# GENETIC ANALYSIS OF COTTON (*Gossypium hirsutum* L.) GENOTYPES FOR DROUGHT TOLERANCE

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BY

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**Approved by:**

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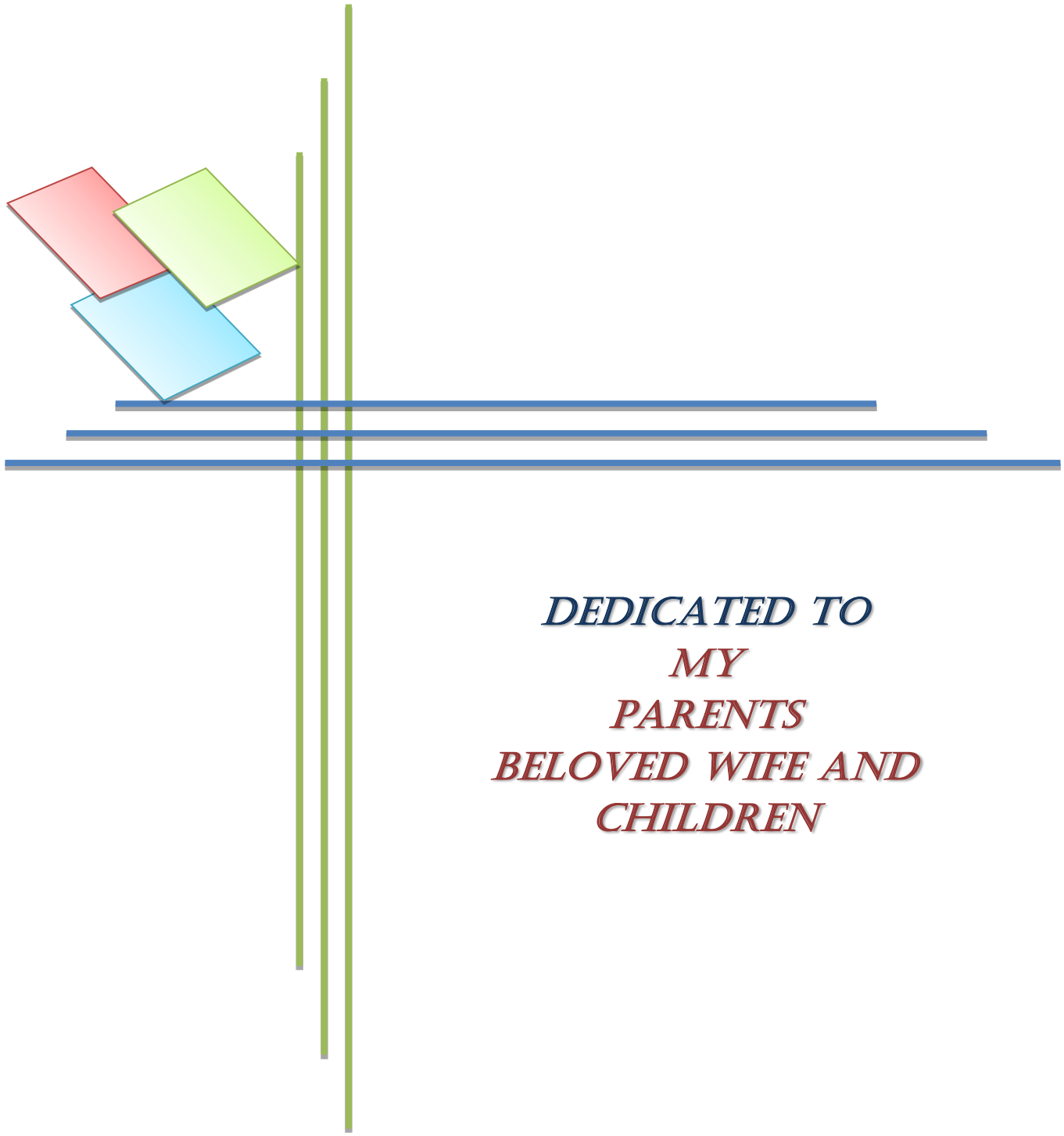
# CERTIFICATE

*This is to certify that thesis entitled "Genetic analysis of cotton (Gossypium hirsutum L.) genotypes against drought stress" submitted to the faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***DOCTOR OF PHILOSOPHY IN GENETICS AND PLANT BREEDING,*** *embodies the result of a piece of bona fide research work carried out by MOHAMMAD ZUBAIR ISLAM TALUKDER, Registration No: 17-08217 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

*I further certify that such help or source of information, as has been availed of during the course of this investigation has been duly been acknowledged by him.*

**Dated: December 2020** **(Prof. Dr. Naheed Zeba)**

**Place: Dhaka, Bangladesh** **Supervisor**



*DEDICATED TO*
*MY*
*PARENTS*
*BELOVED WIFE AND*
*CHILDREN*

## Some commonly used abbreviations

| Full word | Abbreviation | Full word | Abbreviation |
|---|---|---|---|
| Accession | Acc. | Journal | *J.* |
| Agriculture | *Agric.* | Lint Index | LI |
| Agricultural | *Agril.* | Least Significant Difference | LSD |
| Agro-ecological zone | AEZ | Maturity Ratio | MR |
| Analysis of variance | ANOVA | Membrane Stability Index | MSI |
| And others / Co-workers | *et al.* | Micro gram | µg |
| Applied | *Appl.* | Micrometer | µm |
| Archives | *Arch.* | Micronnaire | mic |
| Backcross | BC | mille-mole per liter | mmolL-1 |
| Bangladesh Agricultural Research Council | BARC | milliequivalent per gram | m.equiv.g-1 |
| | | Millilitre | Ml |
| Biology | *Biol.* | Millimeter(s) | mm |
| Botany | *Bot.* | Millimolar | mM |
| Centimeter | cm | Ministry of Agriculture | MoA |
| Coefficient of variation | CV | Muriate of Potash | MOP |
| Completely Randomized Design | CRD | Nitrogen | N |
| | | Number | No. |
| Correlation Coefficient | R | parts per million | ppm |
| Cotton Development Board | CDB | Percentage | % |
| Critical Difference | CD | Phenotypic Coefficient of Variation | PCV |
| Days After Sowing | DAS | | |
| Degrees of Freedom | df | Phenotypic index | Pi |
| Degree Celsius | °C | Phenotypic standard deviation | $\sigma_{ph}$ |
| Deviation from Regression | $S^2d$ | Population mean | $\bar{x}$ |
| Drought Response Index | DRI | Power of hydrogen ions concentration | pH |
| Electrical Conductivity | EC | | |
| Fibre Strength | FS | Principal component analysis | PCA |
| Food and Agriculture Organization | FAO | Principal co-ordinate analysis | PCO |
| | | Randomized Complete Block Design | RCBD |
| For Example | e.g. | | |
| GCA variance | $\sigma^2g$ | Reflectance degree | Rd |
| Genetic advance | GA | Regression co efficient | Bi |
| Genotype by Environment interaction | GXE | Relative Water Content | RWC |
| | | SCA Variance | $\sigma^2s$ |
| Ginning Out Turn | GOT | Seed Index | SI |
| Genetics | *Genet.* | Sher-e-Bangla Agricultural University | SAU |
| Genotypic Coefficient of Variation | GCV | | |
| | | Short Fibre Index | SFI |
| Gram | g | Soil Moisture Content | SMC |
| Hectare | ha | Upper Half Mean Length | UHML |
| Heretability in broad sense | $h^2bs$ | Weight | wt. |
| High Volume Instrument | HVI | Yellowness | +b |

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***The author***

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# GENETIC ANALYSIS OF COTTON (*Gossypium hirsutum* L.) GENOTYPES FOR DROUGHT TOLERANCE

**BY**

**MOHAMMAD ZUBAIR ISLAM TALUKDER**

## ABSTRACT

Drought is a major constraint that adversly affect the cotton yield and its fibre quality. In order to ascertain drought tolerant genotypes of cotton, three experiments based on morphological, physiological, fibre quality, yield and yield components of cotton genotypes under drought condition were conducted at two different locations. The morphological and physiological study was performed at Sher-e-Bangla Agricultural University, Dhaka. The fibre quality and yield experiment was conducted in the farmers' field at Godagari, Rajshahi. The fibre quality tests were executed at Fibre testing laboratory, Dhaka and Cotton Research Farm, Sreepur, Gazipur of Cotton Development Board. The duration of the experiments was from April, 2017 to March, 2020. Fifty cotton genotypes and four different treatments for drought stress were outlined in CRD for morphological and physiologica experiment and RCBD for fibre quality and yield experiment with three replications. Significant genotypic variations were observed for all the characters studied in all three experiments. Among all genotypes CB-12 is the highest ranked genotype for number of reproductive branches at early flowering stage and BC-413 is the highest ranked genotype for root length. Heritability values in broad sense were relatively high for almost all the characters except number of vegetative branches. There is significant positive correlation between the number of reproductive branches and shoot length, shoot root length ratio, root diameter and total biomass of root both at genotypic and phenotypic level. Path analysis also revealed positive direct effect of these four traits on number of reproductive branches indicating these traits would help in further selection progress. According to DRI values, among fifty genotypes, twenty could be included in tolerant group at early flowering stage of cotton. Diversity studies revealed, fifty cotton genotypes were grouped into 8 clusters. The genotypes with high shoot length and no. of reproductive branch was observed in cluster IV. High root diameter and no. of lateral root in drought stress remain together in a cluster VII. Based on relative selection index (RSI) and drought response index (DRI) Ra-16 and BC-442 could be selected as tolerant genotype to drought at early flowering stage. In physiological studies at early flowering stage, among all genotypes CB-14 is the highest ranked genotype for pollen viability followed by water retension capacity and water uptake capacity. SR-16 is the highest ranked genotype for proline content. BC-394 was also higher ranked genotype for proline content as well as for water saturation deficit and relative water content. High heritability coupled with high genetic advanced in percent of mean was recorded for water saturation deficit, water retention capasity, water uptake capacity, membrane stability index and proline content indicating additive gene action controlling these traits and selection based on these traits will be rewarding. Correlation coefficient revealed positive and significant correlation among pollen viability and total chlorophyll as well as nitrogen content. Path analysis also showed positive direct effect of chlorophyll and nitrogen content on pollen viability. Based on RSI and DRI, BC-512, Ra-3, BC-413, CB-14, BC-385 and BC-394 could be selected as drought tolerant genotypes based on physiological study at early flowering stage. Among twenty five selected genotypes from previous two experiments, BC-433 had the highest rank for seed cotton yield per hectare followed by JA-13/R, BC-272, BC-510. The lowest days to first boll bursting rank was found in CB-8 followed by Ra-16 and CB-10. The highest rank for Ginning Out Turn (GOT) was found in BC-272 followed by CB-11 and BC-442. High heritability coupled with high genetic advance at

percent of mean was found for the traits, no. of vegetative and fruiting brunches, no. of bolls per plant, seed cotton yield per hectare indicating additing gene action controlling these traits and selection would be effective. Significant positive correlation with yield was found for the characters plant height, days to first square initiation, days to first boll split, no. of fruiting branch, no. of bolls per plant, single boll weight and seed index. Path analysis revealed positive direct effect of plant height, no. of bolls per plant and single boll weight on yield. Based on RSI and DRI values BC-415 is best ranking genoype for yield followed by BC-433 and BC-442, CB-14, CB-8 and BC-394. Regarding quality traits, genotypes JA-13/R had the longest fibre length, reflectance degree and fibre strength followed by BC-385, BC-433, CB-14, Ra-4, Ra-16 and BC-442. RA-08/9 had the highest micronnaire followed by BC-385 and CB-13. Ra-16 had the highest fibre strength followed by JA-13/R, Ra-3. Uniformity index had significant positive correlation with fibre length both at genotypic and phenotypic level. Path analysis also showed positive direct effect of uniformity index on fibre length. Based on SRI and DRI value, BC-510 is the highest ranking genotype followed by Ra-4, BC-385, BC-433, BC-413 and BC-462. Five genotypes as BC-415, BC-433, BC-442 and CB-14 for highest yield and three genotypes as BC-510, Ra-4, BC-385, BC-433, BC-413 and BC-462 for best quality fibre could be recommended to the farmers' of northern region of Bangladesh. Based on days to first square initiation, days to first flower initiation, days to first boll split and days to first boll bursting, BC-462 required further trial for earliness under drought prone areas.

# CHAPTER I
# INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is the most important textile fibre crop and the world's 2nd important oil seed crop after soybean. Cotton is cultivated in 70 countries of the world with the total coverage of 33.1 m ha, production of 116.6 m bales and a productivity of 76.6 kg lint $ha^{-1}$ (Megha *et al*., 2017). During 2019-20 seasons, cotton was cultivated in 44,430 ha of land and the lint production was 32,375.43 ton that met only 2-3% of our national demand. But among these ten countries China, USA, Russia, India, Brazil, Pakistan, Turkey, Egypt, Mexico and Sudan are accounted for 85-90% of the total production. The economy of Bangladesh is largely dependent on agriculture. However, the Textile sector including Ready–Made Garments (RMG) sector has emerged as the biggest earner of foreign currency. Now Bangladesh is the 2nd largest apparel producer of the world. It also provides employment to around 5 million people, mainly women. Cotton is the basic raw materials of the textile sector. Bangladesh imports 8-8.2 million bales of raw cotton every year. Present government has taken several steps to increase cotton production for the sustainability of the textile sector in the country (CDB, 2020).

Water stress affects the cotton plant by limiting fibre yield and lint quality. Suggested the development of drought tolerant cultivars to get economic yield in drought prone areas. Cotton fibre is the main raw materials of textile industries in Bangladesh as well as cash crop for the farmers. Thus, to save foreign currency for importing cotton fibre. Although cotton is considered to be a drought tolerant crop, its sensitivity varies greatly among genotypes (Naidu *et al*., 1998; Gorham, 1996).

Drought is the most important factor limiting crop productivity around the world. Among the environmental stresses, drought is one of the most adverse factors for plant growth and productivity (Makbul *et al*., 2011) and is a complex physical-chemical process (Moaveni, 2011; Apel and Hirt, 2004). Recently evaluations have shown that approximately 64% of the world's soils are located in desert or in areas with limited water availability and that 57% of the potentially arable area is located in soils for dry-land crops (FAO, 2000). Leaf, stem and root growth rate are very sensitive to water stress because they are dependent on cell expansion (Hearn, 1994).

Cotton is highly responsive to high temperature, cool injury, humidity, flood and drought, which may affect its yield, yield components and fiber properties. Therefore, genetic and environmental variability for seed cotton yield, morphological, physio-chemical and fiber quality traits should be estimated in different environments to conduct suitable breeding program (Gul *et al*., 2016). Seed cotton yield is polygenic trait and thus, it is mostly influenced by soil moisture factors, so the phenotypic response of different genotypes are determined by the genetic and environmental effects upon it, which is the genotype by environment interaction (Ali *et al*., 2005). Such interaction, in the process of widely selected genotypes, constitutes one of the great problems in breeding programs and when recommendation of genotypes for drought condition is to be considered (Gul *et al*., 2014). Genotype × location, genotype × year and genotype × environment interaction components were found to be significant for seed cotton yield in past studies (Campbell *et al*., 2012).

Even though cotton likely is adapted to periodic drought episodes, its optimum production for high lint yield requires between 2,158 and 3,906 $m^3$ of water each growing season, depending on local cultivation practices and meteorological patterns (Mc Williams, 2003). Consequently, the timing, duration and severity of water deficit throughout the life cycle of cotton dictate potential yield losses (Boman and Lemon, 2006).

The average annual rainfall of Bangladesh varies from 1,329 mm in the northwest to 4,338 mm in the northeast region (Shahid *et al*., 2005). The rainfall is very much seasonal, almost 77% of rainfall occurs during monsoon. It is a recurrent phenomenon in different areas of the country, but the northwestern region is mostly drought prone because of high rainfall variability (Shahid & Behrawan, 2008). This region is more prone to droughts as the area is relatively dry, receiving uneven rainfall compared to the rest of the country (Paul, 1998). It is gradually being reported more in Rajshahi, Natore, Chapai Nawabganj, Naogaon, Rangpur, Bogura, Pabna, Dinajpur, and Kushtia regions because of its moisture retention capacity and infiltration rate characteristics. The drought condition in the northwestern part of Bangladesh is close to that of the Barind tract (Rahman *et al*., 2017).

Bangladesh is experiencing more recurring drought than the past. From 1961 to 1991 Bangladesh faced 19 droughts (Climate Change Cell, 2009). Since its independence in

1971, Bangladesh has suffered severe droughts in 1973, 1978, 1979, 1981, 1982, 1992, 1994, 1995, 2000, 2006 and 2009. The ground water level is dropping, when water is most needed at flowering stage of cotton cultivation. The situation is particularly challenging in northwestern region, the driest part of the High Barind Tract. This is not only increasing irrigation costs but also affecting cotton production (Nadiruzzaman *et al*., 2019).

The water resources of Bangladesh, both surface and ground water at barind areas are limiting to meet the demand of water for irrigated areas. This situation demands the government to take necessary action to develop drought tolerant crops. Clearly the major challenge for the agriculture sector during the $21^{th}$ century is to raise crops with low water supply. Bangladesh needs to increase domestic cotton production. The north western barind tract, an unfavorable ecosystem, is a potential area for expansion of cotton areas. Like most of the crops, cotton production is adversely affected by water stress. Insufficient soil water content during the sensitive growth stages such as the blooming, flowering and fruit setting stages can lead to a reduced plant height, fresh and dry weight, number of fruiting branches, boll shedding, developed bolls and seeds, seed cotton yield and yield attributes. Previous studies reported that there is genetic variability for drought response in cotton. Cotton Development Board has 520 cotton genotypes in its gene bank. These genotypes were evaluated for agronomic traits, however, no study were conducted to know the drought tolerance. Therefore, characterization of drought tolerant cotton genotypes is essential for successful expansion of cotton in Barind tract.

Drought stress is a complex phenomenon that affects the morphology and physiology of cotton plant. Most of the drought related breeding program concentrate on selection of those cotton genotypes that seed cotton yield and fiber quality are well under drought stress. This selection is generally based on identifying different morphological and physio-chemical traits that can be utilized for screening to drought tolerance. Many of such attributes including anatomical traits (Shoot, root characters etc.), physiological traits (soil moisture content, chlorophyll content, relative water contents, cell membrane stability etc.) and biochemical traits i.e. accumulation of proline, Glycine betaine etc. traits (Brito *et al*., 2011) measurement are recognized as important components of drought tolerance in cotton (Iqbal *et al*., 2013).

Drought tolerance is a quantitative trait, which means that it is controlled by polygene and has a complex inheritance. Since cotton originates from areas that are often exposed to drought stress, considerable genetic variability in drought tolerance exists (Ahmad *et al*., 2009). Due to large scale genotypic variability for water deficit tolerant characteristics in upland cotton it has become necessary to evaluate more and newly developed genotypes. Present study was initiated to investigate the inheritance of different morphological, physio-chemical and fibre quality characteristics under drought stress. The information generated by this study would be helpful for plant breeder to select high yielding drought tolerant cotton genotypes.

**Objectives:**

The objectives of this study were:

- To study agro-morphological analysis of cotton genotypes under drought stress conditions.
- To study physiochemical analysis of cotton genotypes under drought stress conditions.
- To select drought tolerant cotton genotypes.

# CHAPTER II
# REVIEW OF LITERATURE

Cotton is one of the vital industrial fiber crops and widely known as "white gold", it is most precious gift of nature to the mankind, contributing by the genus "*Gossypium*" to cloth the people all over the world. The genus *Gossypium* was named by Linneaus in the middle of the $18^{th}$ century. It is in a perennial shrub or tree that belongs to the order *Malvales*, family Malvaceae and Tribe Gossypieae (Wendel and Cronn, 2003; Smith, 1995; Fryxell, 1992), 45 of which are diploid (2n=2x=26) and 5 allotetraploid (2n=4x=52), whose geographical distribution spans the tropical subtropical regions of the world (Wakelyn and Chaudhry, 2010). There are four species in the genus *Gossypium hirsutum* L., *Gossypium barbadense* L., *Gossypium arboreum* L. and *Gossypium herbaceum* L. that were domesticated independently as sources of textile fiber. *Gossypium arboreum* and *G. herbaceum* are diploids with A genome and *G. hirsutum* and *G. barbadense* are allotetraploid species with AD genome. *G. hirsutum* represents over 95% of the cultivated cotton worldwide (Plate-1). Globally, the *Gossypium* genus comprises about 50 species (Wendel *et al*., 2009). Also, the old world (Africa and Asia) cottons are represented by the A, B, E and F genomes, the C, G and K genomes are restricted to Australia, while the D and the tetraploid AD-genome originated from the new world (Wakelyn and Chaudhry, 2010).

The origin of the genus *Gossypium* is dated to around 5–10 million years ago (Wendel and Grover, 2015). *Gossypium* species are distributed in arid to semiarid regions of the tropics and subtropics. Generally shrubs or shrub-like plants, the species of this genus are extraordinarily diverse in morphology and adaptation, ranging from fire-adapted, herbaceous perennials in Australia to trees in Mexico (Wendel *et al*., 2009).

The most ancient archaeological artifacts proving the use of cotton fiber date from the Neolithic period (approx. 6000 BC) and were found at Mehrgarh, Pakistan (Moulherat *et al*., 2002). In according to Wakelyn and Chaudhry (2010), archaeological artifacts that prove the use of cotton fibers for textile weaving were found in the Tehaucan Valley in Mexico (*Gossypium hirsutum*, 3500 BC), at Mohenjo-Daro, in the Indus Valley, Pakistan (*G. herbaceum*, 2700 BC), at Huaca Prieta, Peru (*G. barbadense*, 2500 BC).

| | |
|---|---|
|  |  |
| *Gossypium hirsutum* (2n=4x=52) | *Gossypium barbadense* (2n=4x=52) |
|  |  |
| *Gossypium arboreum* (2n=2x=26) | *Gossypium herbaceum* (2n=2x=26) |

**Plate 1. Four cultivated cotton species**

The center of domestication of *G. hirsutum* probably lies in the Yucatan Peninsula of Mexico (Brubaker and Wendel, 1994). Another Hutchinson (1951) said that the wild perennial race 'yacatanense' possibly represents the primitive form. Race 'punctatum' probably represents the first form of domesticated *G. hirsutum*. Wakelyn and Chaudhry (2010) also stated that the perennial races 'morilli', 'richmondi' and 'palmeri' are photoperiodic forms that are found as sub spontaneous populations in different parts of Mexico. Race 'latifolium', found in Mexico and in Guatemala, is at the origin of the day-neutral types that gave rise to the modern "Upland cotton" cultivars. In addition to day-neutrality, domestication was probably aimed at obtaining shorter and more compact plants that matured earlier with seed showing reduced dormancy, leading to the selection of an "annual" type of cotton.

## 2.1 Climatic and Soil Requirement

Cotton requires a daily minimum temperature of 16°C for germination and 21°C to 27°C for proper crop growth. During the fruiting phase, the day temperature ranging from 27°C to 32°C and cool nights are needed. The sowing season of cotton varies considerably from tract to tract and is generally early July-August in Bangladesh where it is mostly cultivated largely under rainfed or dry land conditions. An annual rainfall of at least 50 centimeters distributed throughout the growing season is required for good yield. The cotton-picking period from mid-November to February must have bright sunny days to ensure a good quality (CDB, 2021). Cotton is successfully grown on all soils except sandy, saline or water-logged types. It is grown in well drained deep alluvial soils, moderately tolerant to salinity and is sensitive to water logging as well as frost and chilling temperature in winter (Singh *et al*., 2015).

## 2.2 Stress

Stress is regarded as a change in any abiotic or biotic factor that has an impact on the lint by affecting its morphological, physiological, biochemical and molecular response to such changes, and damage cell. The term stress is most frequently used different meanings and subjectively, the physiological definition and appropriate term as responses in different circumstances. Stress being a constraint or highly impulsive fluctuations imposed on regular metabolic patterns cause injury, damage, disease or physiological disorders (Jaleel *et al*., 2009). Plants are interpretation to drought, oxidative stress; salinity, heat and temperature stress as well as herbivore restraint that limits the rate of decreases plant's ability to convert energy to bio-mass and reduces photosynthesis and yield (Grime, 1977). Stress is a condition to detrimental influence on the plant, in most cases; stress is a measured in relation to plant resistance, crop yield, growth or the primary absorption processes which are related to overall growth and development.

Generally, plants do not grow up in most advantageous conditions during their every phase of life, but endure many unfavorable conditions that cause different types of stresses, and prevent them from getting growth, development, yield and quality. Additionally, the physiological most advantageous for any one variety varies from what is recognized as the biological optimal, as a result in each exacting case, the plant has to acclimatize to the favorable situations established in its habitation. In

general, the stressful conditions cause a sequence of physiological and biochemical and molecular changes in the plant and improvement of crops for better stress resistance to require the knowledge of physiological mechanisms and genetic control of the causative traits at different plant developmental stages.

### 2.3 Abiotic stress as drought

Drought is a natural cruel environment and meteorological term is generally defined as below standard precipitation in a given region; resulting in a deficit of water supply, whether atmospheric, surface water or ground water. In general, the unavailable water in the soil and atmospheric conditions cause uninterrupted loss of water by higher evapotranspiration. Therefore, a continuous shortage in rainfall (meteorological drought) coupled with higher transpiration or evaporation demand leads to agricultural drought (Mishra and Cherkauer, 2010). It is the lack of plenty of moisture required for normal plant growth and development to complete their life cycle (Manivannan *et al*., 2008). Drought severely affects plant growth with considerable reductions in crop growth rate main consequences of drought in crop plants are reduced rate of cell division and expansion, leaf size, stem elongation and root propagation and disturbed stomatal aperture, plant water and nutrient relations with diminished crop productivity (Farooq *et al*., 2009; Li *et al*., 2009). Drought is a global problem, reduce quality and crop productivity and recent global climate change (green house effect) has made this condition very serious (Apel and Hirt, 2004). The world map of drought hazard calculated for the events taking place in the period between January 1901 and December 2010. Overall, it is perceptible a match between the geographic allocation of global drought hazard, as computed with the WASP index, and the wide range of world dry regions, as represented by the worldwide map of waterlessness calculated by (Spinoni *et al*., 2015) (Figure 3). Authors present the map of global drought exposure computed at the sub-national level with the non-compensatory DEA model. They were reported that predict that unreceptive regions like deserts, tundras, and tropical forests are the least exposed to drought globally (Figure 1). Over the globe, drought exposure is higher for Eastern U.S., Southern Europe, India, East China and Nigeria. In (Figure 2) the global drought vulnerability map consequent from a mathematics compound model merge (a) social, (b) economic and (c) infrastructural factors computed with a non compensatory aggregation diagram of vulnerability sign (Carrao *et al*., 2016). Overall, results indicate that Northwest of South America,

Central and South Asia, Central America, and almost all Africa-with the exception of South Africa, are the most vulnerable regions to drought. World wide drought hazardation distribution is illustrated in Figure 3.

### 2.4 Water stress

Water stress occurs when the demand for water exceeds the available amount during a certain period or when poor quality restricts its use. Water stress causes deterioration of fresh water resources in terms of quantity (aqifer over-exploitation, dryness etc.) and quality (eutrophication, organic matter pollution, saline intrusion, etc.). Plants experience water stress either when the water supply to their roots becomes limiting, or when the transpiration rate becomes intense. Water stress is primarily caused by a water deficit, such as a drought which is discussed below.

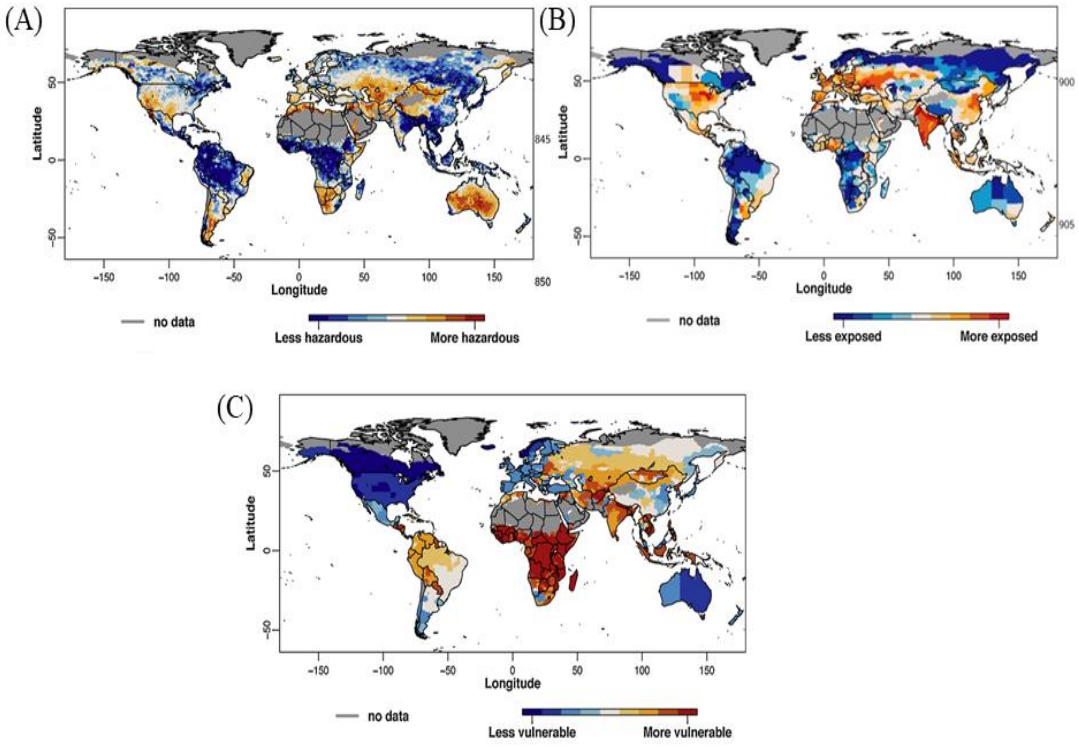



**Figure 1. Global map of drought hazard, expose, and vulnerability (Carrao *et al.*, 2016)**

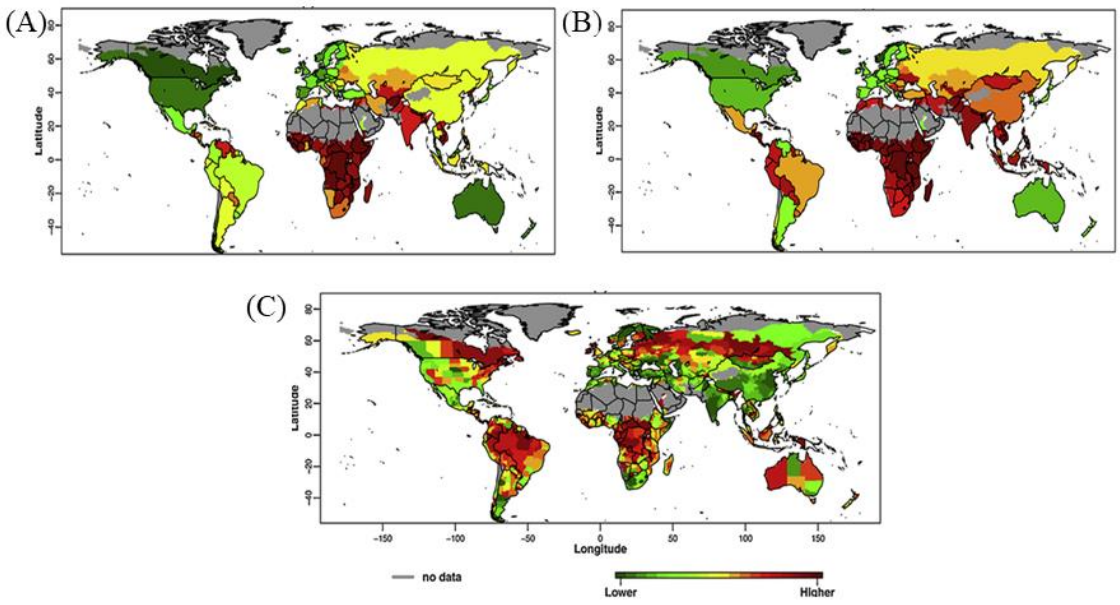



**Figure 2. Global maps of drought vulnerability factors computed with the DEA approach.** (A) social; (B) economic; (C) infrastructural (Carrao *et al.*, 2016)

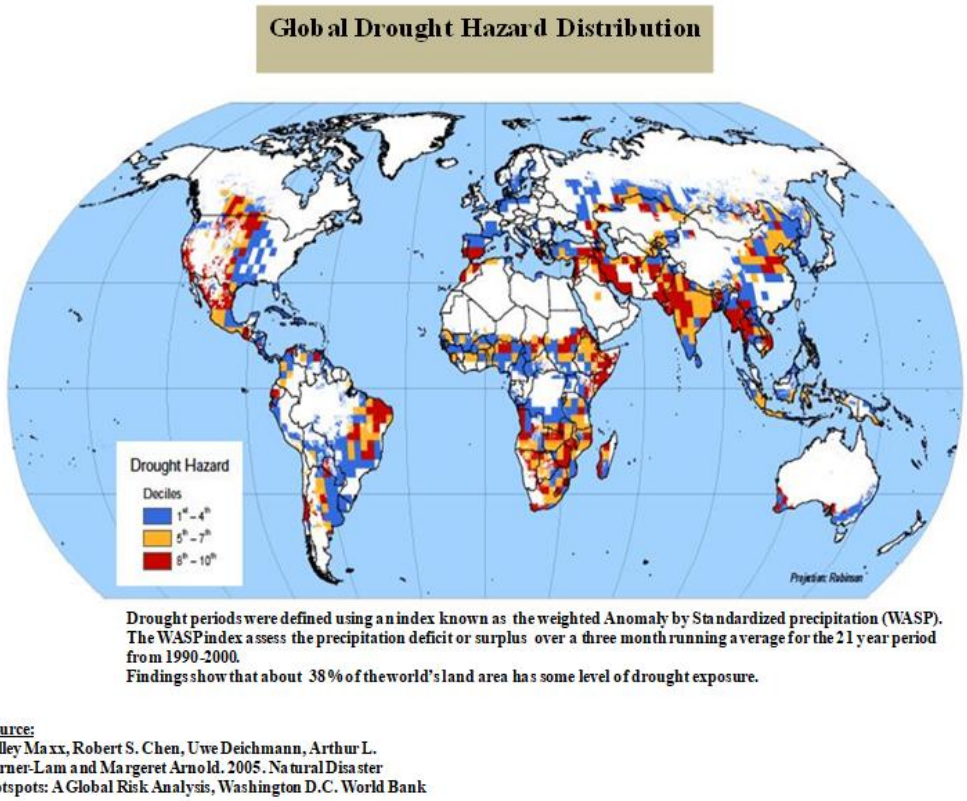



**Figure 3. Worldwide drought hazard distribution**

## 2.5 Drought

A drought is a period of below-average precipitation in a given region; resulting in prolonged shortages in its water supply, whether atmospheric, surface water or ground water. In nature, water is usually the most limiting factor for plant growth. If plants do not receive adequate rainfall or irrigation, the resulting drought stress can reduce growth more than all other environmental stresses combined. It induces various physiological and biochemical adaptations in plants. It has been estimated that up to 45% of the world agricultural lands are subjected to drought (Bot *et al*., 2000). Water deficit leads to the agitation of most of the physiological and biochemical processes and consequently reduces plant growth and yield (Boutraa, 2010). Water deficit reduces the rate of photosynthesis in plants (Cornic, 2000). A plant responds to a lack of water by halting growth and reducing photosynthesis and other plant processes in order to reduce water use. As water loss progresses, leaves of some species may appear to change color usually to blue-green. Foliage begins to wilt and, if the plant is not irrigated, leaves will fall off and the plant will eventually die. Aside from the moisture content of the soil, environmental conditions of high light intensity, high temperature, low relative humidity and high wind speed will significantly increase plant water loss. The prior environment of a plant also can influence the development of drought stress. A plant that has been drought stressed previously and has recovered may become more drought resistant. Also, a plant that was well-watered prior to drought will usually survive drought better than a continuously drought-stressed plant. Drought is by far the most important environmental stress in agriculture and many efforts have been made to improve crop productivity under water-limiting condition. More than 80 years of breeding activities have led to some yield increase in drought for many crop plants. Fundamental research has provided significant gains in the understanding of the physiological and molecular responses of plant to water deficit. Minimizing the 'yield gap' and increasing yield stability under different stress are of strategic importance in guaranteeing food for the future (Anonymous, 2016).

Drought occurs every year in many parts of the world, often with devastating effects on different developmental stages of plant crop production (Ludlow and Muchow, 1990). Worldwide losses in crop yields from drought stress probably exceed the losses from all other abiotic stresses combined (Barnabas *et al.,* 2008). Because water resources for irrigating crops are declining worldwide, the development of more

drought-resistant or drought-tolerant cultivars and greater water-use efficient crops is a global concern (Ludlow and Muchow, 1990). In the last several decades, the most productive agricultural regions were exposed to drought stress in most years and in occasional years with severe drought. Commonly, drought stress synchronizes with extreme temperature, leading to even greater severity of drought stress (Barnabas *et. al.* 2008). The effect of drought on yield is highly complex and involves processes as diverse as reproductive organs, gametogenesis, fertilization, embryogenesis, and seed development stages (Barnabas *et al.,* 2008). Reproductive development at the time of flowering is especially sensitive to drought stress (Samarah *et al*., 2009a; Zinselmeier *et al.,* 1999, 1995). Therefore, an understanding of how a reproductive process affected by drought is of particular interest for improving drought tolerance (Samarah *et al.,* 2009b). The flowering period of a crop is a critical growth stage and a yield determinate factor in normal growing seasons and in drought stressed regions in particular. An understanding of how crop plants respond to drought stress during reproductive stage is important in maximizing yields in water-limited regions.

Drought stress is a main abiotic stress that limits crop pollination by reducing pollen grain availability (Trueman and Wallace, 1999; Agren, 1996), increasing pollen grain sterility (Al-Ghzawi *et al*., 2009; Schoper, 1986), decreasing pollen grain germination and pollen tube growth (Lee, 1988). Drought stress can also reduce megagametophyte fertility (Young *et al.,* 2004), inhibit the differentiation of young microspores (Satake, 1991), lower the number of dehisced anthers (Sawada, 1987), repress anther development (Nishiyama, 1984), and decrease seed set and seed development (Al-Ghzawi *et al*., 2009).

Flowering is one of the most important growth stage affected by drought stress. Drought stress interferes with flower period, flower opening, nectar production, and turgor maintenance of floral organs (Mohan-Ram and Rao, 1984). Drought stress imposed on plants leads to decrease yield through reducing seed set (Al-Ghzawi *et al.,* 2009; Westgate and Boyer, 1986). Low seed set percentages are regularly related to several factors such as reducing pollen grain availability (Trueman and Wallace, 1999; Agren, 1996), increase ovary abortion (Boyer and Westgate, 2004), increase pollen grain sterility (Al-Ghzawi *et al*., 2009; Schoper, 1986; Westgate and Boyer, 1986), slow stigma and style elongation (Westgate and Boyer, 1985b), reducing time of

pollination (Westgate and Boyer, 1986), lower pollen grain germination activity, pollen tube growth, and less development of fertilized seeds (Lee, 1988).

Drought stress affects seed production; many researchers found that drought stress during reproductive growth lowered seed germination and vigor also. Seed quality, estimated by standard germination, was lower for seeds harvested from plants grown under drought than seeds harvested from irrigated plants (Smiciklas *et al.*, 1992).

### 2.6 Perceptions and consequences of drought stress on plants

Drought can be defined as a condition in which plant turgidity and water potential are reduced enough to line with regular functions. Desiccation is considered to be a reasonable loss of water, which leads to restraint of gas exchange and stomatal closure. Drought is a much more widespread loss of water that can potentially lead to gross disturbance of cell structure and metabolism as well as finally to the termination of enzyme catalytic reactions. Generally, drought signs include loss of leaf turgor, reduction of total water potential, water content, drooping, wilting, etiolation, yellowing, and premature leaf downfall, stomatal closure and decrease in cell extension, growth and development of plants (Akhtar and Nazir, 2013; Bhargava and Sawant, 2013; Bernacchia and Furini, 2004) (Figure 4). Additionally, some remarkable symptoms include branch dieback, thinning tree, and bark and twig break, necrosis, furthermore, disruption of metabolism, arrest of photosynthesis, and finally plant death occurs ( Arbona *et al*., 2013; Sapeta *et al*., 2013; Farooq *et al*., 2009; Shao *et al*., 2008). Under drought stress, cell elongation in higher plants is introverted by reduced turgor pressure, water uptake results in a decrease in cell water contents. As a result, turgid is lost. Likewise, drought stress also trim down the photosynthetic rate embarrassment and metabolites required for cell division and ROS production. As a consequence, impaired cell division (mitosis), cell elongation and expansion result in declined growth and development of plants.

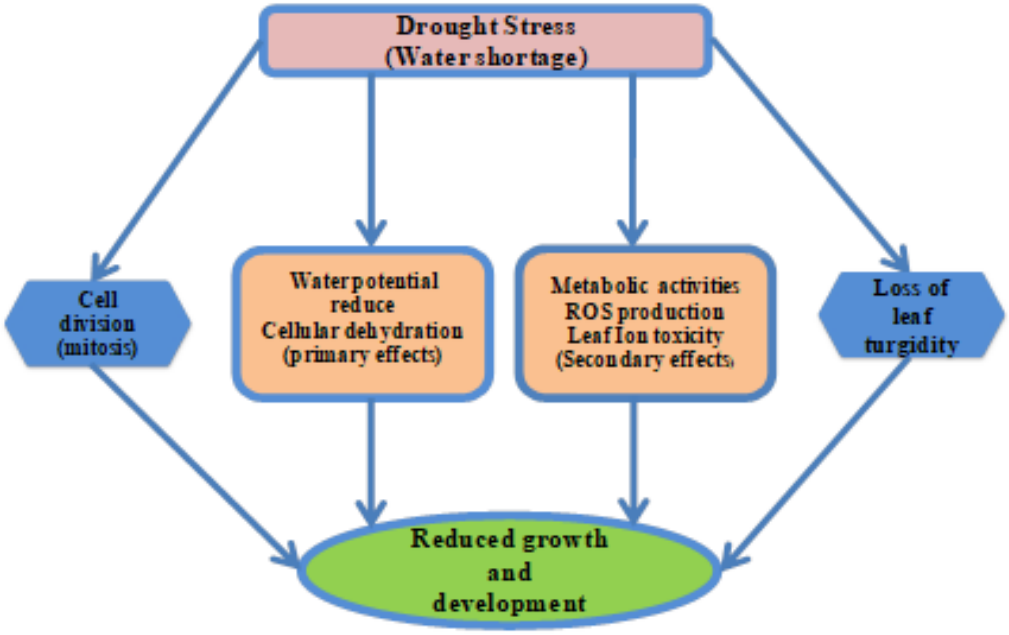



**Figure 4. Potential mechanisms of decreased growth and development under drought stress (Akhtar and Nazir, 2013)**

### 2.7 Economic importance of cotton

Cotton (*Gossypium spp*.) is one of the most important cash crops in the world. Cotton crop not only provides lint for the textile industry, but also plays a role in the fish or cattle feed and edible oil industries with its seed, rich in oil (16 – 20%) and protein (20 – 40%). About 82 thousand people are engaged in cotton production either on farmers' field or in seed cotton or fiber transportation, ginning, baling, storage and marketing. Bangladesh is second raw cotton consumers of the world. Australia and Egypt produce the best quality cotton in the world. Cotton is a major export revenue source for Burkina Faso, Benin, Uzbekistan, Mali, Tajikistan, Ivory Coast, Kazakhstan, Egypt and Syria. Cotton is currently the leading fiber crop worldwide and is grown commercially in the temperate, sub-tropical and tropical regions of more than 50 countries (Australian Government, 2021). The major countries/regions of cotton production include USA, India, China, Pakistan, the Middle East and Australia (Figure 5).

Cotton is a primarily grown as fibre crop or cash crop. It is harvest as "seed cotton" which is then "ginned" to separate the seed and lint. Man has utilized cotton fiber for his benefits since ancient times (Fryxell, 1992). The long fibers have further processed by spinning mills to produce yarn that is knitting or woven into fabrics. The ginned

seed is covered in short, fuzzy fibers, known as “linters”. The cottonseeds could remove before the seed sowing in the fields or crushed for oil, and used in a variety of products including foods. The linters are produce as first or second-cut linters.

The first-cut linters have a longer staple length and used in the production of mattresses, furniture upholstery and wash. The second-cut linters have a much shorter staple length and are a major source of cellulose for both chemical and food uses. They used as cellulose-based products such as high fiber dietary products as well as a viscosity enhancer in ice cream, salad dressings and toothpaste. The second-cut linters used with other compounds to produce cellulose acetate, nitrocellulose and a wide range of other compounds in the chemical industry (Wakelyn and Chaudhry, 2010).

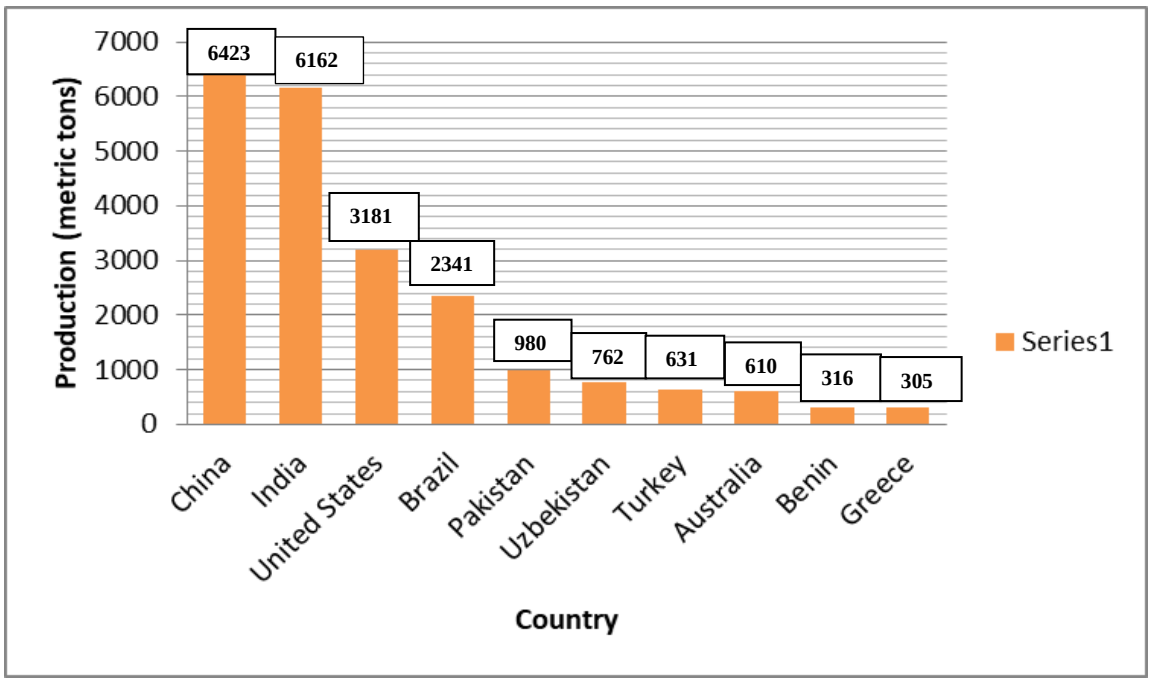



**Figure 5. Cotton productions by country worldwide in 2020-21 (in 1,000 metric tons)**

It is uses in a variety of products including edible vegetable oils and margarine, soap and plastics and paper pulp. Cotton seed derived from it, are also used in edible oil, fish feed products and for animal feed, but this is limited by the presence of natural toxicants (gossypol and cyclopropenoid fatty acids) in the seeds (Australian Government, 2021).

Cotton is one of the vital cash crops and the main raw materials use of textile industry in Bangladesh. It is commonly known as ‘Kapas tula’ in Bangladesh. It is primarily cultivated for its lint, which is spun into yarn. Yarn used for Ready-made Garments industry and others textile industrial uses. Raw cotton is also uses for medical and

surgical purposes. Total cotton cultivated area and productions of cotton in Bangladesh (Table 1).

**Table 1. Area and production of cotton of Bangladesh from 2011-2021**

| Year* | Area Harvested (Hectare) | Production (Lint) | |
|---|---|---|---|
| | | Bales** | Tons |
| 2011/12 | 36,000 | 103,000 | 18,727 |
| 2012/13 | 39,000 | 129,000 | 23,455 |
| 2013/14 | 42,000 | 144,000 | 26,182 |
| 2014/15 | 42,700 | 152,534 | 27,675 |
| 2015/16 | 42,800 | 153,280 | 27,869 |
| 2016/17 | 42850 | 156509 | 28,456 |
| 2017/18 | 43050 | 165269 | 30,049 |
| 2018/19 | 44185 | 171470 | 31,176 |
| 2019/20 | 44430 | 177887 | 32,343 |
| 2020/21 | 44300 | 176286 | 32,052 |

Source: Cotton Development Board (CDB), Government of Bangladesh

*Fiscal Year (July-June)

** 1 bale= 400 lb

### 2.8 Effect of water stress on cotton

Although cotton plant showed an indeterminate growth habit, excessive vegetative growth is restricted by carbohydrate demands placed on the plant primarily by developing bolls. The plant establishes a balance between carbohydrate accumulations according to its demand. Water stress at any stage of growth period will hamper the production and distribution of carbohydrates throughout the plant. The water stress on cotton plant have different impact depending on the development stage of plant, the pressure of stress and the length of time the stress is imposed. Stress during periods of high water demand especially in reproductive stage, have larger impact on reductions in yield. Although, water stress at any stage of the crops growth will reduce significant yield, cotton production loss became double during the stress in peak flowering compared to early or late seasonal stress (Gibb, 1990). Furthermore, the longer duration of drought stress gradually decrease the crop production (Alghabari and Ihsan, 2018).

During the vegetative stage if drought stress occurs, the leaves become smaller at maturity, and less light was intercepted. Boll production is also intrinsically linked to vegetative area ( Garlobo *et al*., 2015; Jackson and Gerik, 2010). Yield is also affected by the timing and drought severity, indicated that water stress reduced the number of fruiting branch as well as the crop growth through the reductions of photosynthesis. Water availability was the most critical part for cotton on the plants from the first square stage until the first flower because early fruit setting were capable of maturing under a short growing period ( Marani and Amirav, 1971; Boyer, 1970).

Kader *et al*. (2015) observed that correlation between yield and morphological traits such as root length, shoot length, root/shoot ratio and physiological traits such as relative water content (RWC), membrane stability index (MSI%), Chlorophyll a, chlorophyll b, total chlorophyll, chlorophyll a/b ratio were significantly affected by drought stress condition.

Plant water deficits depend both on the supply of water to the soil and the evaporative demand of the atmosphere. In general, plant water stress is defined as the condition where a plant's water potential and turgor are decreased such that normal functioning of the plant is inhibited (Loka *et al*., 2011). Plant water deficit can be measured either by relative water content or leaf water potential and the deficit depends on the severity as well as the duration of the stress. Additionally, the genotype of the plant and the growth stage when the stress is imposed, determines the extent of the stress (Kramer, 1983).

Water availability and retention capacity affect the growth and physiological processes of all plants, since water is the major component of actively growing plants, ranging from 70-90% of plant fresh mass (Loka *et al*., 2011). Due to its predominant role in plant nutrient transport, biochemical and physiological reactions, cell expansion and transpiration, water stresses result in anatomical and morphological alterations as well as changes in enzymatic and chemical processes and functions of the plants (Kramer, 1980; Hsiao, 1973).

## 2.9 Effects of drought stress on plant morphological parameters

Cotton is a vital fiber and oilseed crop badly affected by drought stress. Screening of cotton germplasm has prerequisite to identify the cotton genotypes as a drought tolerant. The different morphological parameters (root length, shoot length, root fresh weight, shoot fresh weight, root dry weight, shoot dry weight and lateral root numbers) was assessed for screening suitable genotypes of drought prone areas. The leaf chlorophyll contents have also evaluated. The water stress adversely reduced the values of the above stated parameters excluding root length of some genotypes (Ahmad *et al*., 2020)**.**

Water stress have been considered one of the most important factors adversely affecting plant development and yield performance around the world (Boyer, 1982). Numerous studies have been conducted in the past to determine the effects of water stress on the morphology and development of cotton plants. Water-deficit stress results in stunted growth because of reduced cell growth and leaf expansion, reduced stem elongation (Gerik *et al*., 1996; Ball *et al*., 1994; Turner *et al*., 1986; McMichael and Hesketh, 1982; Jordan *et al*., 1970). Shoot and root growth rate are considered to be very sensitive to water stress since they are dependent on cell expansion (Hsiao, 1976; Hearn, 1994). Krieg and Sung (1986) reported that water stress caused a reduction to the whole plant by decreases in the branch and leaf numbers rather than the leaf size. The authors attributed this decrease to reduced initiation of new leaves instead of leaf abscission due to senescence. Significantly Pace *et al.* (1999) reported fewer nodes and plant biomass dry weights of water-stressed plants compared to those of the control. McMichael and Quisenberry (1991) observed that plants grown under severe water stress conditions decreased shoot/root ratio and Malik *et al.* (1979) reported that root growth shows to be less affected by drought than shoot growth. Several researchers (Pace *et al*., 1999; Ball *et al*., 1994; McMichael and Quisenberry, 1991; Creelman *et al*., 1990) observed that seedlings of water-stressed cotton showed increased root elongation with a reduction of root diameter.

A correlation between leaf abscission and low plant water potentials has been reported by many researchers (Bruce *et al*., 1965; Addicott and Lynch, 1955). McMichael *et al*. (1972) assessed a linear relationship between the rates of leaf abscission and the levels of the imposed water-deficit stress, reporting however, that

leaf abscission occurred after the water stress was relieved and at the period of stress occurs. This is in accordance with Addicott and Lynch (1955), who speculated that formation of the separation layers is dependent on the plant's turgor. In addition, McMichael *et al*. (1973) observed that younger leaves were not as prone to abscission as older ones. Hafeez *et al*. (2015) reported that plant height, root length, fresh and dry biomass and total leaf area were decreased under drought stress condition. Mvula *et al*. (2018) revealed significant impact to minimize the adverse effects of drought on cotton tap root length, lateral root number, fresh root weight, dry root weight, fresh shoot weight, dry shoot weight, shoot length and root biomass. s. Mvula *et al*. (2018) also reported that the association between growth parameters and total biomass had positive correlation coefficients implying that selection for taproot length, lateral root number, shoot fresh weight, shoot dry weight, root fresh weight, root dry weight, shoot length, root volume, stem diameter and number of leaves might improve total biomass under water stressed conditions. Correlation analysis further suggested that simultaneous improvement could be possible for shoot fresh weight, shoot dry weight and shoot length due to positive and highly significant correlation between these traits. These traits showed significant correlation and strongest association with total biomass, revealing their importance for selecting genotypes with drought tolerance and higher biomass. The mentioned traits are easy and more practical to use for indirect selection. Paytas (2009) reported that any reduction in biomass production in cotton decreases final yield. Taproot length and lateral root number correlated significantly and positively with total biomass in this study. Kohel and Lewis (1984) noted that the correlations of taproot length and vigorous laterals with dry matter production suggested that root vigor may allow superior strains to be better competitors for limited soil water. In the current study, most of the parameters were significantly and positively correlated with each other, thereby providing a chance for selection of desirable genotypes with desirable traits.

Irum *et al.* (2011) reported that genetic variability in plant material is necessary for the development of an effective plant breeding program and selection because it is pre-requisite to find out nature and extent of association among various yield and seedling traits. Phenotypic co-efficient of variability (PCV) were higher than genotypic co-efficient of variability (GCV) for all the parameters under investigation except yield. This indicated that these traits were influenced by the environment, although yield was

relatively less influenced by environment in this investigation. Heritability provides information on the relative practicability of selection. Heritability is a measure of the phenotypic variance attributable to genetic causes (Songsri *et al*., 2008). It estimates genetic advance for selection under certain environment. When heritability estimates are higher, selection procedures are simpler (Khan *et al*., 2008). The high heritability does not necessarily, means that the character would show high genetic gain but such associations accrued, the additive gene effects were most important (Sardana *et al*., 2007). High h2 coupled with high genetic advances for yield of seed cotton ha-1, root length and shoot weighty indicated the presence of more additive genetic variance for these traits under this study. Similar results were also found by Soomro *et al*. (2010) who stated that seed cotton yield showed 81.14% broad sense heritability coupled with high genetic advance 60.18%. Moderate heritability with moderate genetic advance for shoot length / root length indicates the presence of non-additive genetic component, which is dominance and epitasis for the controlling of this parameter. Similar results were reported by Idahosa *et al*. (2010) who found moderate heritability estimate for 100-seed weight under combined locations. Dewey and Lu (1959) suggested that genetic causes were more important to effect genotypic association and also the masking effect of environment on association of these traits. An early application of correlation coefficients and path analysis in plant breeding in the study of crested wheat grass. This technique was used in segregating cotton plant material so that the strategy with respect to selection of desirable plant may be made. The genetic correlations were further portioned to their direct and indirect effects to know the importance of different traits for yield. The highest direct effect on yield of seed cotton was exhibited by root weight followed by root length. Root shoot weight ratio had highest indirect effect on yield of seed cotton through root length followed by root shoot length ratio through root length.

### 2.9.1 Shoot length

Shoot length is an important parameter for determining the morphological features relating to plant type and canopy development in cotton. It is also one of the important characters of growth and development of cotton and sensitively influenced by both genetic and environmental factors. (Petterson and Highsmith, 1989) subjected cotton plants to soil moisture stress by withholding water. They reported that water stress

reduced the plant height, branch number, total dry weight, root length in comparison with water stressed and control.

Zhou and Oosterhuis (2012) reported that drought tolerance of eight cotton cultivars using various growth and morphological traits. They also reported that drought intensities caused a significant effect on shoot length and water stress tolerance varied in different genotypes, also identified that early period of drought had drastic effects on shoot length. Pace *et al*. (1999) reported that shoot length, number of branch and the biomass of shoots were less in the drought-treated plants than in the control. Veesar *et al*. (2020) observed that drought stress significantly affected shoot length, root length, number of lateral roots. Several other investigations have reported that drought stress imposed during the vegetative growth phase may be responsible for reduction in the shoot length, root length and plant biomass in many plant species.

Irum *et al.* (2011) reported that the values of phenotypic co-efficient of variability (PCV) were higher than genotypic co-efficient of variability (GCV) for all the parameters under investigation except yield. The heritability estimates were significant at 5% probability level for all traits except seedling shoot length. The highest h2 (0.987) was observed in seed cotton yield and followed by root length (0.592). Moreover, seed cotton yield ha-1, root length, root weight, shoot weight and shoot root length ratio recorded high genetic advance. They also revealed that genotypic correlation coefficients were generally higher in magnitude than their corresponding phenotypic correlation coefficients. The shoot length had negative statistically non-significant genotypic relationship with root length at seedling stage, whereas the phenotypic relationship between these two traits was positive. Shoot length had positive statistically significant genotypic and phenotypic correlations with shoot root length ratio. Correlation between shoot length and shoot weight, as well as root weight at genotypic and phenotypic level was positive and statistically significant. The both correlations between shoot length and S/R weight ratio were positive and statistically non-significant. Shoot length was significantly and positively correlated with yield. The association between root length and shoot root ratio by length was negative and statistically significant.

Veesar *et al*. (2020) results indicated that when shoot length increases; it correspondingly increases the plant roots, smaller lateral roots, leaf area, RWC and

stomatal count per unit area. Root length showed significant positive associations with number of lateral roots, leaf area and relative water content, while significantly negative association of root length was observed with stomatal conductance and number of lateral roots. The negative correlations of root length with stomatal conductance and lateral roots revealed that as the length of roots increase, it causes more evapo-transpiration.

### 2.9.2 Root length

The cotton genotypes evaluated under water stress responded differentially to drought stress. Veesar *et al*. (2020) reported that water stress reduced the root length of varieties CIM-499, CRIS-342, NIAB-78, Chandi, BH-160 and Bt-cotton by -4.75, -4.63, -2.75, -2.50, -1.00, and -0.75 cm, respectively, yet cultivars CRIS342 and CIM-499 were found more susceptible to drought stress because these cultivars recorded higher reductions in root length attributable to moisture stress. Contrary to above findings, the root length of varieties like CIM-534, CRIS-134, CIM-506, Sindh-1, CIM496 and Sadori were increased rather declined by 4.75, 4.50, 3.75, 3.38, 3.25 and 3.00 respectively under water stress indicating their drought tolerance. In consonance with our findings, observed that moderate water stress at seedling stage caused increase in root length while moisture stress at reproductive stage or longer period have condensed the root development.

Decrease in shoot and root length under drought stress might be due to suppression of cell expansion and cell growth, or due to low turgor pressure (Jaleel *et al*., 2008; Liu *et al*., 2004; Yang and Hsiang, 1992). Boyer (1982) showed that total biomass of root and root length account for major share of the differences in drought tolerance and it may be genetic difference in the ability of roots to penetrate deep soil layers. A combination of plant physiology and root morphology with water stress tolerance should affect drought resistance in cotton. Deeper roots allow for the greater extraction of water (Ludlow and Muchow, 1990). Several researchers reported shoot and root growth of cotton genotypes after a brief drought and subsequent recovery period. They also observed that the plant height, number of branches and the dry weights of the shoots were less in the drought-treated plants than in the controls (Pace *et al*., 1999). They also reported that root growth was not decreased in the drought-treated plants, compared with the controls, when the shoot: root ratio was less in the drought treated plants than the controls. They concluded that when cotton is in a

drought stress situation, its taproot would be longer and thinner than that of well water saturated cotton.

Ranjan *et al*. (2012) studied the drought tolerant genotypes showed a longer root length than did by drought sensitive. Several researchers evaluated the water deficit effects, in initial phenological stages of cotton plants from seeds on shoot and root growth. They observed that the tap root was longer in the drought-treated plants than in the controls and this response may allow cotton plants to survive drought (Ferreira *et al*., 2014). McMichael and Quisenberry (1991) they evaluated genetic variability in twenty-five cottons (*Gossypium* spp.) for root and shoot traits grown under conditions of soil moisture deficit and various atmospheric evaporative demands. They observed root-shoot ratios increased in plants grown in the more stressful conditions resulting from a significant increase in root dry weights with little change in shoot dry weights. Ball *et al*. (2010) they were observed changes in root length for net house grown cotton (*Gossypium hirsutum* L.) during drought. About 85% of visible roots showed elongation growth under conditions of adequate soil moisture and followed by a reduction in root diameter. The larger rooting population of produced longer root length than the smaller rooting population under water deficit condition (Basal *et al*., 2003).

Irum *et al.* (2011) reported that root length was positively and significantly correlated with shoot weight and seed cotton yield at genotypic and phenotypic levels. Shoot / root ratio by length was negatively significantly correlated with shoot weight at genotypic and phenotypic levels. They also revealed that Shoot length positively and indirectly affected the yield of seed cotton through seedling root length, seedling shoot root ratio by length, root weight and seedling shoot weight. Seedling root length had positive direct effect on yield and genotypic correlation between these two parameters was also positive. Seedling root length influenced yield indirectly and negatively by seedling shoot length and seedling shoot root ratio by length.

### 2.9.3 Root diameter

Pace *et al*. (1999) they examined shoot and root growth of different season cotton cultivar after a different period of drought and subsequent recovery period. They observed that drought stressed cotton plants had thinner root system than that of control.

### 2.9.4 Biomass of root

Zhou and Oosterhuis (2012) investigated effects of nitrogen on tolerance to water-stress in cotton (*Gossypium hirsutum* L.) seedlings. They showed that fresh root biomass highest in the low-nitrogen rate and decreased by water stress. Jamal (2015) studied that the effect of drought stress on root traits in *Gossypium arboretum.* Plants were grown in plastic bags with different drought conditions (5% and 15% drought) and control condition. They reported that fresh root biomass in cotton line FDH-786 reduced under drought stress condition while increased under control condition. Hafeez *et al*. (2015) studied that fresh and dry biomass of root and total leaf area were found to be decreased under drought stress in both the FDH-786-*Gossypium arboreum* and CIM-496-*Gossypium hirsutum* varieties, but significant reduction was observed in case of CIM-496-*Gossypium hirsutum*.

### 2.9.5 Root shoot ratio

Kader *et al*. (2016) and Sumartini *et al*. (2013) observed that drought tolerant genotype by maintaining the highest values of root length shoot length and root/shoot ratio under drought stress. Some other researchers although R/S ratio decreased under severe water stress conditions (McMichael and Quisenberry, 1991). Pace *et al*. (1999) showed that shoot: root ratio was less in the drought treated plants than the controls.

Irum *et al.* (2011) reported Positive but non-significant relationships existed between seedling shoot root ratio by length and seedling shoot root ratio by weight. The value of correlations was positive and significant between seedling shoot root ratio by length and yield of seed cotton ha-1. The phenotypic correlation coefficient between these two traits was also positive but very small. Seedling ratio of shoot root by length influenced on yield of seed cotton positively. The shoot root ratio by length had positive indirect effect on yield through path viz shoot length, root length and shoot weight. The negative indirect effects were produced by root weight and shoot root ratio by weight.

### 2.9.6 Number of lateral root

Veesar *et al*. (2020) studied that water stress significantly affected number of lateral roots and correlation coefficient revealed that stomatal conductance was negatively associated with no of lateral roots. They also revealed that exposure of water stress reduced the number of lateral roots in cultivars NIAB-78, CIM-499, Bt-cotton,

Chandi, CRIS-342 and BH-160 and by -3.00, -3.00, -3.00, -2.75 -1.75, and -1.25 roots respectively (Table 3). Inversely, the number of lateral roots of varieties like Sindh-1, CRIS-134, Sadori, CIM-534, CIM499 and CIM-506 were increased by 5.50, 5.00, 4.50, 4.00, 3.75, and 3.50 respectively revealing their water stress tolerance. Ahmad *et al*. (2020) observed water stress adversely reduced the values of number of lateral roots. Mvula *et al*. (2018) revealed that significant differences among genotypes on number of lateral roots for response to drought stress.

### 2.9.7 Vegetative and reproductive branches

Drought stress disrupts the boll development and distribution as the higher fruiting branches have smaller and fewer bolls (Wang *et al*., 2016a). Drought stress at the time of early reproductive growth results in shorter plants with a smaller number of nodes, but plants compensate yield if sufficient water is available at latter stages (Ibrahim *et al*., 2019; Ullah *et al*., 2017).

## 2.10 Effects of drought stress on plant physiology

The effects of drought stress on different plant biochemical and physiological processes are complex and interrelated. Cellular water content largely controls chlorophyll synthesis and stomatal conductance directly affects photosynthetic carbon fixation, which in turn affects metabolic functions such as osmotic potential, cell turgor and stabilization of membranes. However, for ease of discussing these physiological functions, we have addressed each function separately. Chen *et al*. (2019) reported that drought tolerance of cotton by regulating many genes that related to drought stress and multiple organ responses to drought, including root growth, the stomata aperture and photosynthesis.

### 2.10.1 Water relations

Relative water content, stomatal movements, transpiration, water use efficiency are important characteristics to persuade plant water relations. Relative water content represents plant water status including water uptake by the roots and water loss by transpiration through plant canopy, as a result reflect the biochemical activities of plant tissue, hence used as a most important trait index for drought tolerance. Khan *et al*. (2018) reported that water availability is a key driver for sustainable cotton production, its scarcity can adversely affect physiological and biochemical processes of plants, leading towards lint yield reduction**.**

Nayyar and Gupta (2006) reported that drought stress effect causes to decrease of the relative water content (RWC) in wide variety of plants. Furthermore, plants exposed to drought stress substantially decreased the relative water content and transpiration rate (Nezhadahmadi *et al*., 2013; Siddique *et al*., 2000). Water unavailability affects the different components of plant water relations and especially stomatal movement is more strongly affected. Moisture stress tolerance can be achieved through the capability of plants to minimize evaporation via stomatal shutting and modifications in leaf phenotype. Veesar *et al*. (2020) studied that twelve most popular upland cotton cultivars with diverse characters under water stress conditions and showed water stress significantly affected relative water content, excised leaf water loss and stomatal conductance. They also reported that drought stress caused considerable declines in RWC% of the genotypes under screening and the reduction ranged from -26.50 to -48.50% (Table 4). The maximum reductions in RWC% due to drought stress was recorded in varieties CIM-499 (-48.50%) closely followed by NIAB-78 (-47.50%) and Bt-cotton (-45.50%). Kader *et al*. (2015) also reported that all genotypes were significantly affected by drought but some genotypes such as Tamcot C. E. x Deltapine, Giza 90x (Giza 90X Australian) and Giza 80x Deltapine by maintaining the highest values of relative water content under drought stress. Oxidative injury at the cellular level under water stress has high lipid peroxidation which decreased stability of cell membrane and led to lose more water from cells (Abdalla and Khoshiban, 2007; Sanchez-Blanco *et al*., 2006 and Sairam and Saxena, 2000). Saleem *et al*. (2015) were conducted some genetic analysis for relative water content with cotton yield and fiber quality against drought and Correlation analysis showed that the genes involved in maintaining high relative water content had genetic linkage with those controlling bolls per plant, fibre length and fibre strength.

Water use efficiency (WUE) is an important parameter connecting plant biomass production with water consumption. Physiologically WUE is defined as the ratio between photosynthetic and transpirational rates, while agronomically is illustrated as the ratio between dry matter produced and quantity of water used. Due to its nature of definition, high water use efficiency produced high cotton yield under water deficit conditions, hence water use efficiency has always been an alluring parameter to determine and correlate with drought tolerance. However, measurements of water use efficiency are difficult and often variable. Abiotic factors, such as solar radiation, high

temperature, humidity, CO2 ambient concentrations as well as soil characteristics and soil water availability significantly affect water use efficiency used as measurement tools (Reddy *et al*., 1995; Reich *et al*., 1985; Zure and Jones 1984; Lin and Ehleringer, 1982; Constable and Rawson, 1980). Additionally, water use efficiency is dependent upon plant characteristics such as plant canopy along with cultural practices, such as plant distance and density (Rosenow *et al*., 1983; Krieg, 2000). Hence, whole plant water use efficiency evaluations are mostly based on the total dry matter production and water consumption, measurements that are even more difficult to accurately calculate. Farquhar *et al*. (1982b) showed that in C3 plants carbon isotope discrimination is associated with the ratio between the intercellular CO2 concentration (Ci) and the ambient CO2 concentration (Ca). Ehleringer *et al*. (1993) reported that the Ci/Ca ratio controls the δ 13C discrimination ratio. Water use efficiency was studied to correlate positively with the δ13C discrimination ratio, providing in that way a more reliable technique for its evaluation. However, limitations of this technique have been observed since any change in Ci concentration has an effect on δ13C discrimination.

A number of studies of water use efficiency have been evaluated for cotton. Eaton and Belden (1929) and Gustein (1969) reported that Acala (*G. hirsutum*) cultivars had lower water requirements compared to Pima (G. barbadense) cultivars under various abiotic stress conditions. Rawson and Constable (1980) studied greenhouse experiments and reported that water use efficiency of individual leaves was dependent on their age 31 and the leaf position on the plant. Wullschleger and Oosterhuis (1989) in field-grown cotton experiments reported that differences in water use efficiency on main-stem and sympodial leaves at node 10 were dependent on the leaf age as well as on the position along the branch. Quisenberry *et al*. (1991, 1976) reported that intraspecific variation in water use efficiency was present in cotton. They also reported that primitive cultivars, characterized by indeterminate growth patterns, had much higher water use efficiencies compared to the modern determinate cultivars concluding that water use efficiency was positively correlated with the indeterminate growth habit. Radin (1992) observed that a positive correlation existed between photosynthetic rates and water use efficiency values of field grown plants. Leidi *et al*. (1999, 1993) reported a positive correlation between carbon isotope discrimination and yield in field experiments in Spain; however the results were inconsistent across

the years, which is in contrast with Gerik *et al*. (1996) who observed a consistent positive relation between carbon isotope discrimination and yield.

Reduction in RWC was detected in the leaf, which was recovered. It may be due to higher contents of sugars, polyphenols, proline, and amino acids, which are compatible solutes (Parida *et al*., 2007). Parida *et al*. (2007) found significant decrease in chlorophyll content, carotenoids, proteins, and starch after applying drought stress for 7 days. Generated data were compared using drought susceptibility indices, drought tolerant indices, and other absolute values.

### 2.10.2 Chlorophyll content

Chlorophyll is one of the major elements of photosynthesis, and chlorophyll content changes under drought stress. This has also been considered for pigment photo-oxidation and chlorophyll degradation and as a result develops the various symptoms of oxidative stress. Drought stress caused a significant decline in the chlorophyll a content, the chlorophyll b content, and the total chlorophyll content in different sunflower varieties (Manivannan *et al*., 2007). Barley plants grown under drought condition showed decrease in chlorophyll synthesis as shown in reduced SPAD values (Zhao *et al*., 2010).

Chlorophyll a fluorescence analysis is a sensitive method for the identification and measurement of changes induced in the photosynthetic apparatus (Guo *et al*., 2016). The chlorophyll fluorescence is based on the calculate of fluorescence signal of dark-adapted plants exposed to continuous light (Govindje, 2006). Dark-adapted samples show significant changes in the intensity of chlorophyll fluorescence during the illumination by continuous lights and this effect is called fluorescence induction of Kautsky´s effect. Drought treated barley plants showed the maximum quantum yield of PSII (*Fv/Fm*) decrease which are the reliable sign of photo inhibition (Guo *et al*., 2009a).

Ullah *et al*. (2017) reported that physiological responses including stomata closing, cellular adaptations, photosynthesis against drought stress in cotton. Dimitra A. Loka (2012) also observed drought stress during flowering significantly compromised leaf gas exchange functions resulting in decreased photosynthesis and affected carbohydrate metabolism of both leaf and pistil. Kader *et al*. (2015) 21 cotton genotypes (6 parents and their 15 F1 crosses) were evaluated under drought condition.

They observed that Chlorophyll a, chlorophyll b, total chlorophyll, chlorophyll a/b ratio, chlorophyll stability index (CSI)) were significantly affected by drought stress. They also showed that under drought treatment, it's found that yield was positively and significantly correlated with total chlorophyll, chlorophyll 'b', chlorophyll 'a', membrane stability index and relative water content % and negatively and significantly correlated with electrolyte leakage %. The decrement of chlorophyll content during drought stress could be related to photo-oxidation resulting from oxidative stress which reduces photosynthetic process (Hamayun *et al*., 2010; Ashraf, 2009; Delfine *et al*., 1998). Ahmad *et al*., (2020) were also evaluated 10 cotton leaf chlorophyll contents and observed that water stress adversely reduced leaf chlorophyll. Hafeez *et al*. (2015) observed chlorophyll content and photosynthesis rate of cotton plant under drought stress were also sharply decreased.

### 2.10.3 Nitrogen concentration

Nitrogen (N) metabolism regulation is very crucial for tolerance against environmental stresses (e.g. drought) due to its involvement in the majority of the physiological processes of plants (Lawlor, 2002). Drought stress disturbs the plant metabolism by affecting the uptake and translocation of N to above ground parts through reduction in transpiration (Xiong *et al*., 2018). Application of N to cotton plants under water deficit conditions can help in improving the drought stress tolerance through antioxidant enzymes activation, leading to decrease lipid peroxidation and better root growth (Zhou and Oosterhuis, 2012). Likewise, exogenous N supply improved the N uptake, photosynthesis, relative water contents of cotton leaves under drought stress conditions. Further, high N concentration in plants helped in mitigating the drought induced stomatal limitations, enhanced the osmoprotectants synthesis (soluble proteins and free amino acids), activities of antioxidant (SOD, POD, and CAT) enzymes and N assimilating enzymes (nitrogen reductase, glutamine synthetase, glutamate synthase and glutamate dehydrogenase) (Iqbal *et al*., 2020).

### 2.10.4 Regulation of ROS levels

One of the most common stress tolerance strategies in plants is the over production of different types of compatible organic solutes, such as proline (Pro) and glycine-betaine (GB) (Serraj and Sinclair, 2002). Compatible solutes are highly soluble

compounds; low molecular weight that are usually non-toxic function at high cytosolic concentrations. Proline, GB and sugars facilitate water uptake in response to cell osmotic stress like drought stress (Ashraf and Foolad, 2007 ; Hare *et al*., 1998). In addition, these osmolites are important for protecting cells against increased levels of ROS accumulation under drought conditions.

Proline accumulates in the cytosol and the vacuole during drought condition shelters cotton plant cells against shrinkage caused by $1O_2$ or $HO^-$ (McNeil *et al*., 2002; Matysik *et al*., 2002). Proline plays a vital role to protect proteins, DNA and membranes by quenching $^1O_2$ and directly scavenging $HO^-$ (Smirnoff and Cumbes, 1989). In addition to directly scavenging of $HO^-$, Pro bind to redox-active metal ions and protect biological tissues against cell rupture caused by $HO^-$ formation (Smirnoff and Cumbes, 1989). Hafeez *et al*. (2015) studied the comparative analysis to evaluate the two genotypes, FDH-786 (*Gossypium arboreum)* and CIM-496 (*Gossypium hirsutum*) under different levels of drought stress and proline was sharply decreased in CIM-496 as compared to FDH-786 during relative expression level of drought responsive genes (TPS, PIP, Gh-POD and LHCP-PSII) were observed under different drought stress conditions.

Osmolytes are organic compounds that exist in a stable form inside the cells and are not easily metabolized. In general, they do not have an effect on cell functions, even when they have accumulated in considerably high concentrations, i.e. more than 200mM (Hare *et al*., 1998; Sakamoto and Murata, 2002). Compatible solutes include sugars and sugar alcohols (polyols) (Yancey *et al*., 1982), amino acids such as proline (Aspinall and Paleg, 1981; Bonhert *et al*., 1995) and its analogues. Osmolytes production is a general method in plants to maintain osmotic potential and cell turgor, as stated above; however they have protection of cells by scavenging for reactive oxygen species (Pinhero *et al*., 2001). They also have secondary roles such as stabilization of membranes and maintenance of proper protein conformation at low leaf water potentials (Papageorgiou and Morata, 1995), as well as regulation and integration in the metabolism of stressed photosynthetic tissues (Lawlor and Cornic, 2002). Their synthesis and accumulation varies among plant species, as well as among genotypes of the same species, and they are most often confined to the chloroplasts and cytoplasmic compartments that according to occupy less than 20% of the total volume of mature cells.

Proline plays a multifunctional role in the defense mechanisms. It acts as an intermediary of osmotic adjustment, a scavenger of free radicals, a stabilizer of subcellular structure, an energy sink and a stress-related signal (Nanjo *et al*., 1999). A strong correlation between the accumulation of Pro and tolerance of drought stress has been demonstrated by overexpression of the $^{\Delta}$1-pyrroline-5-carboxylate synthase gene P5CS or by antisense suppression of the proline dehydrogenase (ProDH) gene in various plants (Bartels and Sunkar, 2005) (Figure 6).

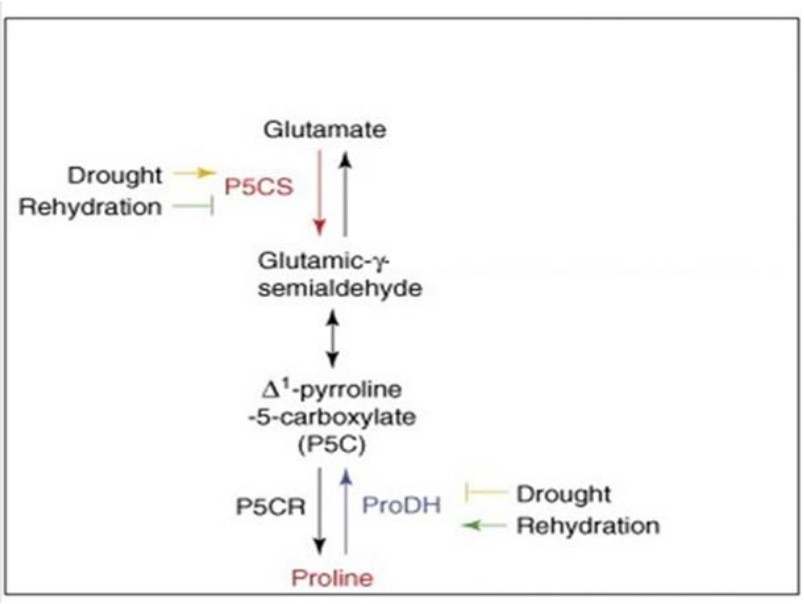



**Figure 6. Regulation of proline biosynthetic and catabolic pathways in plants** Here, P5CDH, P5C dehydrogenase; P5CR, P5C reductase; P5CS, P5C synthase; ProDH, proline dehydrogenase.(Seki et al., 2007).

Eid *et al*. (2022) revealed that significantly decreased relative water content, membrane stability index, chlorophyll content, plant height, yield components, and fiber quality traits. Otherwise, phenolic compounds, proline contents, as well as antioxidant enzyme activities increased in concomitance with an increase in electrolyte leakage and malondialdehyde content.

Mahmood *et al*. (2021) variability of drought tolerance indices was explained for the PCA1 ($F_1$) and PCA2 ($F_2$). Biplot demonstrating overall variability of 55.89% explained for all traits. Vector magnitude of biochemical traits clarified more relative, indicating the importance of these traits for selecting cotton genotypes at early seedling stages under drought stress. Distribution and position of drought-tolerant genotypes including DTV-9, BT-992, and MNH-886 fall near to the vectors of biochemical parameters including PC, POX, NOX, APX, H2O2, and SOD, which indicated the response of these genotypes for biochemical parameters. Variance, and

Heritability Estimates Broad sense heritability (H2) and narrow-sense heritability (h2) displayed remarkable variation under cross environments. Germination percentage (GP) had a minimum H2 (0.901) and ChT had a maximum (0.998) among all the traits. In terms of h2, DS, BW, and PH had higher values (0.78, 0.72, and 0.722), respectively.

### 2.10.5 Membrane Stability Index (MSI)

Various defense mechanisms e.g. maintenance of membrane stability, have been found play a vital role in plant survival under moisture stress (Khan *et al*., 2018). Kader *et al*. (2015) evaluated the correlation between yield and physiological trait membrane stability index (MSI%) under normal and drought treatments. They concluded that all genotypes were significantly affected by drought and membrane stability index could be used as selection criteria for high yield under drought stress. The plasma membrane is generally protected from desiccation-induced damage by presence of membrane compatible solutes, such as sugars and amino acid. Therefore, a link may exist between the capacity for osmotic adjustment and degree of membrane protection (Sibet and Birol, 2007). The drought stress induces decreasing in membrane stability which indicates that the extent of lipid peroxidation caused by active oxygen species (Sibet and Birol, 2007; Menconi *et al*., 1995 and Dhindsa *et al*., 1981). Saleem *et al*. (2015) also observed that the genes involved in maintaining high cell membrane stability had genetic linkage with those controlling bolls per plant, fibre length and fibre strength.

Rahman *et al*., (2008) reported that the significant positively associated were found with seed cotton yield under the water-limited regime between cell membrane stability and osmotic adjustment implicates the role of osmolytes in the protection of various cellular functions, including those associated with cellular membranes and inversely correlated with the drought susceptibility index. Hafeez *et al*. (2015) also observed cell membrane stability was found to be decreased under drought stress.

### 2.10.6 Pollen viability content

Burke and Ulloa (2017) observed that pollen development stability and mature pollen viability across a range of environmental stress to stabilize and enhance cotton yield. Razzaq *et al*. (2019) reported that abiotic stress reduce the photosynthates production, thus genotypes also reduce the reserve mobilization for tapetum cells, which induce

the significant reduction in pollen fertility. Pollen viability in the field is highly variable, indicating that differences in microenvironment may have a profound effect on pollen viability (Bots and Mariani, 2005). Burke (2002) observed that after the Cotton flowers were saturated with water, pollen dehisced resulted in the osmotic disruption of the pollen grains and prevented self-pollination of the cotton flowers. Burke *et al.* (2004) also observed that water stress responses environmental stress–related yield reductions and germinating cotton (*Gossypium* spp.) pollen in vitro.

WeiHu *et al.* (2020) reported that drought reduced the deposition of starch, the hydrolysis of sucrose into hexoses, the generation of adenosine triphosphate (ATP) in anthers, restricting pollen viability, inhibited male fertility and germination of cotton. SamiUl-Allah *et al.* (2021) observed that drought stressed cotton plant has poor assimilate translocation towards reproductive tissues, leading to poor pollen functioning, reproductive failure and inferior fiber quality. The viability of pollen depends on the health of anthers. Drought stress severely affects the anther growth and development which affects pollen viability (Zhang *et al*., 2020). Drought stress reduced starch accumulation and its breakdown into hexoses in the anthers of cotton which in turn restrict the productions of ATPs (Hu *et al*., 2020b). This results in less availability of energy to developing pollens and leads to the production of less viable or unviable pollens and results in premature abortion of buds and flowers (Hu *et al*., 2020a; Echer *et al*., 2014) and the biomass allocation to reproductive organs reduced (Wang *et al*., 2016a).

### 2.11 Effects of drought stress on plant morphology and yield

Hafeez *et al*. (2019) reported that drought stress changes the morphological, physio-chemical and molecular characteristics of cotton plants, which became the major cause of yield reduction. Rahman *et al*. (2017) observed that agricultural practice in Barind area based on groundwater irrigation is vulnerable to drought. Kamruzzaman *et al*. (2019) studied the characteristics of agricultural droughts in Bangladesh during 1981–2015 and showed that the northwestern areas were prone to extreme droughts during the Kharif (wet) and Rabi (dry) seasons.

### 2.11.1 Growth and development

Plant responses to water deficit are involving adaptive changes and/or adverse effects on growth is through cell division, cell development and rivets morphological, physiological, ecological, biochemical and molecular event and their complex correlations. The quality of plant growth and development depends on these functions, which are affected by water stress. Cell division is one of the most drought susceptible physiological events due to the decreases in turgidity (Taíz and Zeiger, 2010). Reduced cell and plant growth, inhibition of cell enlargement as well as reduction in cell wall synthesis results occurred in drought stress (Chaitanya *et al*., 2003). Drought influences the normal metabolic events of the cell such as energy charge, carbon-reduction cycle, light reactions and leads to the production of toxic molecules. Consequently, most of the mechanisms were development by plants to tolerate abiotic stresses like drought which is schematically showed in Figure 7.

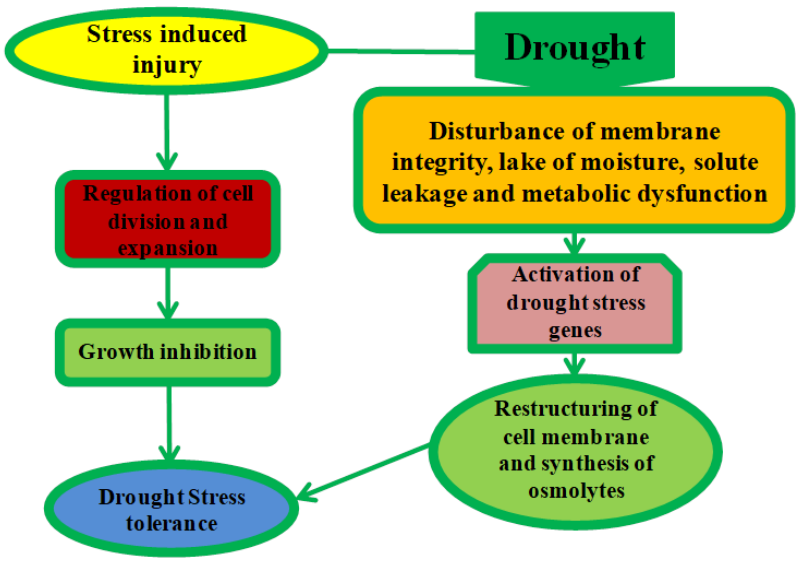



**Figure 7. Plausible drought tolerance mechanisms in plants**

### 2.11.2 Yield

Many physiological processes are involved in quantitative trait as seed cotton yield. Many lint yield estimating physiological processes in plants respond to drought stress. Due to the involvement of pathways and metabolic complex processes, it is difficult to understand how plants accumulate and activate physiological processes over the life cycle of crops. For drought stress, severity, timing and duration of stress and plants

responses after stress reduction and correlations between stress and other biotic and abiotic factors are very important (Khan *et al*., 2018). Drought stress reduced cotton (*Gossypium hirsutum*) lint yield, severity, duration and speed of growth. Lint yield was usually reduced due to boll formation because of lower number of flowers and greater boll abortions due to increase in drought stress severity and length during reproductive stage (Pettigrew, 2004).

Adversely affect the growth and development as well as the production of the cotton (Figure-8). In general, drought stress harshly hampers cotton growth and development, such as affecting plant height, plant dry weight, root development, node number, sympodial branch number, cotton seed, lint weight and fiber quality (Loka *et al*., 2011). Particularly, net photosynthetic rate, transpiration rate and water potential of cotton leaves were reduced significantly under drought stress conditions (Kumar *et al*., 2001). The detrimental effects of water stress on cotton 50% dry matter accumulation of *Gossypium barbadense* was limited; also the photosynthetic rate and transpiration rate were also reduced under drought stress condition (Hejnák *et al*., 2015). Cotton has acquired a wide range of morphological and physiological mechanisms in response to abiotic stresses that enable them to tolerate and/or avoid drought stress.

In evaluation, existing drought might reduce the morphological such as plant height, leaf dry weight, stem dry weight; root development, node number, fiber quality and physiological traits as well as decreases photosynthetic rate of cotton leaves under drought stress condition (Ullah *et al*., 2017).

Drought stress is a major cause for significant compromises in plant development and productivity around the world (Boyer, 1982). In reproductive development stage, many crops are the most drought-stress-sensitive after seed germination and seedling establishment has been observed (Saini, 1997). In cotton however, there is still debate about the most vulnerable period to drought stress during development in relation to seed cotton yield, even though water sensitivity during flowering and boll development has been well established (Turner *et al*., 1986 and Constable and Hearn, 1981). However, adverse affect to the growth and development as well as the production of the cotton is shown in Figure 7. According to Reddell *et al*. (1987) the early flowering stage is the most sensitive to drought stress, whereas Orgaz *et al*. (1992) concluded that drought stress during peak flowering had the most adverse

effects on cotton yield. On the other hand, a number of reports (de Cock *et al*., 1993; Radin *et al*., 1992 and Plaut *et al*., 1992) state that boll development, after the end of effective flowering, is the most moisture deficit sensitive period for cotton. Additionally, in an earlier experiment Harris and Hawkins (1942) reported that moisture stress at fruiting could prevent yield reduces due to excessive vegetative growth. Similar results were observed from Singh (1975) who supplied irrigation until wilting was reached in the morning during the pre-flowering stage and reported higher number of flowers and bolls per plant as well as increased yield. However, Lashin *et al*. (1970) and Stocton *et al*. (1961) observed that increased

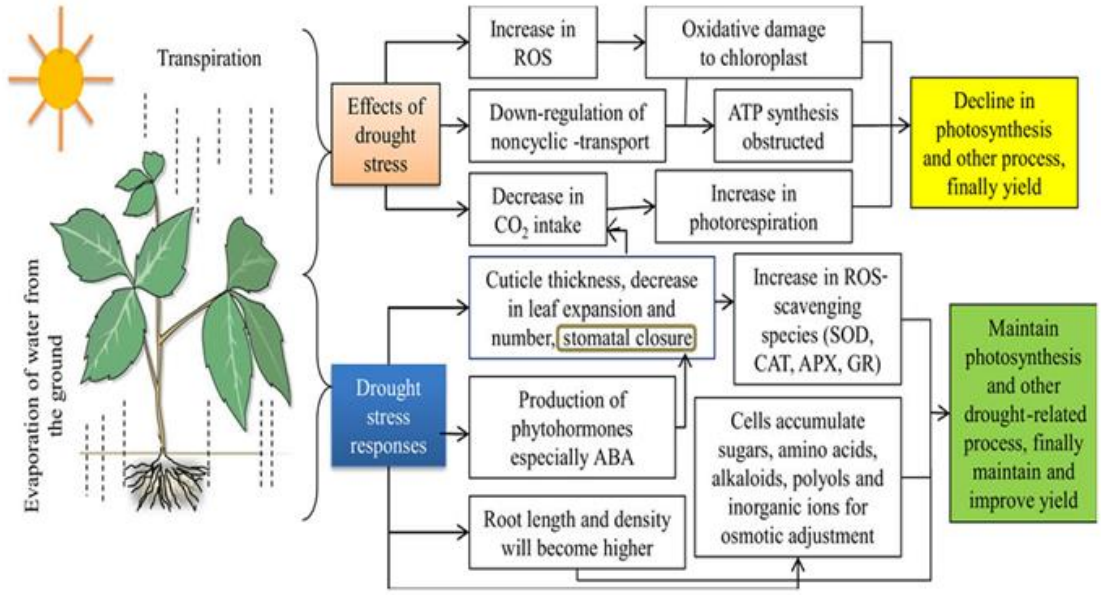



**Figure 8. Adverse affect to the growth and development as well as the production of the cotton (Loka *et al*., 2011)**

irrigation resulted in higher flowering. Guinn *et al*. (1981) concluded that a moderated drought stress early in the season could be beneficial to the plants since it would mildly retard growth, however either delaying or limiting water supply could lead to stunted growth.

Cotton is not the only crop where various opinions exist concerning the extent of sensitivity of each growth stage to drought stresses. A similar criticism has also been reported in grain crops such as wheat, rice, barley and maize where all stages of reproduction (meiosis, anthesis, pollen fertility, fertilization, gametophyte fertility and zygote development) are considered to be scarcely affected by drought stress (Saini and Westgate, 2000). Cotton however, provides a various challenges due to its

indeterminate growth habit, which results in an inability to distinct growth stages. That inability in combination with the drought stress affects cotton plants, explains the lack of understanding concerning the effects of drought stress on cottonseed set and development.

Lint yield is generally lower under water-stress because of bring down boll formation, primarily due to the production of lower flowers and bolls (Gerik *et al*., 1996; Grimes, 1969 and Stocton *et al*., 1961) but also because of higher rates of boll abortion when the stress is extreme and occurs during reproductive development (Turner *et al*., 1986; Grimes and Yamada, 1982 and McMichael and Hesketh, 1982). In addition, Pettigrew (2004) observed that the exposed of the bolls, both vertically and horizontally was detrimentally by water stress, with the moisture stressed plants retaining higher number of bolls at first initiation and forming lower bolls above node n=11 compared to the control. He speculated that the reduction investigated in lint yield production was due to the loss of these fruiting stages as well as lower lint per number of seeds.

Yagmur *et al*. (2014) observed that a drought stress increased, values of traits including plant height, boll number, seed cotton yield, and 100-seed weight decreased in spite of increasing boll weight, first harvest ratio, and ginning percentage. Bakhsh *et al*. (2019) studied performance of 23 cotton genotypes was compared for seed cotton yield and fiber quality traits under water stress and nonstress conditions. They observed that drought stress were caused a reduction of 13% in days to first square formation, 14% in days to first flower formation, 19% in plant height, 18% in monopodial branches, 26% in sympodial branches, 27% in number of bolls per plant, 14% in boll weight, 4% in ginning out turn and 37% in seed cotton yield. They also observed that GeFH-326 was showed better performance for sympodial branches, bolls per plant, fibre strength and seed cotton yield under water stress and non-stress conditions. Ahmad *et al*. (2009) studied $F_1$, $F_2$ and backcross generations of six crosses under drought conditions in the field to find gene action of the traits, plant height, number of fruiting branches per plant, number of vegetative branches per plant, number of bolls per plant, boll weight, ginning out-turn and analysis indicated that all three kinds of gene effects (additive, dominance & interactions) were involved in the inheritance of the studied traits. Kamaran *et al*. (2016) observed that seed yield was showed harmful effects of drought stress as compared with those assessed in non-stressed condition. Rahman *et al*. (2008) observed that reduction in seed cotton yield

due to water deficit was 20 to 43% and relative yield traits were losses due to drought stress ranging from 20 to 74%. Karademir *et al*. (2011) reported that seed cotton yield (48.04%) and fiber yield were decreased (49.41%), due to drought stress.

Mahdi *et al*. (2014) noted that seed cotton yield was reduced by drought stress (%47.03), Sahito *et al*. (2015) showed that all the growth and yield components of cotton were significantly ($P < 0.01$) affected by varieties and irrigation frequencies, Hamoud *et al*. (2016) found significant ($p \leq 0.01$) genetic differences between cotton well-watered and water-stressed treatments, Gao *et al*. (2020) noted that fiber quality was significantly affected by drought level, Shilpa and Chandrasekhar (2020) found that fiber fineness and bundle strength decrease in inferior direction as reduction of soil moisture levels. The reduction in yields could be mainly due to the decrease in lint index, boll weight and seed index rather than a decrease in bolls/plant. Bakhsh *et al*. (2019) noted that water stress caused a reduction of 14% in days to first flower formation, 27% in number of bolls/ plants, 14% in boll weight and 37% in seed cotton yield.

### 2.11.3 Fiber Properties

Fiber characteristics have been reported to be insensitive to drought stress (Hearn, 1994; Marani and Amirav, 1971; Bennet *et al*., 1967), unless the drought stress is extremely severe. Drought stress has also been reported to cause a significant lower in fiber micronaire (Marani and Amirav, 1971; Eaton and Ergle, 1952).Timing of water-deficit stress is also a significant factor, since Marani and Amirav (1971) showed that water stress initial in the flowering stage, had no effect on fiber quality but stress, however when the water stress occur shortly after flowering it significantly decreased fiber length. Dhindsa *et al*. (1975) observed that cotton fiber was a process primarily dependent on turgor and carbohydrate supply, the reductions in plant water status and photosynthesis that occur under drought stress condition would result in reduction in fiber growth. Cosgrove (1993) who reported that increased volume of growing plant cells depends on the water uptake by the vacuole. However, Lewis *et al*. (2000) observed that lint yield was a function not only of fiber properties but also a function of number of fibers per seed and number of seeds per unit area. Rabadia *et al*. (1999) also observed that a strong correlation exists between plant water retention and accumulation of dry matter of the developing fiber and seed which implies that quick

water uptake is required in order to hold up seed development. Yagmur *et al*. (2014) reported that lint properties such as fiber length, fineness, uniformity, and strength were reduced under limited water levels, except for short fiber index. Saleem *et al*. (2015) observed that the genes involved in maintaining high relative water content and cell membrane stability had genetic linkage with those controlling fibre length and strength.

Osmotic stress, at fiber initiation and elongation, reduces the fiber cell division leading to a smaller number of total fiber cells (Zhang *et al*., 2020) and shortens the fiber length. Drought stress reduces the fiber length by reducing the leaf water potential causing a decrease in the rate of fiber elongation. Studies have shown that the force and duration of the cell turgor regulate the fiber elongation process (Gao *et al.*, 2020; Zhao *et al*., 2019a; Tang *et al*., 2017; Wang *et al*., 2016a;). Drought stress disturbs the fiber cell turgor pressure (Ullah *et al*., 2017; Wang *et al*., 2016a) leading to reduced fiber length, uniformity, and strength; while the increase in fiber micronnaire. Snowden *et al.* (2014) reported that drought stress at early and full bloom have similar effects on reproductive development of cotton but on full bloom, it has more detrimental effect on fiber length and fineness than early bloom stress. Droughts stress at the secondary wall deposition stage mainly affects fiber thickness and strength which are the main contributors to lint weight (Gao *et al*., 2020). The mature fiber has thicker secondary wall, smaller middle cavity and high strength (Zhang *et al*., 2019). Fiber thickness development involves largely synthesis and accumulation of cellulose; and it depends on amount and quality of deposited cellulose (Pettigrew, 2001). Limited water availability during the fiber thickening (stage of secondary wall deposition) affects carbohydrate metabolism in developing fibers leading to lower fiber sucrose contents and insufficient UDP-glucose (Gao *et al*., 2020; Tang *et al*., 2017) resulting in cellulose synthesis instead of cellulose and results in weak fibers. Drought stress disturbs fiber development by decreasing leaf water potential, cell expansion, and carbohydrate metabolism, resulting in reduced the quality of developing fiber of upland cotton by lowering the length, uniformity, and strength of developing fiber (Witt *et al*., 2020).

## 2.12 Variability Analysis

Adeela *et al*. (2021) reported that the phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all studied traits. Plant height, monopodial branches, total number of bolls, lint index, seed index, and seed cotton yield displayed high heritability in a broad sense with maximum genetic advance. A similar trend was also observed for the values of environmental coefficients were low as compared with the genotypic coefficient of variation. This indicated that the influence of environment was less on these characters. Plant height, monopodial branches, the number of bolls, lint index, seed index, and seed cotton yield displayed high heritability with maximum genetic advance per percent mean. A similar trend was observed for the phenotypic coefficient of variation (Shakeel *et al*., 2015a). Plant height, the number of monopodial branches, the number of bolls, lint index, seed index, and seed cotton yield displayed high heritability with maximum genetic advance per percent mean. Similar results were reported by many researchers including Dhivya *et al*. (2014), Khan *et al*. (2017), Shar *et al*. (2017) and Hayat and Bardak (2020). Fiber attributes displayed high phenotypic variance values in comparison with genotypic variance as reported by Shakeel *et al*. (2015). Heritability was maximum for micronaire and fiber strength with low genetic advance as revealed by Nawaz *et al*. (2019). Rehman *et al*. (2020) estimates of heritability were high for all of the traits except number of sympodial branches per plant and boll weight. Plant height was positively linked with sympodial branches per plant, number of bolls per plant, GOT, seed cotton yield, staple length and fibre fineness. Azhar and Ajmal (1999), Rao and Gopinath (2013) and Shahzad *et al*. (2015) also had similar findings. Tulasi *et al*. (2012) also observed positive association with GOT, fibre length and fineness. Heritability (B.S) for plant height was 74.48%. Kapoor and Kaushik (2003), Ahmad *et al*. (2011) and Baloch *et al*. (2015) also found high heritability 94%, 81% and 96.4% correspondingly for plant height. High heritability estimates indicated that selection for plant height can be effective. Bolls per plant had positive association with plant height, boll weight, sympodial branches per plant, seed index, seed cotton yield and fibre strength. Ahmad and Azhar (2000), Djaboutou *et al*. (2005), Gul *et al*. (2014), Magadum *et al*. (2012), Alkuddsi *et al*. (2013) and Farooq *et al*. (2014), also found same results. Heritability value for bolls per plant was 53.87% (Table 3). Desalegn *et al*. (2009), Ahmad *et al*. (2011), Baloch *et al*. (2015) and Rathinavel *et al*.

(2017) estimated 59%, 88%, 93% and 60.21% high broad sense heritability respectively for bolls per plant. High estimates of heritability revealed that successful and effective selection can be helpful in the improvement of this trait.

Sympodial branches per plant had positive relationship with plant height, number of bolls per plant, boll weight, seed cotton yield, GOT, staple length and fibre fineness. Pujer *et al*. (2014), Anandan (2009), Joshi *et al*. (2006) indicated that sympodial branches/plant positively correlated with seed cotton yield, plant height, GOT and boll weight. Whereas, Killi *et al*. (2005) found that sympodial branches per plant were positively linked with fibre strength. Rauf *et al*. (2004) also observed that sympodial branches per plant had positive relationship with number of bolls per plant and fibre fineness. Kulkarni *et al*. (2011), Neelima and Reddy (2008), Mustafa *et al*. (2007) and Ahmed *et al*. (2006) also observed medium heritability 50.72%, 59%, 61.30% and 43% respectively for sympodial branches per plant. Boll weight was positively linked with bolls per plant, sympodial branches per plant, 100 seed weight, staple length and fibre fineness. Jatt *et al*. (2007) revealed that boll weight had positive association with yield of seed cotton. Abdullah *et al*. (2016) and Shaheen and Yaseen (2014) observed that boll weight was positively correlated with fibre length, fibre fineness and sympodial branches per plant. Do Thi *et al*. (2008) and Kale *et al*. (2007) reported that boll weight positively linked with seed index and number of bolls per plant. Whilst heritability value was moderate 46.66% for this trait. Huangjun and Myers (2011), Naveed *et al*. (2004) and Ahmed *et al*. (2006) estimated 57%, 22% and 50.0% medium heritability respectively for boll weight. Monicashree and Balu (2018), Pujer *et al*. (2014) and Chattha *et al*. (2013) observed that GOT had positive linkage with plant height and sympodial branches per plant and yield of seed cotton. Shahzad *et al*. (2015) observed that GOT had positive association with staple length. Heritability for GOT was 90.65%. Devidas *et al*. (2017), Shahzad *et al*. (2015), Kumar and Katageri (2017) and Jarwar *et al*. (2018) found high heritability values 72.5%, 80.73%, 90.0% and 85.46% for GOT. Seed index had positive linkage with bolls per plant, boll weight and fibre length. Komala *et al*. (2018), Memon *et al*. (2017), Isong *et al*. (2017), Shabbir *et al*. (2016), Méndez *et al*. (2012), Patil (2010) and Ashokkumar and Ravikesavan (2010) depicted similar findings. Heritability (B.S) for this trait was 53.42%. Latif *et al*. (2015), Majeedano *et al*. (2014), Joshi *et al*. (2006) and Gite *et al*. (2006) indicated that seed cotton yield was positively linked with plant height,

sympodial branches per plant and number of bolls/plant. Monisha *et al*. (2018) determined positive correlation among GOT, fibre strength and seed cotton yield. Heritability value for seed cotton yield was 54.56%. Hussain *et al*. (2010), Ullah *et al*. (2015), Ahmad *et al*. (2011), Desalegn *et al*. (2009) and Reddy and Reddy (2007) estimated 61%, 80%, 50%, 98% and 76% heritability respectively for this trait. Fiber length was positively linked with plant height, boll weight, GOT, seed index, fibre fineness and seed cotton yield. Fiber length had negative correlation with fibre strength. Ali and Awan (2009) and Echekwu (2001) indicated that fiber length was negatively associated with fibre strength. Yaqoob *et al*. (2016), Tang and Xiao (2014), Zeng and Meredith (2009) and Ali and Awan (2009) found positive linkage between fibre fineness and fibre strength. Abbas *et al*. (2013) and Altaher and Singh (2003) revealed that fibre fineness had positive linkage with plant height, sympodial branches per plant. Abdullah *et al*. (2016) reported that fibre fineness was positively correlated with boll weight. Heritability value for fibre fineness was 70.42%. Hendawi *et al*. (1999) and Lu *et al*. (2002) estimated 67% and 73% heritability respectively for fibre fineness.

### 2.13 Diversity analysis

Cluster analysis has been used as most widely technique in order to classify the different genotypes into homogeneous groups. It works on a matrix of similarity (or dissimilarity) indexes for all possible pairs of genotypes (Ghaderi *et al*., 1980). Cluster analysis was performed to study the patterns of groupings of genotypes. The dendrogram was generated from the UPGMA (Un-weighted Pair Group Method with Arithmetic Mean) clustering method of genotypes based on Euclidean distances. Mugheri *et al*. (2017) classified the 26 Bt cotton genotypes into 9 small clusters, reflecting the presence of wide genetic diversity among the tested genotypes. Based on obtained results, it is suggested that the genotypes clustered together into cluster one, possessing desirable gene combinations for seed cotton yield plant-1, offering that these Bt cotton genotypes could be used in future breeding programs in order to improve seed cotton yield. They also revealed that genotypes grouped together into cluster eight should not be used in cotton breeding programs since the genotypes of that cluster contain undesirable gene recombination for seed cotton yield and its related traits. It is also recommended that hybridization program should be avoided

between cluster one with cluster eight because later cluster do not possess reliable gene combinations for yield and morphological traits.

The conservation and exploitation of genetic resources could be achieved by partitioning the total variance into its components. It also offers a chance for utilization of proper germplasm in crop development for specific plant characters. PCA is an important tool to get parental materials for successful breeding strategies (Nazir *et al*., 2013). Mugheri *et al*. (2017) reported that out of total eight, first three principal components were extracted having Eigen value more than one. They also showed that First three principal components explained 75.90% variability, which is considerably high and can be utilized for further breeding programs in cotton. The positive and negative loading reveals the occurrence of positive and negative association trends between the components and the variables. Therefore, the given characters which load high positively and negatively contributed more to the genetic variability and they were the ones that most distinguished the clusters. As usual, it is customary to choose one variable from known groups. Elci *et al*. (2014) also derived PCA on morphological data in Turkish cotton varieties where PCA indicated the relationships of genotypes in a more significant manner showing that PCA should be used along with the cluster to achieve a better perceptive of relationships among genotypes.

Adeela *et al*. (2021) revealed that the first 6 principal component analysis (PCs) out of the total fourteen PCs displayed Eigen values (> 1) and had maximum share to total variability (82.79%). The attributes that had maximum share to total divergence included plant height, uniformity index, the number of sympodial branches, seed per boll, GOT, seed cotton yield, and short fiber index. Isong *et al*. (2017) reported similar results. According to scree plot, PC1 displayed the highest variability 22.63% with an eigenvalue of 3.622. Minimum variability was observed for PC13 and PC14 with eigenvalues of 0.038 and 0.002, respectively. PC1 was maximum variability so the genotypes in PC1 should opt for selection. The results were in accordance with the findings of Riaz *et al*. (2019) and Shakeel *et al*. (2015). PCA can explain and describe the important indicators of drought resistance and salt tolerance in germplasm (Kakar *et al*., 2019; Bo *et al*., 2017 and Negrao *et al*., 2017). Ayalew *et al*. (2011) identified three principal components through PCA, which accounted for 70% of the total variation in 14 agronomic traits.

Rizwan *et al*. (2022) reported that contribution of first two PCs was 70.77% in total variation among the strains explored for chlorophyll contents, yield and yield related components (Table 3, Figure 3). While, the left over six components presented only 29.23% contribution towards the total diversity. Maximum factor loadings was presented by PC-I (52.21%) followed by PC-II (18.56%). This indicates that maximum information about genetic diversity among genotypes is present in first two principal components which may be utilized in further selection. In previous studies of different characters, Saeed *et al*. (2014) found major impact of first two PCs in the total diversity. As depicted in Table 4, seed cotton yield contributed with maximum positive loading on PC-I subsequently chlorophyll contents, boll weight, No. of sympodia, seed index and GOT% but plant height had negative loadings. PC-II exhibited maximum positive loadings by plant height subsequently chlorophyll contents and seed cotton yield whereas GOT% presented maximum negative loadings followed by No. of boll plant-1 and seed index. The PC analysis inveterate the amount of diversity for studied traits which may be used in scheming a breeding strategy to improve No. of boll plant-1, No. of sympodia plant-1, boll weight and consequently seed yield of cotton (Nazir *et al*., 2013). Principal component analysis was used for assessment of genetic variation regarding physiological parameters of cotton (Li *et al*., 2008). In biplot, the parameters and strains were super-imposed on the graph as vector and contribution of each parameter with respect to different strains was estimated by their distance on PC-1 and PC-2. While studying different cotton strains, (Saeed *et al*., 2014), also observed main contribution of first two principal components in variation. As depicted in biplot, the traits boll weight, chlorophyll contents, sympodia, seed cotton yield and seed index added maximum contribution in variation among the explored strains. The strength of correlation among characters was also revealed in biplot. Therefore, it was illustrated that boll weight, chlorophyll contents, sympodia, seed cotton yield and seed index have strong positive correlation with each other. These parameters may be considered in further selection for yield improvement. Shakeel *et al*. (2015) also found the importance of PCA for selection of desirable strains presenting better quality and yield. PCA is very useful tool as it discloses the significance of major contributors in the diversity present at each level (Sharma, 2006).

## 2.14 Correlations of co-efficient and path analysis

Adeela *et al*. (2021) revealed that seed cotton yield had a significant positive association with plant height, the number of monopodial or vegetative branches, the number of sympodial (reproductive) branches, ginning out turn (GOT), the number of bolls, seed per boll, seed index, uniformity index, the number of sympodial branches, reflectance and seed index at the genotypic level while a significant positive relationship was observed with plant height, the number of sympodial branches, boll number, and GOT. They also negative significant relation was observed for short fiber index at genotypic level. At the phenotypic level, seed cotton yield was positively and significantly associated with sympodial branches, plant height, GOT (%) and the number of bolls while the significantly negative association with short fiber index. Similar results have been reported by Reddy *et al*. (2019) while Kumbhar *et al*. (2020) reported a significantly positive association of plant height with sympodial branches. Erande *et al*. (2014) and Nandhini *et al*. (2019) reported a non-significant and positive correlation of the number of monopodial branches with GOT. Salahuddin *et al*. (2010) found that at the phenotypic level, yield was positively associated with sympodial and bolls. Shakeel *et al*. (2015) reported that plant height and seed per boll was significantly and positively correlated with the number of sympodial branches. Baloch *et al*. (2015) reported a significant and positive relation of bolls with seed cotton yield at both genotypic and phenotypic levels. A similar association of seeds per boll with other yield and fiber traits was observed by Ali *et al*. (2020), Rai and Sangwan (2020), and Bhatti *et al*. (2020). Seed index was significantly and positively associated with yield and uniformity ratio as displayed by Ahmed *et al*. (2019) and Rai and Sangwan (2020). Erande *et al*. (2014) and Monisha *et al*. (2018) reported a significantly positive association of GOT with yield, the number of bolls and seeds per boll. Rehman *et al*. (2020) revealed that seed cotton yield had significant positive correlation with plant height, number of bolls per plant, number of sympodial branches per plant, GOT, staple length and fibre strength. Staple length and fibre strength were negatively linked with each other.

According to Grimes *et al*. (1969) there is a positive correlation between the yield and the number of bolls retention, however, the physiochemical or metabolic functions affecting boll formation have not been observed. The majority of studies have conducted on the consequences of drought stress on plant height, boll number and

weight, as well as lint yield and their correlations to leaf photosynthesis and plant water relations, without any focus on the physiochemical and metabolic processes of the reproductive parts themselves.

Rizwan *et al*. (2022) depicted in correlation coefficients, leaf chlorophyll contents contributed with significant positive correlation towards boll weight, number of sympodial branches plant-1, seed index and seed cotton yield while it correlated negatively with number of boll plant-1. Boll weight (g) showed noticeable positive relationship with leaf chlorophyll contents, seed index, No. of sympodial branches plant-1 and seed cotton yield. Other traits presented non-significant positive correlation with boll weight except plant height which has negative but non-significant correlation with boll weight. The percentage Ginning out-turn (GOT) presented significant positive association with number of sympodial branches and seed index while non-significant contribution was observed with all other parameters. Seed index also correlated positively and significantly with boll weight, chlorophyll contents, GOT, sympodia and seed cotton yield. Highly positive and significant association of seed cotton yield was observed with boll weight, leaf chlorophyll contents, number of sympodia plant-1 and seed index which specifies that the yield can be upgraded by improving these parameters. These studies are in accordance with (Farooq *et al*., 2014, 2018; Karademir *et al*., 2009) who mentioned significant positive association of leaf chlorophyll and yield with yield contributing traits.

Ginning out turn was negatively and significantly correlated with 100 seed weight as advocated by Kıllı *et al*. (2005). Plant height had positive and significant correlation with number of boll per plant (r=0.436**), number of sympodial branches (r = 0.415**), as well as with boll weight (r = 0.289**) and seed cotton weight per boll (r=0.329**).. Number of monopodial branch was correlated with number of boll per plant (r=0.325**). Similar report was given by Iqbal *et al*. (2006). Number of sympodial branch was correlated with number of boll per plant (r=0.285**). Number of boll per plant was correlated with boll weight (r = 0.254**) as advocated by Manzoor and Azhar (2000) and seed cotton weight per boll (r=0.256**). Finally, boll weight was positively and significantly correlated with seed cotton weight per boll (r=0.985**). The results of correlation coefficient analysis revealed that leaf chlorophyll content was positively and significantly correlated with the seed cotton

yield and ginning out turn, an increase in the leaf chlorophyll content may induce positive impacts on seed cotton yield under drought stress conditions.

Mahdi *et al*. (2021) noted that the phenotypic correlations are shown in Table 8. The correlation of SCY/P under normal irrigation was high with LY/P, Lint %, NB/P, LI and BW, moderate with NS/B and upper half mean length, and low with DFF, Pressley index and negative with Micronaire reading. The picture was different under drought stress in which drought affect lint rather than seeds as mentioned above, the correlation of SCY/P was moderate with lint% (0.5897), fiber length (0.7248), low and negative with LI (-0.1488) and Micronaire reading (-0.4090) indicating that droughtaffected deposition of cellulose which slightly lowered Micronaire and increase fiber strength.

Path coefficient analysis determined direct and indirect effects of all the attributes on dependent variable. It revealed that traits like the number of monopodial branches, plant height, seed per boll, short fiber index, GOT, and boll weight impacted positively and directly on yield. The remaining traits exerted negative direct effects on yield (Adeela *et al.*, 2021). The results of path analysis were in accordance with Nandhini *et al*. (2019) and Kumbhar *et al*. (2020), who suggested direct positive effects of boll weight on yield. Manonmani *et al*. (2019) and Ali *et al*. (2020) reported a direct positive effect of seed per boll on yield. Ahsan *et al*. (2015) observed that GOT had positive and direct effects on yield. Some scientists also reported indirect significant effect of leaf chlorophyll on seed cotton yield (Reddy and Kumari, 2004).

Karademir *et al*. (2009) reported that number of monopodial branches (0.125), plant height (0.263) and ginning out turn (0.312) had positive direct effect on seed cotton yield. Similar results were reported by Baloch *et al*. (2001). Chlorophyll content (0.155) had positive direct effect on seed cotton yield as advocated by Reddy and Kumari (2004), also it had positive indirect effect via ginning out turn (0.100). 100 seed weight had positive direct effect on seed cotton yield (0.241), but it had negative indirect effect via ginning out turn (-0.110). From the Tab. it can be seen that the direct effect of seed cotton yield per boll is negligible (0.067). Number of sympodial branch had negative direct effect (-0,026) on seed cotton yield but it had positive indirect effect via plant height (0.109).On the other hand, number of boll per plant and boll weight had negative and non-significant direct effect on seed cotton yield. Similar

findings were reported by Alishah *et al*. (2008), Manzoor and Azhar (2000) and Baloch *et al*. (2001).

Mahdi *et al*. (2021) concluded that the direct and indirect effects of SCY/P components varied greatly under both environments, and LY/P, NB/P and NS/B should be considered as selection indices under normal irrigation, NB/P and NS/B under stress when selection practiced for SCY/P. Farooq *et al*. (2014) found positive direct effect of boll weight on seed cotton yield / plant. Ahsan *et al*. (2015) found that bolls plant1 had maximum direct effect (0.945) followed by the boll weight (0.062), seed index (0.007) and lint index (0.040). Wadeyar and Kajjidoni (2014) and latif *et al*. (2015) noted that the correlation and path analysis together indicated that number of bolls / plant and boll weight should be considered when selection practiced for seed cotton yield / plant. Joshi and Patil (2018) found that number of bolls/plants had positive indirect effect on seed cotton yield/plant, seed index, lint index, fiber strength etc. Boll weight was responsible for high yield through seed index and lint index.

**2.15 Selection for drought tolerant genotypes**

Drought tolerance is a quantitative trait, which means that is inhibited by poly genes and has a complex inheritance. Since cotton originates from areas that are often exposed to drought stress, considerable genetic variability in water stress tolerance exists (Saranga *et al*., 1998; Pettigrew and Meredith, 1994). Past research focused on physiological traits such as photosynthesis (Jones *et al*., 1999; Nepomuceno *et al*., 1998; Leidi *et al*., 1993), plant turgor maintenance (Quisenberry *et al*., 1982), water use efficiency (Saranga *et al.*, 1999; Quisenberry and McMicheal, 1991), biomass accumulation (Hatfield *et al*., 1987; Quisenberry *et al.*, 1981) , root growth and root-shoot ratio (McMichael and Quisenberry, 1991; Cook, 1985; Quisenberry *et al*., 1981), cell membrane stability (Rahman *et al*., 2008) and fruiting pattern (Lopez *et al*., 1995; Sharp and Davies, 1989; Burke *et al*., 1985a). However, none of the above physiochemical traits has so far been correlated positively and continuously with drought tolerance. Molecular studies have also been conducted for identification of quantitative trait loci (QTLs) accountable for enhance cotton production under drought conditions (Saranga *et al*., 2008, 2004) while use of genetic engineering and transgenic plants has been shown to result in supportive correlations (Parkhi *et al*., 2009; Lv *et al*., 2007). Healthy plant seedlings have a significant role in crop yield

performance, but drought stress unswervingly reduces the growth of plants by affecting their normal growth at early seedling stages (Dugasa *et al*., 2019). A significant reduction in plant total biomass (PTDW), including other morphological traits was observed under the DS condition, which indicates the reduction in nutrient uptake from the soil due to the low water potential of soil under osmotic stress. Meanwhile, less water and nutrient uptake affect plant membrane stability and permeability (van Bavel, 1996). Such nutrition imbalances forced the plant to stunt its normal growth by enhancing the nutrient uses compared to nutrient uptake and energy resources, which causes a reduction in the plant total biomass (Hu *et al*., 2006). In the results, a severe decline in plant biomass, cell membrane stability, including various morpho-physiological traits, was observed under DS conditions, which was also consistent with the results of Hassan *et al*. (2015).

# CHAPTER III
# MATERIALS AND METHODS

This chapter illustrates information concerning materials and methods those were used in conduct of the experiments. The experiments were executed in four years for drought stress at 2017-2020. The experiments for drought stress were then executed into three segments viz., morphological study of cotton genotypes against drought at early flowering stage, physiological and biochemical study of cotton genotypes against drought at early flowering stage and selection of drought tolerant cotton genotypes in AEZ of Barind tract. The different steps of drought experiments are stated here chronologically in section III.

## 3.1 Experiment 1. Morphological study of cotton genotypes for drought tolerance at early flowering stage

The effect of drought stress on different genotypes of cotton was studied based on agromorphogeneic traits. The agromorphogenic traits included days to germination, number of germinations, root length, shoot length, shoot-root length ratio, root diameter, total biomass of root, number of lateral root, number of vegetative branches and number of fruiting branches.

### 3.1.1 Experimental site

The experiment was conducted in a polythene screen house in front of Kazi Nazrul Islam Hall and near the net house of the department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207 during the periods from April to June in the years of 2017. Location of the site is 23°74' N latitude and 90°35' E longitude with an elevation of 8 meter from sea level in Agro-ecological zone of "Madhupur Tract" (AEZ-28) (Quddus, 2009). The experimental site is shown in Appendix I.

### 3.1.2 Planting materials

A total number of fifty genotypes of upland cotton were used in this study (Table 2). All upland cotton genotypes were collected from Cotton Research Centre, Cotton Development Board (CDB), Mahigonj, Rangpur, Bangladesh.

**Table 2. Name and source of collection of fifty upland cotton genotypes used in the study**

| Sl. No. | Genotypes No. | Materials used | Source of collection |
|---|---|---|---|
| 1 | $G_1$ | CB-1 | Gene Bank, Cotton Research Centre, Cotton Development Board, Mahigonj, Rangpur |
| 2 | $G_2$ | CB-2 | |
| 3 | $G_3$ | CB-3 | |
| 4 | $G_4$ | CB-4 | |
| 5 | $G_5$ | CB-5 | |
| 6 | $G_6$ | CB-6 | |
| 7 | $G_7$ | CB-7 | |
| 8 | $G_8$ | CB-8 | |
| 9 | $G_9$ | CB-9 | |
| 10 | $G_{10}$ | CB-10 | |
| 11 | $G_{11}$ | CB-11 | |
| 12 | $G_{12}$ | CB-12 | |
| 13 | $G_{13}$ | CB-13 | |
| 14 | $G_{14}$ | CB-14 | |
| 15 | $G_{15}$ | CB-15 | |
| 16 | $G_{16}$ | Ra-2 | |
| 17 | $G_{17}$ | Ra-3 | |
| 18 | $G_{18}$ | Ra-4 | |
| 19 | $G_{19}$ | Ra-5 | |
| 20 | $G_{20}$ | Ra-9 | |
| 21 | $G_{21}$ | Ra-15 | |
| 22 | $G_{22}$ | Ra-16 | |
| 23 | $G_{23}$ | JA-08/9 | |
| 24 | $G_{24}$ | JA-11/M | |
| 25 | $G_{25}$ | JA-10/55 | |
| 26 | $G_{26}$ | JA-08/B | |
| 27 | $G_{27}$ | JA-11/L | |
| 28 | $G_{28}$ | JA-09/H | |
| 29 | $G_{29}$ | JA-13/R | |
| 30 | $G_{30}$ | SR-15 | |
| 31 | $G_{31}$ | SR-16 | |
| 32 | $G_{32}$ | SR-17 | |
| 33 | $G_{33}$ | BC-272 | |
| 34 | $G_{34}$ | BC-385 | |
| 35 | $G_{35}$ | BC-394 | |
| 36 | $G_{36}$ | BC-397 | |
| 37 | $G_{37}$ | BC-410 | |
| 38 | $G_{38}$ | BC-413 | |
| 39 | $G_{39}$ | BC-415 | |
| 40 | $G_{40}$ | BC-419 | |
| 41 | $G_{41}$ | BC-423 | |
| 42 | $G_{42}$ | BC-430 | |
| 43 | $G_{43}$ | BC-433 | |
| 44 | $G_{44}$ | BC-435 | |
| 45 | $G_{45}$ | BC-442 | |
| 46 | $G_{46}$ | BC-462 | |
| 47 | $G_{47}$ | BC-509 | |
| 48 | $G_{48}$ | BC-510 | |
| 49 | $G_{49}$ | BC-511 | |
| 50 | $G_{50}$ | BC-512 | |

### 3.1.3 Treatments in the experiment

The two factorial experiment was studied to evaluate the performance of fifty upland cotton genotypes under different water stress treatments. Factor A was cotton genotypes where fifty cotton genotypes were used. Factor B was different water stress (drought) treatments. Water stress treatments were employed by witholding of water after thirty two days of seed sowing in the plastic pot. Four treatments were, $T_1$ (0 days witholding of water/Control), $T_2$ (watering after 7 days interval), $T_3$ (watering after 14 days interval) and $T_4$ (watering after 21 days interval).

### 3.1.4 Design and layout of the experiment

The experiment was expended and evaluated during Kharif season in Completely Randomized Design (CRD) using two factors. Factor A included 50 genotypes and Factor B included 4 drought treatments with 3 replications.

### 3.1.5 Climate and soil

Experimental site was in the subtropical climatic zone, set aparted by sufficient of sunshine, rainy and high temperature prevails during April to May (Kharif season) which is suitable for cotton growing in Bangladesh.

### 3.1.6 Manure and fertilizers application

Soil was well pulverized and dried in the sun and only well decomposed cow dung was mixed with the loamy soil according to the Fertilizer Recommendation Guide, BARC, 2012. Well decomposed soil was calculated for each pot considering the dose of 1 hectare soil. On an average each plastic pot was filled with soil containing 100 g decomposed cow dung (10 tons/hectare). Total decomposed cow dung was applied before sowing the cotton seed to plastic pots.

### 3.1.7 Pot preparation and sowing of cotton seed

Weeds and stubbles were completely removed from soil which was used for sowing. Pots were filled up two days before sowing. Each pot was filled with 7 kg of soil. The pot size was 20 cm in height, 30 cm in top diameter and 20 cm in bottom diameter. Three pores were made in each plastic pot that excess water could easily drain out. The sowing was carried out on April in the plastic pot. Before sowing, seeds were

treated with Imitaf for 30 minutes. Five seeds were sown at 4 to 5 cm depth in each pot by dibbling method. Thinning was performed after 10 and 20 days of seed sowing. Seed sowing of all genotypes were raised in 600 pots in front of Kazi Nazrul Islam residential student Hall of the out side of the net house of Genetics and Plant Breeding Department, Sher-e-Bangla Agricultural University, Dhaka-1207. Seedlings were raised using regular nursery practices of the poly house. Recommended cultural practices were taken up before and after sowing the seeds.

### 3.1.8 Application of drought treatments

Fifty upland cotton genotypes were studied under different drought treatments (T1- Control condition or 0 Days withholding of water; T2- watering after 7 days interval, T3- watering after 14 days interval and T4- watering after 21 days interval. Water stress treatments were employed by witholding of water after thirty two days of seed sowing in the plastic pots. Plants in control treatments (T1) were not exposed to drought, whereas plants in T2, T3 and T4 treatments were exposed to drought for 74 days. Plants in control treatments (T1) were always irrigated with fresh water. T2, T3 and T4 drought treatments were employed on plants in the plastic pots 7, 14 and 21 days, respectivly after 32 days of seed sowing in the pots. The four treatments condition of cotton plants in the poly house are shown in Plate 2(A-C).

### 3.1.9 Intercultural operations

Necessary watering and intercultural operations were provided as and when required. Weeding was performed in all pots as and when required to keep plants free from weeds. Aphid, Jassid and Spotted Bollwarm were the main insects of cotton crops. Experimental cotton seeds were treated with Imitaf and Ripcord to prevent unwanted insects' problem @ 2 ml/l. The insecticides were sprayed twice, first at vegetative growth stage and next to early flowering stage to manage insects. When plants were well established, stalking was done by bamboo stick between 30-35 DAS to keep the plants erect. Proper tagging and labeling were done for each plant.

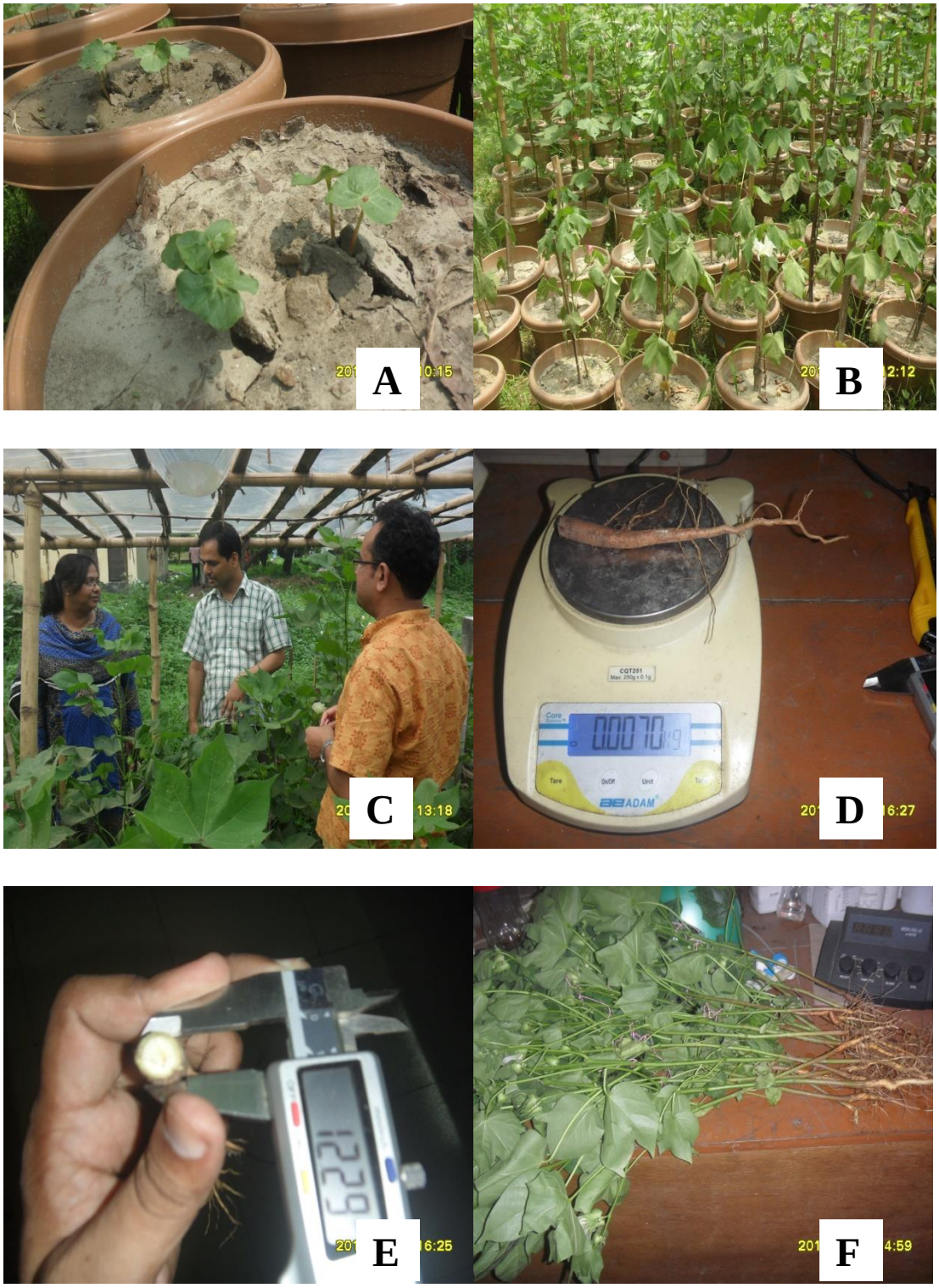



**Plate 2. Drought treatment in the poly house and data recording. A. Establishes seedling. B. drought stress given to the cotton plants at early flowering stage in the pot, C. Chairman and Member of Advisory committee were visited the experiment plot, D-F. Data collection**

### 3.1.10 Sample collection and processing

Cotton plant with root was upholding from pot for evaluating morphological traits against drought. Samples were collected for each treatment for data collection.

### 3.1.11 Data recording

Data were recorded from each pot based on different agromorphological traits. A view of data collection in the laboratory is presented in Plate 2(D-F). Data were recorded in respect of the days to germination, number of germinations, root length, shoot length, shoot-root length ratio, root diameter, total biomass of root, number of lateral roots, number of vegetative branch, number of fruiting branch, days to first square initiation and days to first flowering.

#### 3.1.11.1 Days to germination

The number of days to first germination was counted from the date of cotton seed germinating to date of seed sowing.

#### 3.1.11.2 Number of germinating seed

The number of germinating seed was counted after seven days from the date of seed sowing.

#### 3.1.11.3 Shoot length

Shoot length of each plant at early flowering stage measured in cm using meter scale and replicated mean was calculated.

#### 3.1.11.4 Root length

At end of the early flowering stage, plants were uprooted from soil and root length of each plant was measured in cm using meter scale and replicated mean was calculated.

#### 3.1.11.5 Shoot/Root length ratio

At end of the early flowering stage, plants were uprooted from soil and the shoot and root length of each plant was measured using meter scale and ratio was calculated.

#### 3.1.11.6 Number of lateral roots

At end of the early flowering stage, plants were uprooted from soil and the count of number of lateral root and replicated mean was calculated.

#### 3.1.11.7 Total biomass of root

At end of the early flowering stage, plants were uprooted from soil and measured using electric balance in gm and replicated mean was calculated.

#### 3.1.11.8 Root diameter

At end of the early flowering stage, plants were uprooted from soil and the root diameter of each plant was measured using Digital Caliper-515 (DC-515) in millimeter (mm) and replicated mean was calculated.

#### 3.1.11.9 Number of vegetative branches

At end of the early flowering stage, the vegetative branches were counted and replicated mean was calculated.

#### 3.1.11.10 Number of fruiting branches

At end of the early flowering stage, the fruiting branches were counted and replicated mean was calculated.

#### 3.1.11.11 Days to first flowering

The number of days to first flowering was counted from the date of cotton seeds were sowing to date of first flowering.

### 3.1.12 Statistical analysis

Analysis of variance (ANOVA) was calculated to determine the significant effect of genotype, treatment, and interaction at both 1% and 5% level of significance. To provide the basic information of variables, descriptive statisctics was performed. Mean value of genotypes, treatment and their interaction were calculated for each of the variables. ANOVA and mean values were calculated using stats, ggplot2 and tidyverse in R software (version 4.2).

### 3.1.12.1 Estimation of reduction (%)

% Reduction of each trait of each genotype under four drought stress were calculated using the following formula:

$$\% \text{ Reduction} = \frac{\text{value at control condition} - \text{value at stress condition}}{\text{value at control condition}} \times 100$$

Genotypic reduction at each drought treatments for eight traits has been visualized using the ggplot2 and tidyverse packages in R program (version 4.2).

### 3.1.12.2 Estimation of regression coefficient

Regression coeeficient for each character was calculated using the mean values of different treatments for each genotype of this experiment taking the genotypic effect on the dependent and treatment effect as independent variables following the method as cited by Zaman *et al*., 1982. The formula used as follow:

$$b_{yx} = \frac{\Sigma xy - \frac{(\Sigma x)(\Sigma y)}{n}}{\Sigma x2 - (\Sigma xy)2}$$

Where,

b= regression coefficient

x= values of independent variable (drought dose)

y= values of dependent variable (geotypic mean)

n=total number of observations

Regression coefficient was calculated using the lme4 packages in R (version 4.2).

### 3.1.12.3 Ranking of the genotypes for each character

Ranking of each genotype for each character was done based on the regression coefficient value.

### 3.1.12.4 Estimation of drought response index (DRI)

DRI value represents the relative changes of each trait caused by drought stress. The DRI value was calculated from the observed phenotypic value of each trait using the following formula (Ashraf and Waheed, 1990).

$$\text{Drought response index (DRI)} = \frac{\text{value from drought treatment}}{\text{value from control}} \times 100$$

### 3.1.12.5 Drought tolerant grouping scale

All the genotypes in this study were classified as tolerant, moderately tolerant, moederately susceptible and susceptible based on their DRI valuses for eight drought reposne characters.

**Table 3. Drought tolerant grouping scale**

| Sl No. | Scale | % DRI values | Drought tolerant group |
|---|---|---|---|
| **1** | I | >90 | Tolerant |
| **2** | II | 80-90 | Moderately tolerant |
| **3** | III | 70-80 | Moderately susceptible |
| **4** | IV | <70 | Susceptible |

### 3.1.12.6 Estimation of genetic parameters

Genetic parameters including the variability, heritability, genotypic and phenotypic correlation, path coefficient was calculated in R using the variability packages in R software (version 4.2).

#### 3.1.12.6.1 Estimation of genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficient of variation was calculated by the formula suggested by Burton (1952)

Genotypic co-efficient of variation, GCV (%) = $\frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$

Where,

$\sigma^2_g$ = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

The phenotypic co-efficient of variation was calculated from the following formula.

Phenotypic co-efficient variation, PCV (%) = $\frac{\sqrt{\sigma^2 ph}}{\bar{x}} \times 100$

Where,

$\sigma^2_{ph}$= Phenotypic variance

$\bar{x}$ = Population mean

**3.1.12.6.2 Estimation of heritability**

Broad-sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

Heritability, $h^2_b$ (%) = $\frac{\sigma^2 g}{\sigma^2 ph} \times 100$

Where,

$h^2_b$ = Heritability in broad sense

$\sigma^2_g$ = Genotypic variance

$\sigma^2_{ph}$ = Phenotypic variance

**3.1.12.6.3 Estimation of genetic advance**

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance, GA = K. $h^2$. $\sigma_p$

Or Genetic advance, GA = K. $\frac{\sigma^2 g}{\sigma^2 ph} . \sigma_{ph}$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

$\sigma_{ph}$ = Phenotypic standard deviation

$h^2_b$= Heritability in broad sense

$\sigma^2_g$ = Genotypic variance

$\sigma^2_{ph}$ = Phenotypic variance

**3.1.12.6.4 Estimation of genetic advance mean's percentage**

Genetic advance as a percentage of the mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance (GA)}}{\text{Population mean } (\bar{x})} \times 100$$

**3.1.12.6.5 Estimation of simple correlation coefficient**

Simple correlation coefficients (r) was estimated with the following formula (Singh and Chaudhary, 1985).

$$r = \frac{\sum xy - \frac{\sum x . \sum y}{N}}{\sqrt{[\{\sum x2 - \frac{(\sum x)2}{N}\}\{\sum y2 - \frac{(\sum y)2}{N}\}]}}$$

Where,

$\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

**3.1.12.6.6 Estimation of genotypic and phenotypic correlation coefficient**

For calculating the genotypic and phenotypic correlation coefficient for all possible combinations the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The covariance components were

used to compute the genotypic and phenotypic correlation between the pairs of characters as follows:

Genotypic correlation, $r_{gxy} = \frac{GCOVxy}{\sqrt{GVx.GVy}} =$

Where,

$\sigma_{gxy}$ = Genotypic co-variance between the traits x and y

$\sigma^2_{gx}$ = Genotypic variance of the trait x

$\sigma^2_{gy}$ = Genotypic variance of the trait y

Phenotypic correlation ($r_{pxy}$) = $\frac{PCOVxy}{\sqrt{PVx.PVy}} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px}.\sigma^2_{pv})}}$

Where,

$\sigma_{pxy}$ = Phenotypic covariance between the trait x and y

$\sigma^2_{px}$ = Phenotypic variance of the trait x

$\sigma^2_{py}$ = Phenotypic variance of the trait y

Pearson correlation coefficient was analysed and visualized using the corrplot and Rcolorbrewer packages in R software (version 4.2).

**3.1.12.6.7 Estimation of path co-efficient**

It was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using phenotypic correlation coefficient values. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects on yield per hectare. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3….and 7 on number of reproductive branches y, a set of simultaneous equations (twelve equations in this example) is required to be formulated as shown below:

$r_{1.y} = P_{1.y} + r_{1.2} P_{2.y} + r_{1.3} P_{3.y} + r_{1.4} P_{4.y} + r_{1.5} P_{5.y} + r_{1.6} P_{6.y} + r_{1.7} P_{7.y}$

$r_{2.y} = r_{1.2} P_{1.y} + P_{2.y} + r_{2.3} P_{3.y} + r_{2.4} P_{4.y} + r_{2.5} P_{5.y} + r_{2.6} P_{6.y} + r_{2.7} P_{7.y}$

$r_{3.y} = r_{1.3} P_{1.y} + r_{2.3} P_{2.y} + P_{3.y} + r_{3.4} P_{4.y} + r_{3.5} P_{5.y} + r_{3.6} P_{6.y} + r_{3.7} P_{7.y}$

$r_{4.y} = r_{1.4} P_{1.y} + r_{2.4} P_{2.y} + r_{3.4} P_{3.y} + P_{4.y} + r4_{1.5} P_{5.y} + r_{4.6} P_{6.y} + r_{4.7} P_{7.y}$

$r_{5.y} = r_{1.5} P_{1.y} + r_{2.5} P_{2.y} + r_{3.5} P_{3.y} + r_{4.5} P_{4.y} + P_{5.y} + r_{5.6} P_{6.y} + r_{5.7} P_{7.y}$

$r_{6.y} = r_{1.6} P_{1.y} + r_{2.6} P_{2.y} + r_{3.6} P_{3.y} + r_{4.6} P_{4.y} + r_{5.6} P_{5.y} + P_{6.y} + r_{6.7} P_{7.y}$

$r_{7.y} = r_{1.7} P1.y + r_{2.7} P_{2.y} + r_{3.7} P_{3.y} + r_{4.7} P_{4.y} + r_{5.7} P_{5.y} + r_{6.7} P_{6.y} + P_{7.y}$

Where,

$r_{1y}$ = Genotypic correlation coefficients between y and I th character (y = No. of reproductive branches)

$P_{iy}$ = Path coefficient due to i th character (i= 1, 2, 3,….7)

1 = Root length

2 = Shoot length

3 = Shoot root length ratio

4 = Root diameter

5 = Total biomass of root

6 = No. of lateral roots

7 = No. of vegetative branches.

Total correlation, say between 1 and y i. e., $r_{1y}$ is thus partitioned as follows:

$P_{1.y}$ = the direct effect of 1 on y

$r_{1.2} P_{2.y}$ = indirect effect of 1 via 2 on y

$r_{1.3} P_{3.y}$ = indirect effect of 1 via 3 on y

$r_{1.4} P_{4.y}$ = indirect effect of 1 via 4 on y

$r_{1.5} P_{5.y}$ = indirect effect of 1 via 5 on y

$r_{1.6} P_{6.y}$ = indirect effect of 1 via 6 on y

$r_{1.7} P_{7.y}$ = indirect effect of 1 via 7 on y

Where,

$P_{1.y,}$ $P_{2.y,}$ $P_{3.y.}$ …… $P_{7.y}$ = Path coefficient of the independent variables 1, 2, 3,….,7 on the dependent variable y, respectively.

$r_{1.y}, r_{2.y}, r_{3.y}, \ldots, r_{7y}$ = Correlation coefficient of 1, 2, 3,…., 7 with y, respectively.

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula (Singh and Chaudhary, 1985) given below

$P^2_{RY} = 1- (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} + \ldots\ldots\ldots\ldots\ldots + r_{7.y}P_{7.y})$

Where,

$P^2_{RY} = R^2$

and hence residual effect, $R = (P^2_{RY})^{1/2}$

$P_{1.y}$ = Direct effect of the i th character on No. of reproductive branches y.

$r_{1.y}$ = Correlation of the i th character with No. of reproductive branches y.

### 3.1.12.7 Principal Component Analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. The contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

Principal component analysis was carried out in R software (version 4.2) using the Factoextra, prcomp and FactoMineR packages. Components with their eigen value and explained variances were calculated. Variables with their individual contributions in PC1 and PC2 has been presented. Biplot was prepared to find out the similiraites and dissimilirities among genotypes and treatments.

### 3.1.12.8 Hierarchical K means clustering analysis

Dendogram for fity genotypes was prepared based on their overall performance in term of eight agromorphogenic traits. Dendogram revaled the cluster presence among the genotypes. Hierarchical clustering was prepared using the factoextra and biotools packages in R (version 4.2).

### 3.1.12.9 Intra and inter cluster distance analysis

Based on the K means hierarchical clustering, intra and inter cluster distance was calculated using the biotools packages in R (version 4.2).

### 3.1.12.10 Cluster mean analysis

Mean value of each character were estimated for each of the cluster using FactomineR and Factoextra package in R software.

### 3.1.12.11 Selection Index

A selection index is an efficient method of plant selection for yiled and quality based on the components traits that go to make up the crop yield and their relationship between traits and yield. This forms the basis for information of selection index that serves to assess the importance or efficiency in selection for yield and quality in crop plants and it seems as a basis of superiror genotypes. Selections indices involve decriminate function based on the relative economic importance of the various characters. Discriminate functions were by R software using select. Index packages in R software. Selection indices were constructed yielding the methods developed by Smith (1936) based on the discernment function. Methodology was followed as per the book of Singh and Choudhury (1985).

Selection index has been worked out as, suggested by Smith (1936).

Selection index (SI) = $b_1p_1$+ $b_2p_2$ +…….+ $b_np_n$

Where,

$b_1$, b2, $b_3$…..$b_n$ are the vectors of selection coefficient

$p_1$, $p_2$, $p_3$…..$p_n$ are the phenotypic performance of various characters of experiment-1

By using this function, the index value of each 50 genotypes was computed and ranked. Highest drought tolerant genotypes were selected on the basis on their performance over the respective mean values.

## 3.2 Experiment 2. Physiochemical study of cotton genotypes against drought at early flowering stage

The effect of drought stress on different genotypes of cotton was studied based on Physioligical and biochemical traits. The physiochemical traits included soil moisture content, relative water content (RWC), water saturation deficit (WSD), water retension capacity (WRC), water uptake capacity (WUC), Proline content, total chlorophyll content, nitrogen content, membrane stability index (MSI) and pollen grain content (% of pollen viability).

### 3.2.1 Experimental site

The experiment was conducted in rooftop net house of the department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207 during the periods from September to November in the years of 2018. Location of the site was 23°74' N latitude and 90°35' E longitude with an elevation of 8 meter from sea level in Agro-ecological zone of "Madhupur Tract" (AEZ-28) (Quddus, 2009). The experimental site is shown in Appendix I.

### 3.2.2 Planting materials

A total number of fifty upland cotton were used in this study (Table 1). All upland cotton genotypes were collected from Cotton Research Centre, Cotton Development Board (CDB), Mahigonj, Rangpur, Bangladesh.

### 3.2.3 Treatments in the experiment

The two factorial experiment was studied to evaluate the performance of fifty upland cotton genotypes under different water stress treatments . Factor A was cotton genotypes where fifty cotton genotypes were used. Factor B was different water stress (drought) treatments. Water stress treatments were employed by witholding of water after thirty two days of seed sowing in the plastic pot. Four treatments were, $T_1$ (0 days witholding of water/Control) , $T_2$ (watering after 7 days interval), $T_3$ (watering after 14 days interval) and $T_4$ (watering after 21 days interval).

### 3.2.4 Design and layout of the experiment

The experiment was expended and evaluated during Kharif season in Completely Randomized Design (CRD) using two factors. Factor A included 50 genotypes and Factor B included 4 drought treatments with 3 replications.

### 3.2.5 Climate and soil

Experimental site was located in the subtropical climatic zone, set aparted by sufficient of sunshine, rainy and medium high temperature prevails during September to November (Kharif season) which is suitable for cotton growing in Bangladesh.

### 3.2.6 Manure and fertilizers application

Soil was well pulverized and dried in the sun and only well decomposed cow dung was mixed with the loamy soil according to the Fertilizer Recommendation Guide, BARC, 2012. Well decomposed soil was calculated for each pot considering the dose of 1 hectare soil. On an average each plastic pot was filled with soil containing 100 g decomposed cow dung (10 tons/hectare). Total decomposed cow dung was applied before sowing the cotton seed to plastic pots.

### 3.2.7 Pot preparation and sowing of cotton seeds

Weeds and stubbles were completely removed from soil which was used for sowing. Pots were filled up two days before sowing. Each pot was filled with 7 kg of soil. The pot size was 20 cm in height, 30 cm in top diameter and 20 cm in bottom diameter. Three pores were made in each plastic pot that excess water could easily drain out. The sowing was carried out on September 2018 in the plastic pot. Before sowing, seeds were treated with Imitaf for 30 minutes. Five seeds were sown at 4 to 5 cm depth in each pot by dibbling method. Thinning was performed after 10 and 20 days of seed sowing. Seed sowing of all genotypes were raised in 600 pots in the rooftop of the net house of Genetics and Plant Breeding Department, Sher-e-Bangla Agricultural University, Dhaka-1207. Seedlings were raised using regular nursery practices of the poly house. Recommended cultural practices were taken up before and after sowing the seeds.

### 3.2.8 Application of drought treatments

Fifty upland cotton genotypes were studied under different drought treatments (T1- Control condition or 0 Days withholding of water; T2- watering after 7 days interval, T3- watering after 14 days interval and T4- watering after 21 days interval. Water stress treatments were employed by witholding of water after thirty two days of seed sowing in the plastic pots. Plants in control treatments (T1) were not exposed to drought; whereas plants in T2, T3 and T4 treatments were exposed to drought for 74 days. Plants in control treatments (T1) were always irrigated with fresh water. T2, T3 and T4 drought treatments were employed on plants in the plastic pots 7, 14 and 21 days respectively after 32 days of seed sowing in the pots. The four treatments condition of cotton plants in the net house are shown in Plate 3(A-B).

### 3.2.9 Intercultural operations

Necessary watering, weeding and other intercultural operations were provided as and when required. Experimental cotton seeds were treated with Imitaf @ 2 ml/l to reduce the infestation of Aphid, Jassid and Spotted Bollwarm. It was spread twice, first at vegetative growth stage and next to early flowering stage to manage insects. When plants were well established, stalking was done by bamboo stick between 30-35 DAS to keep the plants erect. Proper tagging and labeling were done for each plant.

### 3.2.10 Sample collection and processing

Cotton leaves, flowers, plants with root were upholding from pot for evaluating physiological and biochemical traits against drought. Samples were collected for each treatment for data collection.

### 3.2.11 Data recording

Data were recorded from each pot based on different physiological and biochemical traits *viz*., Soil Moisture Content (SMC), water content (RWC), water saturation deficit (WSD), water retension capacity (WRC), water uptake capacity (WUC), Proline content, Chlorophyll-a content, chlorophyll-b content, total chlorophyll content, nitrogen content, membrane stability index (MSI) and pollen grain content (% of pollen viability. A view of data collection in the laboratory is presented in Plate 3(C-F) and 4(A-F).


**Plate 3. Drought treatment in the net house and data recording. A. Cotton seed sowing in the pots. B. Member of Advisory committee were visited the experiment plot. C-F. drought stress given to the cotton plants at early flowering stage in the pot and data collection**


**Plate 4. Drought treatment in the net house and data recording. A-D. Measuring different biochemical test E. Collecting anther for measuring pollen viability. F. Chairman of the Advisory committee was observed pollen viability test**

### 3.2.11.1 Determination of Soil Moisture Content (SMC)

Soil moisture content was measured by using Tentiometer. The soil moisture content was measured from soil stressed at different drought treatments from the pot soil and then averaged for analysis. Measuring of soil moisture content by Tentiometer is shown in Plate 4D. From the Tentiometer reading obtained from experimental pot soil, the respective soil moisture content was estimated by standard curve of soil moisture was used for calibration.

#### 3.2.11.1.1 Preparation of soil moisture standard curve

Consider a sample of moist soil within a glasswear such as a petridish. The weight of the moist soil consists of the weight of the dry soil particles plus the weight of the water within the soil. When expressing the results of an experiment such as the nutrient content of a soil, use of the dry weight basis provides standardization of the final result. Weigh both of the petridishes. Aliquot approximately 50 g of moist soil into each petridish and reweigh the petridishes. Hence, the moist weight of the soil sample is now known. Dry the soil of 72 hours at 60°C in the oven. Remove the petridishes from the oven and allow them to cool. Reweigh the petridishes plus the oven dry soil. Now the weight of the dry soil is known. Calculate the moisture content of the soil by using following formula:

$$\text{Soil moisture } (\%) = \frac{\text{weight of moist soil} - \text{weight of oven dried soil}}{\text{weight of oven dried soil}} \text{x } 100$$

By plotting the tension (centibar) in 'X' axis and obtained soil moisture (%) reading in 'Y' axis a standard curve was prepared. From the moisture reading obtained from graph, their respective moisture content was estimated in percentages by using moisture standard curve.

#### 3.2.11.1.2 Determination of relative water content

The relative water content (RWC) was estimated according to Barrs and Weatherly (1962). The fresh weight of the whole plant was recorded. The plant was floated in water under night until the weight stayed constant to attain full turgid and turgid weight was recorded. Then the plant was kept in hot air oven at 60°C for 72 hours and

the dry weight was recorded. The relative water content (RWC) was calculated by using following formula,

$$\text{Relative water content (\%)} = \frac{\text{Fresh weight} - \text{Dry weight}}{\text{Turgid weight} - \text{Dry weight}} \text{ x } 100$$

**3.2.11.2 Water Saturation Deficit**

The relative water content (RWC) was estimated according to Barrs and Weatherly (1962). The fresh weight of the whole plant was recorded. The plant was floated in water under night until the weight stayed constant to attain full turgid and turgid weight was recorded. Then the plant was kept in hot air oven at 60°C for 72 hours and the dry weight was recorded. The Water Saturation Deficit (WSD) was calculated by using following formula,

$$\text{Water Saturation Deficit (WSD)} = \frac{\text{Turgid weight} - \text{Fresh weight}}{\text{Turgid weight} - \text{Dry weight}} \text{ x } 100$$

**3.2.11.3 Water Retention Capacity (WRC)**

The relative water content (RWC) was estimated according to Barrs and Weatherly (1962). The fresh weight of the whole plant was recorded. The plant was floated in water under night until the weight stayed constant to attain full turgid and turgid weight was recorded. Then the plant was kept in hot air oven at 60°C for 72 hours and the dry weight was recorded. The Water Retention Capacity (WRC) was calculated by using following formula,

$$\text{Water Retention Capacity (WRC)} = \frac{\text{Turgid weight}}{\text{Dry weight}}$$

**3.2.11.4 Water Uptake Capacity (WUC)**

The relative water content (RWC) was estimated according to Barrs and Weatherly (1962). The fresh weight of the whole plant was recorded. The plant was floated in water under night until the weight stayed constant to attain full turgid and turgid weight was recorded. Then the plant was kept in hot air oven at 60°C for 72 hours and the dry weight was recorded. The Water Uptake Capacity (WUC) was calculated by using following formula

$$\text{Water Uptake Capacity (WUC)} = \frac{\text{Turgid weight} - \text{Fresh weight}}{\text{Dry weight}}$$

### 3.2.11.5 Determination of proline content

Proline accumulation was determined by the method as described by Sadasivam and Manickam (1996). Different steps of proline determination are stated below.

#### 3.2.11.5.1 Proline extraction

Fresh cotton leaves (0.5 g) were grinded in mortar and pestle with 10 mL of 3% sulphosalicyclic acid and the homogenate was centrifuged at 18000×g. The homogenate was filtered, and 2 mL of filtrate was added to the 2 mL of glacial acetic acid and 2 mL of acid ninhydrin and test tubes were kept for 1h at 100°C in water bath, followed by ice bath. The reaction mixture was vortexed with 4 mL of toluene. Toluene layer was separated, and absorbance was read at 520 nm. A standard curve of proline was used for calibration.

#### 3.2.11.5.2 Preparation of proline standard curve

80 mg of pure proline was dissolved into 100 mL of distilled water to get 800 ppm proline stock solution for preparing proline standard curve. By diluting this solution, 50 ppm, 100 ppm, 200 ppm, 400 ppm and 800 ppm solution were prepared in 20 mL each. The absorbance was measured with the help of Spectrophotometer at 520 nm. By plotting the concentration of proline (ppm) in 'X' axis and obtained absorbance reading in 'Y' axis a standard curve was prepared . From the absorbance reading obtained from samples, their respective proline content was estimated in ppm by using proline standard curve and converted into micro gram per gram (µg/g) unit using the following formula:

$$\text{Amount of proline}(\mu g/g) = \frac{x}{2} \times \frac{10}{500} \times 1000$$

### 3.2.11.6 Measuring of chlorophyll content

Leaf chlorophyll content was measured by using SPAD-502 plus Portable Chlorophyll meter. The chlorophyll content was measured from leaves stressed at different drought treatments from four different portion of the leaf and then averaged for analysis. Measuring of chlorophyll content by Spad meter is shown in Plate 4C. From the Spad meter reading obtained from cotton leaves, the respectives Chlorophyll-a, chlorophyll-

b and total chlorophyll content were estimated in mg/g by using the following formula:

y=0.0346X – 0.1933 (X= Spad meter reading)

y=0.0115X – 0.0936 (X= Spad meter reading)

Total Chlorophyll= Chlorophyll-a + Chlorophyll-b

### 3.2.11.7 Nitrogen Concentration (%)

Leaf chlorophyll content was measured by using SPAD-502 plus Portable Chlorophyll meter. The chlorophyll content was measured from leaves stressed at different drought treatments from four different portion of the leaf and then averaged for analysis. Measuring of chlorophyll content by Spad meter is shown in Plate 4C. From the Spad meter reading obtained from cotton leaves, the respectives Nitrogen Concentration (%) was estimated in mg/g by using the following formula:

y= 0.0396X – 0.0747 (X= Spad meter reading)

### 3.2.11.8 Determination Membrane Stability Index (MSI)

Membrane stability index (MSI) was measured from fully expanded fresh leaves that were plucked at least after four weeks of 50 cotton genotypes into fresh or normal irrigated and drought soil. After plucking the fresh leaves from five plants within each treatment, leaves were washed using distilled water and dried with tissue paper separately. Then 2 g of leaf sample of each treatment within each replication was placed in a test tube containing 10 ml of distilled water. These test tubes were placed in a water bath for 30 min having 40°C temperature. After the prescribed time passed test tubes were taken out, cooled at room temperature and electrical conductivity (EC) of water extract within the tubes was determined using HANNA EC meter (Model HI763064, HANNA Instruments,) which considered as $EC_1$. Subsequently, same test tubes were once more placed in a water bath at 100°C. Test tubes were again taken out after 30 min, cooled at room temperature and $EC_2$ of water extract within the tubes was determined. Both $EC_1$ and $EC_2$ were used to determine MSI of each genotype for all levels of drought after following the equation given by Sairam (1994);

$$MSI = (1 - \frac{EC1}{EC2}) \times 100$$

### 3.2.11.9 Determination Pollen grain content (% of pollen viability)

Fresh pollen or mature but undehisced anthers were squashed in 1% acetocarmine on a microscope slide. The pollen was observed under a microscope. All deeply stained pollen grains were considered viable.

Percentage viability of pollen grains by this test was calculated as:

$$\text{Percentage pollen viability} = \frac{\text{No.of viable pollen grains}}{\text{No.of viable pollen grains+No.of non-viable pollen grains}} \text{ x } 100$$

### 3.2.12 Statistical analysis

Statistical analyses were carried out as summarized in the section of 3.1.12.

## 3.3 Experiment 3. Selection of drought tolerant cotton genotypes in AEZ of Barind tract

### 3.3.1 Experimental site

The experiment was conducted in Udpur village, Mouja-Baje udpur, Bosontopur union of Godagari upazila in a translucent polythene screen house under Rajshahi district in the division of Rajshahi, Bangladesh during the period from July 2019 to March 2020. Location of the site in between 24° 41' and 24°48' north latitudes and in between 88° 42' and 89°28' east longitudes (Google GPS mobile tracking) in Agro-ecological zone of "High Barind Tract" (AEZ-26) (Quddus, 2009). The experimental site is shown in the map of AEZ of Bangladesh in (Appendix I).

### 3.3.2 Planting materials

25 (twenty-five) genotypes of upland cotton seeds were taken based on the previous experiments. The source of collection of these genotypes was gene bank of Cotton Research Centre, Cotton Development Board (CDB), Mahigonj, Rangpur where 19 (Nineteen) of them were lines and 6 (Six) varieties (Table 4)

**Table 4. Name and source of collection of twenty-five upland cotton genotypes used in the study**

| Sl. No. | Genotypes No. | Materials used | Source of collection |
|---|---|---|---|
| 01 | G1 | CB-1 | Gene bank of Cotton Research Centre, Cotton Development Board (CDB), Mahigonj, Rangpur |
| 02 | G2 | CB-2 | |
| 03 | G8 | CB-8 | |
| 04 | G10 | CB-10 | |
| 05 | G11 | CB-11 | |
| 06 | G12 | CB-12 | |
| 07 | G13 | CB-13 | |
| 08 | G14 | CB-14 | |
| 09 | G15 | CB-15 | |
| 10 | G17 | Ra-3 | |
| 11 | G18 | Ra-4 | |
| 12 | G22 | Ra-16 | |
| 13 | G23 | JA-08/9 | |
| 14 | G29 | JA-13/R | |
| 15 | G30 | SR-15 | |
| 16 | G33 | BC-0272 | |
| 17 | G34 | BC-0385 | |
| 18 | G35 | BC-0394 | |
| 19 | G38 | BC-0413 | |
| 20 | G39 | BC-0415 | |
| 21 | G43 | BC-0433 | |
| 22 | G45 | BC-0442 | |
| 23 | G46 | BC-0462 | |
| 24 | G48 | BC-0510 | |
| 25 | G50 | BC-0512 | |

### 3.3.3 Climate and soil

Experimental site was located in the tropical climates have monthly temperature $9^0$C to $15^0$C in coolest season and $25^0$C to $35^0$C in hottest season of the year and typically a pronounced dry season, with the driest month having precipitation less than 60 mm precipitation. Weather information and physicochemical properties of the soil are described in Appendix II and III. The soil was clay in texture having pH 6.0-6.5.

### 3.3.4 Land preparation

The experimental plots were ploughed and brought into a fine tilth and raised the ridge, applied the recommended dose of fertilizers and farm yard manures (FYM) as Vermi-compost. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. The final land preparation was done on July 8, 2019. Prepared land for sowing is shown in Plate 6A.

### 3.3.5 Design and layout of the experiment

The experiment was laid out and evaluated under field condition during Kharif-2 to Robi 2019 in Randomized Complete Block Design (RCBD). The 25 genotypes were selected acceding to top ranking, 4 cultivars and 2 descending genotypes based on selection scores (Expt-1 and Expt-2). These 25 genotypes were used as a plant material for the next experiments for yield contributing and fibre quality characters (Expt 3) and selection suitable genotypes for Barind tract. The number of treatments was four with three replications. The spacing was 90 cm × 45 cm. The line-to-line distance was 90 cm and plant to plant distance was 45 cm. The plot size was 46 m x 23.4 m (1076.4 $m^2$). The number of seedlings/replication was two and total numbers of seedlings were 600.

### 3.3.6 Seed sowing

The sowing was carried out on July 09, 2019 in the plot. Before sowing, seeds were treated with Imitaf for 30 minutes. Seeds were sown of plant-to-plant distance at 45 cm and row to row distance at 90 cm. Recommended cultural practices were taken up before and after sowing the seeds. When the seedlings become 12 days old, those were first thinning in all treatments. After 20 days old of seedlings, second times

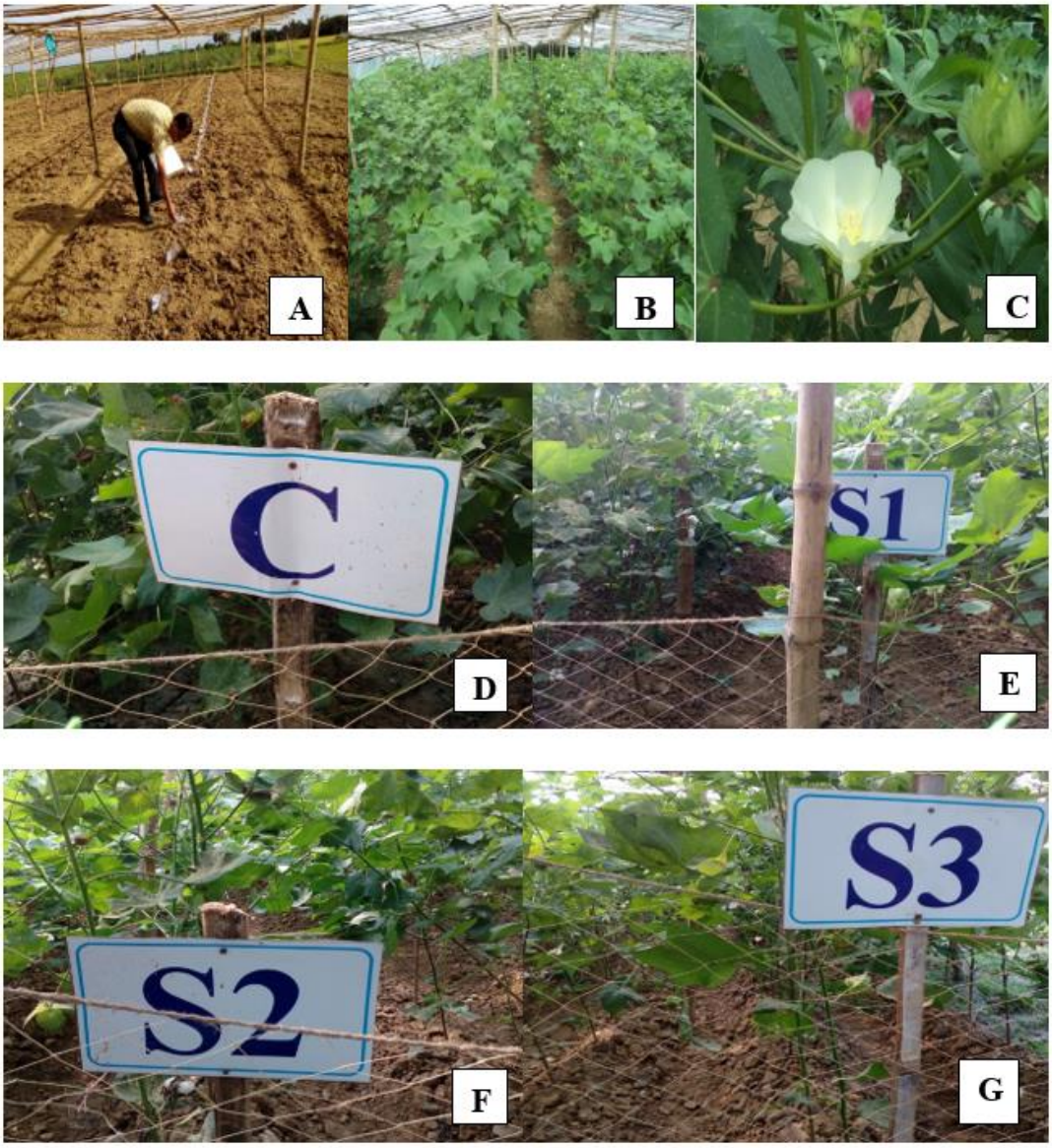



**Plate 5. Different steps of the experiment in Godagari, Rajshahi for the performance against drought stress. A. Cotton seed sowing in the experimental plots. B. Vegetative stage of the cotton. C. Flowering stage of the cotton field. D-G. Measuring different stress treatments of the experiment**

thinning were also done and become established one seedling and are shown in Plate 6B.

### 3.3.7 Manure and fertilizers application

Total Vermi-compost organic manure and half of total Triple Super Phosphate (TSP) were applied in the field during final land preparation.The another chemical fertilizers were applied in the plot after three (21days after seed sowing), six (42 days after seed sowing) and nine (63 days after seed sowing) weeks of transplanting. Remaining Urea, boron and Muriate of Potash (MOP) were applied after 12 weeks of transplanting as foliar spray. Doses of manure and fertilizers used in the study are presented in Table 5.

**Table 5. Doses of manures and fertilizers used in the experimental field**

| Sl. No. | Name of Fertilizers | Amounts of fertilizer (kg) with Dose | | | | Foliar spray (g) | Total amount of fertilizer (kg) |
|---|---|---|---|---|---|---|---|
| | | Basal Dose or 1st dose | 2nd dose | 3rd dose | 4th dose | | |
| 01. | Vermi-compost | 50 | - | - | - | - | 50 |
| 02. | Urea | - | 5 | 6 | 6 | 200 | 17.20 |
| 03. | Triple Super Phosphate (TSP) | 14 | - | 14 | - | 150 | 28.15 |
| 04. | Muriate of Potash (MoP) | - | 8 | 10 | 10 | 150 | 28.15 |
| 05. | Borax | - | 0.5 | 0.5 | - | 150 | 1.15 |
| 06. | Zinc Sulphate | - | 1.0 | - | - | - | 1.0 |
| 07. | Gypsum | - | 5 | 5 | - | - | 10 |
| 08. | Magnesium Sulphate | | 0.5 | 0.5 | - | - | 1.0 |

Source: Fertilizer Recommendation Guide 2012 and Cotton Development Board

### 3.3.8 Application of drought treatments

Twenty-five upland cotton genotypes were studied under different drought treatments (T1- Control condition or 0 Days withholding of water; T2- one irrigation after 40 days of sowing, T3- without irrigation after sowing and T4- two irrigation after 40 and 60 days of seed sowing. Plants in control treatments (T1) were not exposed to drought; whereas plants in T2, T3 and T4 treatments were exposed to drought upto harvesting. Plants in control treatments (T1) were always irrigated with fresh water. T2, T3 and T4 drought treatments were employed on plants in the plots 40, 0, 40 & 60 21 days respectivly after seed sowing in the pots. The four treatments condition of cotton plants in the polythene screen house are shown in Plate 6(A-F).

### 3.3.9 Intercultural operations

When the seedlings were well established, first thinning and gap filling was done after 15 days, and weeding was done uniformly after 20 days in all the plots. Second thinning was done after 21 days, and weeding was done after 21 days of all treatments. After 42 days of seed sowing, the third weeding with earthing up of soil was done of tratments. Aphid, Jassid, Red cotton bug and Spotted Bollwarm were the main insects of cotton crops. Experimental cotton seeds were treated with Imitaf and Volume flexi to prevent unwanted insects' problem @ 2 ml/l. The insecticides were sprayed twice, first at vegetative growth stage and next to early flowering stage to manage insects. Fungicide application, irrigation, removal of old leaves and after-care was also done as per requirement. Raising of seedlings, growth condition of plants, intercultural operation, flowering, and fruiting of cotton plant are shown in Plate 6.

### 3.3.10 Harvesting and processing

All of the cotton genotypes used in this experiment was indeterminate types. So, harvesting continued for about two and half month because cotton boll bursting of different genotypes matured progressively at different dates and harvest seed cotton by three times. The seed cottons were collected and dry on the roof by sun and stored at room temperature for future use. Harvesting was continued from first week of December, 2019 to March, 2020. After seed cotton harvesting, the dried seed cotton was ginned by mini ginning machine of the cotton research, training and seed multiplication farm, sreepur, Gazipur. Seeds of 25 genotypes were dried and store at $4^{o}$C for future use and

lint sent to fibre testing laboratory at Cotton Development Board, khamarbari, Dhaka for the measurement of different fibre characteristics.

### 3.3.11 Data recording

Three plants in each genotype were used for recording observations for the following morphological at field and fibre characters at fibre testing laboratory by High Volume Tester (HVT). Views of data recording are presented Plate 6(B-F).

#### 3.3.11.1 Morphological characteristics

Data recorded on morphological characteristics are stated below.

##### 3.3.11.1.1 Plant height (cm)

The plant height was measured from ground level to tip of the plant expressed in centimeters (cm) and mean was calculated.

##### 3.3.11.1.2 Days to first square initiation

The number of days was counted from the date of sowing to days to first square initiation in four stress treatment.

##### 3.3.11.1.3 Days to first flower initiation

It was counted from the date of sowing to days to first flower initiation.

##### 3.3.11.1.4 Days to first boll split

It was counted from the date of sowing to first boll split in four stress treatment.

##### 3.3.11.1.5 Number of vegetative branches per plant

The number of vegetative branches per plant was recorded at the time of harvesting. Then the average number of vegetative branches was calculated.

##### 3.3.11.1.6 Number of fruiting branches per plant

The number of fruiting branch in each plant was counted. Then the average number of fruiting branch per plant was calculated.


**Plate 6. Different steps of the experiment in Godagari, Rajshahi for the performance against drought stress. A. Experimental plots with Chairman of the advisory committee. B. Fruiting stage with data recording. C. Measurement of moisture by Tensiometer. D. Measurement of light intensity by lux meter. E. Seed cotton drying by the sunshine. F. Ginning of the seed cotton by mini ginning machine at cotton research, training, and seed multiplication farm, Sreepur, Gazipur**

#### 3.3.11.1.7 Number of bolls per plant

Total number of bolls per plant was counted and the average of them was calculated.

#### 3.3.11.1.8 Days to first boll bursting

It was counted from the date of sowing to days to first boll bursting.

#### 3.3.11.1.9 Single boll weight per plant (g)

It was measured in gm at maturity 20 bolls per plant were randomly selected and the average weight was calculated.

#### 3.3.11.1.10 Seed cotton yield (g)

The Seed cotton yield (g) per plant was calculated by using following formula and the average weight was calculated.

Seed cotton yield (g) = Number of bolls per plant x Single boll weight per plant (g)

#### 3.3.11.1.11 Ginning out turn (GOT)

Ginning is the process of separating lint from seed by meachanical means. Ginning out turn was calculated of weight of lint or fibre and weight of seed cotton was measured at lb or gm and GOT was calculated of % using the following formula-

$$\text{Ginning out turn (\%)} = \frac{\text{Weight of lint}}{\text{Weight of seed cotton}} \text{ x } 100$$

#### 3.3.11.1.12 Seed Index (SI)

Weight of 100 seeds per plant were measured and the average weight was calculated. The seed index was calculated by using following formula-

Seed Index = Weight of 100 seeds

#### 3.3.11.1.13 Fiber cotton yield (g)

Yield of fibre or lint per plant was calculated by following formula and the average yield was measured.

$$\text{Fibre cotton yield (g)} = \text{Seed cotton x} \frac{\text{Ginning out turn (GOT)}}{100}$$

#### 3.3.11.1.14 Lint index

Lint index was calculated by following formula and the average lint index was measured.

$$\text{Lint index} = \frac{\text{Weight of lint}}{\text{Weight of seed}} \text{ x Seed index}$$

#### 3.3.11.1.15 Yield per hectare (YPH)

The number of plants/ha was 24690. Yield per hectare (ton) was calculated by using following formula and the average weight was calculated.

$$\text{Yield per hectare (ton)} = \frac{\text{Weight of seed cotton per plant (kg) x 24690}}{1000}$$

### 3.3.11.2 Fibre characteristics

Fiber properties have been studied since the early 1900s, but electronic and physical sciences have been employed in measuring quality parameters only since the 1950s (Chaudhry and Guitchounts, 2003). High Volume Instrument (HVI) was machines for measuring quality characteristics in cotton. The following fibre properties were measured by using HVT machine.

#### 3.3.11.2.1 Fibre length

Cotton fibre length was measured and reported as the upper half mean length (average length of the longest 50% of fibre) to an accuracy of one hundredth of an inch. The following length grouping was used in stating the trade staple:

Average: (25-35 mm)

| Sl. no. | UHML (inch) | UHML (mm) | Cotton description |
|---|---|---|---|
| 01 | < 1.01 | < 25.8 | Short length |
| 02 | 1.02-1.13 | 25.9-28.7 | Medium length |
| 03 | 1.14-1.35 | 29.0-34.3 | Long length |
| 04 | > 1.36 | > 34.5 | Extra long length |

#### 3.3.11.2.2 Uniformity Index

Very weak cottons tend to rupture during processing both in blow room & carding, creating short fibres & consequently deteriorate yarn strength and uniformity. The

uniformity index calculated the ratio of mean length of UHML.The following scale of value was used:

| Sl. no. | Uniformity index (%) | Description of parameter level |
|---|---|---|
| 01 | < 77 | Very low |
| 02 | 77 to 80 | Low |
| 03 | 81 to 84 | Medium |
| 04 | 85 to 87 | High |
| 05 | > 87 | Very high |

**3.3.11.2.3 Short fibre index (SFI)**

The short fiber index is an indication of the percentage of fibers that are shorter than 12.7 mm (half an inch). The short fiber index was measured on the basis of following groups:

| Sl. no. | Short fibre index | Description of parameter level |
|---|---|---|
| 01 | < 6 | Very low |
| 02 | 7 to 9 | Low |
| 03 | 10 to 13 | Medium |
| 04 | 14 to 17 | High |
| 05 | > 18 | Very high |

**3.3.11.2.4 Fibre strength (FS)**

Fibre strength was measured by breaking the fibres held between clamp jaws. It's was calculated as grams per tex, which was the force in grams required to break a bundle of fibres one tex unit in size. A tex unit is equal to the weight in grams of 1000 meters of fibre. The fibre strength was measured based on following groups:

| Sl. no. | Fibre strength (g/tex) | Description of parameter level |
|---|---|---|
| 01 | < 21 | Very weak |
| 02 | 21 to 24 | Weak |
| 03 | 25 to 27 | Medium |
| 04 | 28 to 30 | Strong |
| 05 | > 31 | Very strong |

**3.3.11.2.5 Micronaire (Mic)**

Micronaire was measures a combination of fibre fineness and maturity. Micronaire is indirectly determined according to the airflow principle. A mass of coarse fibres permits more airflow and thus expresses higher micronaire value. Low micronaire values could be an indication of low intrinsic fineness (diameter) or low maturity. The

optimum micronaire value is 3.8-4.3 µg/inch. Micronaire (µg/inch) was calculated on the basis of following groups:

| Sl. no. | Micronaire (µg/inch) | Description of parameter level |
|---|---|---|
| 01 | < 3.0 | Very thin/fine |
| 02 | 3.0 to 3.6 | Thin/Fine |
| 03 | 3.7 to 4.7 | Medium thick/coarse |
| 04 | 4.8 to 5.4 | Thick/Coarse |
| 05 | > 5.5 | Very thick/coarse |

**3.3.11.2.6 Elongation**

Elongation refers to the distance that the fibres extend before they break, and the value was expressed as a percent of the initial sample length. The elongation was measured based on following groups:

| Sl. no. | Elongation (%) | Cotton description |
|---|---|---|
| 01 | < 5.0 | Very small elongation |
| 02 | 5.0 to 5.8 | Small elongation |
| 03 | 5.9 to 6.7 | Medium elongation |
| 04 | 6.8 to 7.6 | Good elongation |
| 05 | > 7.7 | Very good elongation |

**3.3.11.2.7 Maturity ratio (MR)**

The maturity ratio or index indicates the degree of cell wall thickness within a cotton sample. The maturity ratio was measured based on following groups:

| Sl. no. | Maturity ratio | Cotton description |
|---|---|---|
| 01 | < 0.75 | Rarely appear |
| 02 | 0.75 to 0.85 | Immature |
| 03 | 0.86 to 0.95 | Mature |
| 04 | > 0.95 | Very mature |

**3.3.11.2.8 Moisture content/regain**

Moisture is the amount in the tested sample, compared to dry weight, and is, expressed as percent moisture regain. The moisture content was measured based on following groups:

| Sl. no. | Moisture content (%) | Cotton description |
|---|---|---|
| 01 | < 4.5 | Very low |
| 02 | 4.5 to 6.5 | Low |
| 03 | 6.5 to 8.0 | Medium |
| 04 | 8.0 to 10.0 | High |
| 05 | > 10.0 | Very high |

#### 3.3.11.2.9 Reflectance degree (Rd) value

Reflectance expresses the whiteness of the light that is reflected by the cotton fibre. Low Rd levels indicate dullness or greyness while high Rd levels indicate brightness or lack of grey. It expressed in percent (40 to above 80%). The optimum Rd value is above 70%.

#### 3.3.11.2.10 Yellowness (+b) value

The yellowness value is a comparison of the cotton fiber's light reflectance to yellowness. It ranges in 4 to 18.

### 3.3.12 Statistical analysis

Statistical analyses were carried out as described in the section of 3.1.12.

# CHAPTER IV
# RESULTS AND DISCUSSION

The experimental work was accomplished for the evaluation of fifty cotton genotypes to different drought treatments using agromorphogenic and biochemical traits. The field performance of drought tolerant genotypes using yield and yield contributing as well as fiber quality characters in barind tract (Godagari, Rajshahi) of Bangladesh was evaluated. Here, the experimental findings have been put forwarded and discussed. Table(s) and Figure(s) are presented for easy discussion, comprehension and understanding.

## 4.1 Experiment 1. Morphological study of cotton genotypes for drought tolerance at early flowering stage

This investigation was conducted to evaluate the fifty cotton genotypes under four drought stresses based on eight agromorphogenic characters to assess the genetic variation among the genotypes for drought tolerance. The agromorphogenic traits included root length, shoot length, shoot-root length ratio, root diameter, total biomass of root, number of lateral roots, number of vegetative branches and number of reproductive branches. Data are presented in Tables and Figures.

### 4.1.1 Agromorphogenic performance of cotton genotypes under drought stress

Eight agromorphogenic responses of fifty genotypes were observed under four different drought stress conditions. ANOVA showed the significant effect of genotypes, treatment and interaction on all eight agromoprhogenic characters (Appendix IV).

#### 4.1.1.1 Root length

Genotype, treatment and their interaction significantly affected the root length. The highest mean root length (17.0 cm) was observed in T2 drought stress whereas the lowest root length (14.4 cm) was observed in T4 drought stress (Table 6). Among the genotypes, highest root length (18.2 cm) was observed in G45 and lowest (10.4 cm) in G36. Based on the genotype stress interaction, highest root length (24.8 cm) and lowest (5.6 cm) was observed in G26 under T1 and G5 under T4 stress, respectively.

On the basis of b values, the best performance (highest b value) was observed in genotype G38 (0.20) followed by G34 (0.19) and lowest in G5 (-0.68). With the

**Table 6. Root length of fifty genotypes at different drought treatments**

| Genotype | Root length(cm) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 15.5 | 15.9 | 9.4 | 13.6 | 13.6 | -2.6 | 39.2 | 12.3 | 16.3 | 0.01 | 9 |
| G2 | 17.4 | 17.4 | 19.5 | 9.3 | 15.9 | -0.2 | -12.3 | 46.4 | 11.3 | -0.38 | 32 |
| G3 | 18.2 | 16.3 | 9.8 | 15.9 | 15.0 | 10.8 | 46.4 | 13.0 | 23.4 | -0.01 | 11 |
| G4 | 16.2 | 16.5 | 10.5 | 11.3 | 13.6 | -1.6 | 35.2 | 30.2 | 21.3 | -0.12 | 18 |
| G5 | 19.1 | 11.9 | 19.3 | 5.6 | 13.9 | 37.8 | -1.0 | 70.8 | 35.8 | -0.68 | 36 |
| G6 | 17.0 | 13.2 | 8.8 | 12.1 | 12.8 | 22.5 | 48.1 | 29.2 | 33.3 | -0.15 | 19 |
| G7 | 19.3 | 12.6 | 18.9 | 12.7 | 15.9 | 34.8 | 1.7 | 34.3 | 23.6 | -0.37 | 31 |
| G8 | 17.4 | 14.4 | 18.6 | 11.1 | 15.4 | 17.4 | -6.7 | 36.0 | 15.6 | -0.33 | 29 |
| G9 | 16.7 | 12.1 | 13.7 | 10.8 | 13.3 | 27.6 | 18.0 | 35.0 | 26.9 | -0.27 | 26 |
| G10 | 19.3 | 13.3 | 10.4 | 18.3 | 15.3 | 31.0 | 46.0 | 5.0 | 27.3 | 0.00 | 10 |
| G11 | 14.5 | 15.5 | 9.7 | 11.9 | 12.9 | -6.7 | 33.3 | 18.3 | 15.0 | -0.03 | 12 |
| G12 | 17.3 | 11.1 | 15.2 | 18.0 | 15.4 | 36.0 | 12.1 | -3.9 | 14.8 | -0.03 | 12 |
| G13 | 16.3 | 22.2 | 17.7 | 12.1 | 17.1 | -36.5 | -8.8 | 25.4 | -6.6 | -0.11 | 17 |
| G14 | 13.1 | 11.2 | 16.2 | 11.1 | 12.9 | 14.8 | -23.4 | 15.3 | 2.2 | -0.16 | 20 |
| G15 | 18.7 | 17.5 | 19.1 | 17.5 | 18.2 | 6.4 | -2.1 | 6.3 | 3.5 | -0.07 | 15 |
| G16 | 14.1 | 16.4 | 17.6 | 15.3 | 15.9 | -16.5 | -24.6 | -8.7 | -16.6 | 0.04 | 7 |
| G17 | 18.4 | 14.3 | 17.5 | 12.0 | 15.6 | 22.4 | 4.9 | 35.1 | 20.8 | -0.32 | 28 |
| G18 | 16.4 | 15.9 | 10.5 | 11.8 | 13.7 | 3.0 | 36.3 | 28.2 | 22.5 | -0.12 | 18 |
| G19 | 16.9 | 16.4 | 16.7 | 15.6 | 16.4 | 2.8 | 1.0 | 7.5 | 3.8 | -0.06 | 14 |
| G20 | 19.4 | 16.7 | 11.7 | 13.9 | 15.4 | 13.6 | 39.8 | 28.2 | 27.2 | -0.16 | 20 |
| G21 | 17.5 | 15.6 | 14.7 | 18.0 | 16.5 | 11.0 | 16.2 | -2.5 | 8.2 | 0.03 | 8 |
| G22 | 17.3 | 14.4 | 14.6 | 17.5 | 16.0 | 16.7 | 15.6 | -0.8 | 10.5 | 0.00 | 10 |
| G23 | 16.7 | 13.3 | 16.9 | 18.0 | 16.2 | 20.4 | -1.2 | -7.8 | 3.8 | 0.00 | 10 |
| G24 | 17.4 | 13.4 | 17.8 | 18.7 | 16.8 | 23.0 | -2.5 | -7.3 | 4.4 | -0.01 | 11 |
| G25 | 17.1 | 13.2 | 12.6 | 15.8 | 14.7 | 22.6 | 26.1 | 7.4 | 18.7 | -0.05 | 13 |
| G26 | 24.8 | 16.9 | 17.5 | 16.8 | 19.0 | 31.8 | 29.5 | 32.5 | 31.3 | -0.35 | 30 |
| G27 | 13.8 | 11.9 | 11.8 | 16.5 | 13.5 | 13.8 | 14.3 | -19.8 | 2.7 | 0.12 | 3 |
| G28 | 18.8 | 8.7 | 17.2 | 10.6 | 13.8 | 54.0 | 8.8 | 43.9 | 35.6 | -0.48 | 34 |
| G29 | 14.7 | 10.3 | 17.4 | 12.3 | 13.7 | 29.5 | -18.9 | 15.9 | 8.9 | -0.20 | 22 |
| G30 | 23.1 | 13.2 | 20.4 | 13.2 | 17.5 | 42.9 | 11.8 | 43.0 | 32.6 | -0.53 | 35 |
| G31 | 15.5 | 14.3 | 19.6 | 15.5 | 16.2 | 7.3 | -26.7 | 0.0 | -6.5 | -0.08 | 16 |
| G32 | 18.2 | 16.8 | 17.1 | 15.5 | 16.9 | 8.0 | 6.4 | 15.2 | 9.9 | -0.12 | 18 |
| G33 | 18.3 | 11.4 | 23.7 | 11.7 | 16.3 | 37.8 | -29.9 | 36.1 | 14.7 | -0.46 | 33 |
| G34 | 16.3 | 14.0 | 8.1 | 18.8 | 14.3 | 14.5 | 50.4 | -14.9 | 16.7 | 0.19 | 2 |
| G35 | 20.4 | 14.4 | 18.6 | 16.7 | 17.6 | 29.4 | 8.8 | 18.1 | 18.8 | -0.22 | 23 |
| G36 | 16.4 | 7.8 | 6.6 | 10.7 | 10.4 | 52.3 | 59.9 | 34.4 | 48.9 | -0.22 | 23 |
| G37 | 17.5 | 13.6 | 9.0 | 16.3 | 14.1 | 22.4 | 48.9 | 6.8 | 26.0 | 0.01 | 9 |
| G38 | 9.6 | 17.5 | 19.2 | 14.8 | 15.3 | -82.9 | -100.3 | -54.7 | -79.3 | 0.20 | 1 |
| G39 | 17.5 | 13.4 | 12.7 | 14.5 | 14.5 | 23.6 | 27.2 | 17.3 | 22.7 | -0.12 | 18 |
| G40 | 18.8 | 9.1 | 13.4 | 14.5 | 14.0 | 51.6 | 28.7 | 22.9 | 34.4 | -0.25 | 24 |
| G41 | 14.3 | 18.5 | 13.9 | 14.5 | 15.3 | -29.4 | 2.6 | -1.9 | -9.6 | 0.08 | 5 |
| G42 | 16.3 | 15.6 | 18.0 | 12.9 | 15.7 | 4.1 | -10.5 | 20.5 | 4.7 | -0.18 | 21 |
| G43 | 17.0 | 8.2 | 18.7 | 14.5 | 14.6 | 51.5 | -10.2 | 14.5 | 18.6 | -0.26 | 25 |
| G44 | 16.5 | 9.7 | 14.9 | 15.5 | 14.2 | 41.1 | 9.3 | 5.9 | 18.8 | -0.12 | 18 |
| G45 | 18.2 | 15.2 | 21.8 | 17.6 | 18.2 | 16.5 | -19.4 | 3.7 | 0.2 | -0.12 | 18 |
| G46 | 16.3 | 11.8 | 22.0 | 12.4 | 15.6 | 27.5 | -35.2 | 24.0 | 5.4 | -0.31 | 27 |
| G47 | 11.8 | 13.8 | 17.4 | 15.0 | 14.5 | -17.2 | -47.2 | -27.4 | -30.6 | 0.09 | 4 |
| G48 | 13.5 | 13.5 | 16.7 | 15.8 | 14.9 | 0.0 | -24.0 | -17.6 | -13.9 | 0.06 | 6 |
| G49 | 18.0 | 12.1 | 16.8 | 16.0 | 15.7 | 33.1 | 6.8 | 11.3 | 17.1 | -0.15 | 19 |
| G50 | 18.2 | 17.2 | 15.5 | 17.6 | 17.1 | 5.7 | 15.0 | 3.1 | 7.9 | 0.00 | 10 |
| Mean (T) | 17.0 | 13.9 | 15.5 | 14.4 | | | | | | | |

increase of drought stress, root length was decreased as shown in linear regression in Figure 9. The minimum reduction% (-100.3 %) was observed in G38 under T3 drought stress (Figure 10, Table 6). Maximum reduction% (70.8%) was observed in G5 under T4 stress (Figure 10). The result showed the negative effect of drought stress on root length in genotypic dependent manner. Similar results were found in the study of (Veesar *et al*., 2020). The water stress adversely reduced the values of the morphological parameters excluding root length of some genotypes (Ahmad *et al*., 2020). Under drought stress conditions, root length showed both an increase and decrease depending on the genetic structure of cotton genotypes (Mahmood *et al*., 2022; Xiao *et al*., 2020). However, the tolerance mechanisms against the drought stress in cotton depends on the genotypes as described in Mahmood *et al*. (2022). Tolerant genotypes have a mechanism to increase the cell division at the root apical meristem to extend their root system in purpose of water uptake (Polania *et al*., 2017). On the other hand, drought susceptible showed less root development.

#### 4.1.1.2 Shoot length

Genotype, treatment and their interaction significantly affected the shoot length. The highest mean shoot length (88.6 cm) was observed in T1 drought stress whereas the lowest shoot length (42.9 cm) was observed in T4 drought stress (Table 7). Among the genotypes, highest shoot length (84.8 cm) was observed in G22 and lowest (46.1 cm) in G36. Based on the genotype stress interaction, highest shoot length (125 cm) and lowest (18.0 cm) was observed in G5 under T1 and T4 stress. On the basis of b values, the best performance (highest b value) was observed in genotype G12 (-0.29) followed by G19 (-0.31) and lowest in G5 (-4.68). With the increase of drought stress, shoot length was decreased as shown in linear regression in Figure 11. The minimum reduction% (-54.3%) was observed in G12 under T2 drought stress (Figure 12, Table 7). Maximum reduction% (85.6%) was observed in G5 under T4 stress (Figure 12). The result showed the negative effect of drought stress on shoot length in genotypic dependent manner. Some of the genotypes showed an increase in shoot length at mild and moderate drought stress. However, all the genotypes showed a decrease of shoot length under the severe drought stress. Similar result has been observed in Veesar *et al*. (2020). Decrease in shoot and root length under drought stress might be due to suppression of cell expansion and cell growth, or due to low turgor pressure (Jaleel *et al*., 2008; Liu *et al*., 2004).

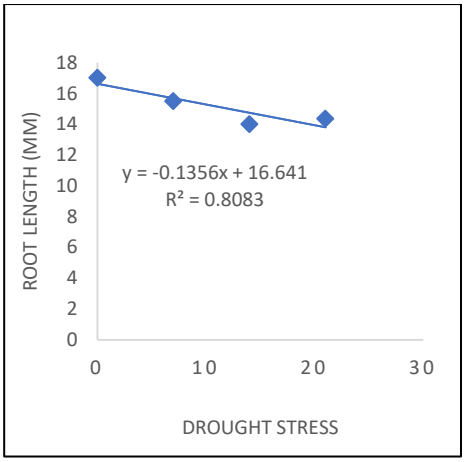



**Figure 9. Relationships between the root length of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

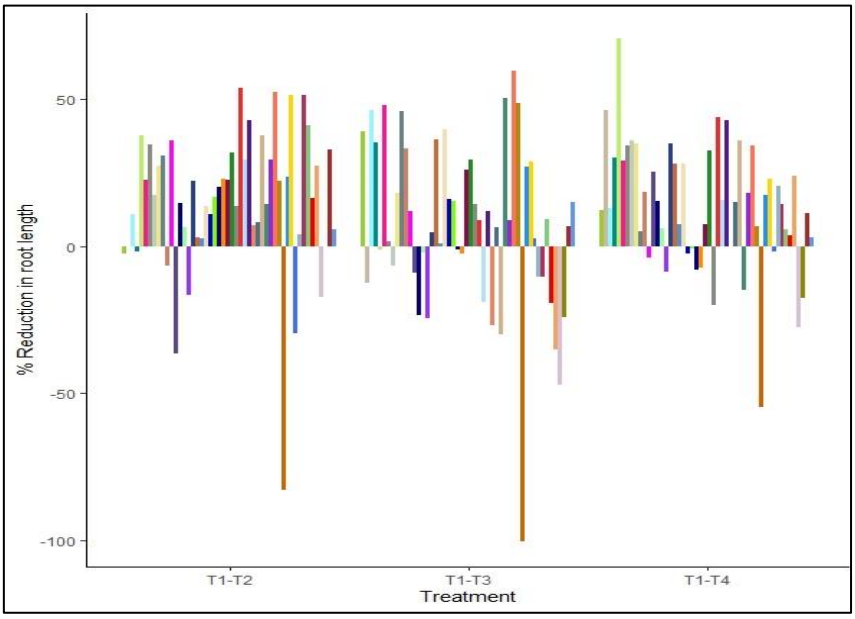
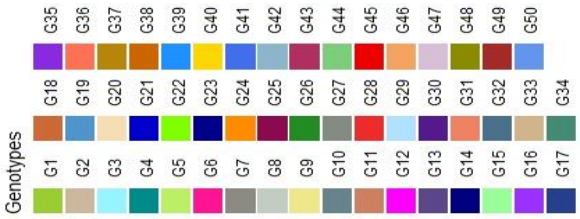



**Figure 10. Reduction percentage of root length of fifty cotton genotypes under different drought stresses compared with control**



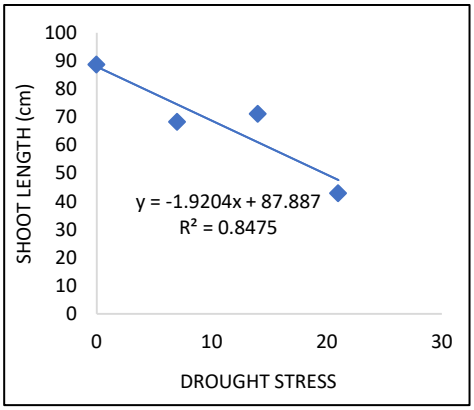




**Figure 11. Relationships between shoot length of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

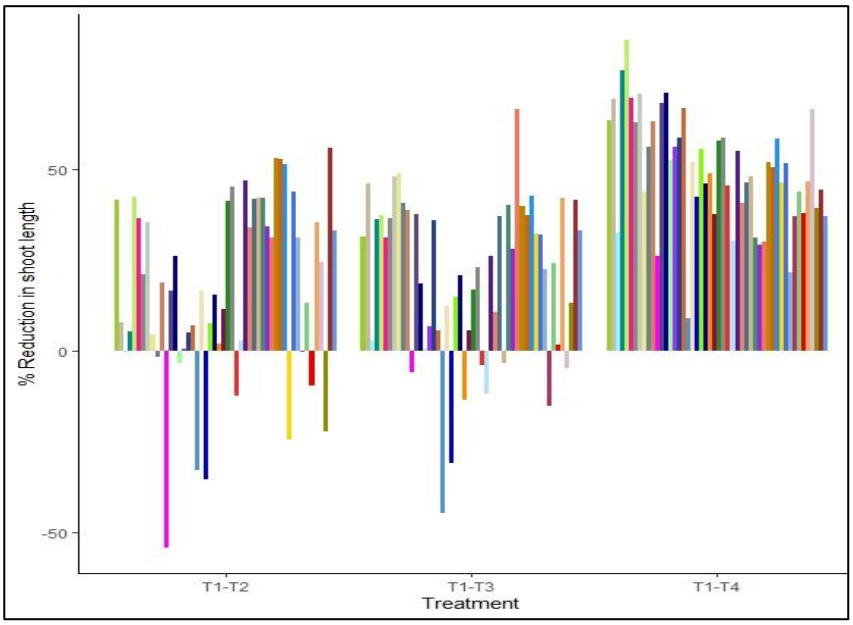



**Figure 12. Reduction percentage of shoot length of fifty cotton genotypes under different drought stresses compared with control**

## Table 7. Shoot length of fifty genotypes at different drought treatments

| Genotype | shoot length (cm) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 83.0 | 48.7 | 57.0 | 30.3 | 54.8 | 41.4 | 31.3 | 63.5 | 45.4 | -2.38 | 30 |
| G2 | 111.0 | 102.3 | 60.0 | 34.0 | 76.8 | 7.8 | 45.9 | 69.4 | 41.0 | -2.70 | 37 |
| G3 | 74.0 | 74.3 | 72.0 | 50.0 | 67.6 | -0.5 | 2.7 | 32.4 | 11.6 | -1.00 | 7 |
| G4 | 103.3 | 98.0 | 66.0 | 23.7 | 72.8 | 5.2 | 36.1 | 77.1 | 39.5 | -2.96 | 41 |
| G5 | 125.0 | 72.0 | 78.3 | 18.0 | 73.3 | 42.4 | 37.3 | 85.6 | 55.1 | -4.68 | 44 |
| G6 | 109.0 | 69.3 | 75.0 | 33.3 | 71.7 | 36.4 | 31.2 | 69.4 | 45.7 | -3.32 | 42 |
| G7 | 104.7 | 82.7 | 66.7 | 39.0 | 73.3 | 21.0 | 36.3 | 62.7 | 40.0 | -2.59 | 35 |
| G8 | 123.3 | 79.7 | 64.3 | 36.3 | 75.9 | 35.4 | 47.8 | 70.5 | 51.3 | -3.51 | 43 |
| G9 | 96.3 | 92.0 | 49.3 | 54.3 | 73.0 | 4.5 | 48.8 | 43.6 | 32.3 | -1.19 | 11 |
| G10 | 100.3 | 102.0 | 59.7 | 44.0 | 76.5 | -1.7 | 40.5 | 56.1 | 31.7 | -1.81 | 20 |
| G11 | 83.7 | 68.0 | 51.3 | 31.0 | 58.5 | 18.7 | 38.6 | 62.9 | 40.1 | -2.02 | 26 |
| G12 | 66.3 | 102.3 | 70.3 | 49.0 | 72.0 | -54.3 | -6.0 | 26.1 | -11.4 | -0.29 | 1 |
| G13 | 97.0 | 81.0 | 60.7 | 31.0 | 67.4 | 16.5 | 37.5 | 68.0 | 40.7 | -2.54 | 34 |
| G14 | 88.7 | 65.7 | 72.3 | 25.7 | 63.1 | 25.9 | 18.4 | 71.1 | 38.5 | -2.80 | 38 |
| G15 | 85.3 | 88.3 | 85.0 | 40.7 | 74.8 | -3.5 | 0.4 | 52.3 | 16.4 | -1.87 | 21 |
| G16 | 87.0 | 86.7 | 81.3 | 38.3 | 73.3 | 0.4 | 6.5 | 55.9 | 20.9 | -2.01 | 25 |
| G17 | 92.3 | 87.7 | 59.3 | 38.3 | 69.4 | 5.1 | 35.7 | 58.5 | 33.1 | -1.91 | 23 |
| G18 | 100.3 | 93.3 | 94.7 | 33.3 | 80.4 | 7.0 | 5.6 | 66.8 | 26.5 | -2.89 | 40 |
| G19 | 56.7 | 75.3 | 82.0 | 51.7 | 66.4 | -32.9 | -44.7 | 8.8 | -22.9 | -0.31 | 2 |
| G20 | 82.3 | 68.7 | 72.3 | 39.7 | 65.8 | 16.6 | 12.1 | 51.8 | 26.9 | -1.88 | 22 |
| G21 | 68.2 | 92.3 | 89.3 | 39.3 | 72.3 | -35.5 | -31.1 | 42.3 | -8.1 | -1.19 | 11 |
| G22 | 105.3 | 97.3 | 89.7 | 47.0 | 84.8 | 7.6 | 14.9 | 55.4 | 25.9 | -2.39 | 31 |
| G23 | 88.3 | 74.7 | 70.0 | 47.7 | 70.2 | 15.5 | 20.8 | 46.0 | 27.4 | -1.68 | 19 |
| G24 | 71.0 | 69.7 | 80.7 | 36.3 | 64.4 | 1.9 | -13.6 | 48.8 | 12.4 | -1.64 | 18 |
| G25 | 55.0 | 48.7 | 52.0 | 34.3 | 47.5 | 11.5 | 5.5 | 37.6 | 18.2 | -0.93 | 6 |
| G26 | 86.0 | 50.7 | 71.7 | 36.3 | 61.2 | 41.1 | 16.7 | 57.8 | 38.5 | -2.43 | 33 |
| G27 | 92.7 | 51.0 | 71.3 | 38.3 | 63.3 | 45.0 | 23.0 | 58.6 | 42.2 | -2.62 | 36 |
| G28 | 67.0 | 75.3 | 69.7 | 36.7 | 62.2 | -12.4 | -4.0 | 45.3 | 9.6 | -1.22 | 13 |
| G29 | 76.3 | 74.3 | 85.3 | 53.3 | 72.3 | 2.6 | -11.8 | 30.1 | 7.0 | -1.14 | 9 |
| G30 | 107.7 | 57.3 | 79.7 | 48.7 | 73.3 | 46.7 | 26.0 | 54.8 | 42.5 | -2.85 | 39 |
| G31 | 79.0 | 52.3 | 70.7 | 47.0 | 62.3 | 33.8 | 10.5 | 40.5 | 28.3 | -1.63 | 17 |
| G32 | 100.3 | 58.3 | 63.3 | 54.0 | 69.0 | 41.9 | 36.9 | 46.2 | 41.6 | -2.06 | 27 |
| G33 | 89.0 | 51.5 | 92.0 | 46.3 | 69.7 | 42.1 | -3.4 | 47.9 | 28.9 | -2.41 | 32 |
| G34 | 85.7 | 49.7 | 51.3 | 59.0 | 61.4 | 42.0 | 40.1 | 31.1 | 37.7 | -1.17 | 10 |
| G35 | 81.0 | 53.3 | 58.3 | 57.3 | 62.5 | 34.2 | 28.0 | 29.2 | 30.5 | -1.09 | 8 |
| G36 | 67.7 | 46.7 | 22.7 | 47.3 | 46.1 | 31.0 | 66.5 | 30.0 | 42.5 | -0.53 | 3 |
| G37 | 99.0 | 46.7 | 59.7 | 47.7 | 63.3 | 52.9 | 39.7 | 51.9 | 48.1 | -2.39 | 31 |
| G38 | 101.0 | 47.7 | 63.3 | 50.0 | 65.5 | 52.8 | 37.3 | 50.5 | 46.9 | -2.41 | 32 |
| G39 | 100.0 | 48.7 | 57.3 | 41.7 | 61.9 | 51.3 | 42.7 | 58.3 | 50.8 | -2.62 | 36 |
| G40 | 85.7 | 106.7 | 58.0 | 46.0 | 74.1 | -24.5 | 32.3 | 46.3 | 18.0 | -1.00 | 7 |
| G41 | 94.3 | 53.0 | 64.2 | 45.7 | 64.3 | 43.8 | 32.0 | 51.6 | 42.5 | -2.25 | 29 |
| G42 | 72.7 | 50.0 | 56.4 | 57.0 | 59.0 | 31.2 | 22.4 | 21.6 | 25.1 | -0.76 | 4 |
| G43 | 80.3 | 80.7 | 92.7 | 50.7 | 76.1 | -0.4 | -15.4 | 36.9 | 7.1 | -1.44 | 15 |
| G44 | 93.3 | 81.0 | 71.0 | 52.7 | 74.5 | 13.2 | 23.9 | 43.6 | 26.9 | -1.60 | 16 |
| G45 | 85.3 | 93.7 | 84.0 | 53.0 | 79.0 | -9.8 | 1.6 | 37.9 | 9.9 | -1.25 | 14 |
| G46 | 102.3 | 66.3 | 59.3 | 54.7 | 70.7 | 35.2 | 42.0 | 46.6 | 41.3 | -1.94 | 24 |
| G47 | 77.7 | 58.7 | 81.3 | 26.0 | 60.9 | 24.5 | -4.7 | 66.5 | 28.8 | -2.54 | 34 |
| G48 | 68.7 | 84.0 | 59.7 | 41.7 | 63.5 | -22.3 | 13.1 | 39.3 | 10.0 | -0.81 | 5 |
| G49 | 104.0 | 46.0 | 61.0 | 58.0 | 67.3 | 55.8 | 41.3 | 44.2 | 47.1 | -2.19 | 28 |
| G50 | 76.7 | 51.3 | 51.3 | 48.3 | 56.9 | 33.0 | 33.0 | 37.0 | 34.3 | -1.21 | 12 |
| Mean (T) | 88.6 | 71.1 | 68.3 | 42.9 | | | | | | | |

#### 4.1.1.3 Shoot root length ratio

Genotype, treatment and their interaction significantly affected the shoot root length ratio. The highest mean shoot root length ratio (5.4) was observed in T2 drought stress whereas the lowest mean shoot root length ratio (3.1) was observed in T4 drought stress (Table 8). Among the genotypes, highest shoot root length ratio (6.0) was observed in G18 and G40 whereas lowest (3.2) in G26. Based on the genotype stress interaction, highest shoot root length ratio was observed in G40 (11.7) under T2 and lowest in G47 (1.7) under T4 stress. Based on b values, the best performance (highest b value) was observed in genotype G28 (0.06) followed by G36 (0.05) and lowest in G38 (-0.32). With the increase of drought stress, shoot root length ratio was decreased as shown in linear regression in Figure 13. The minimum reduction% (-157.6%) was observed in G40 under T2 drought stress (Figure 14, Table 8). Maximum reduction% (74.4%) was observed in G38 under T2 stress (Figure 14). The result showed the negative effect of drought stress on shoot root length ratio in genotypic dependent manner. Many genotypes showed an increase in shoot root length ratio under moderate and mild drought stress. However, all the genotypes showed decrease in shoot root length ration under the severe drought stress except G36. Decrease in shoot root length ratio in cotton under drought stress observed in Sumartini *et al*. (2013).

#### 4.1.1.4 Root diameter

Genotype, treatment and their interaction significantly affected the root diameter. The highest mean root diameter (9.7 mm) was observed in T1 drought stress whereas the lowest root diameter (5.5 mm) was observed in T4 drought stress (Table 9). Among the genotypes, highest root diameter (9.3 mm) was observed in G20 whereas lowest (7.1 mm) in G36. Based on the genotype stress interaction, highest root diameter was observed in G5 (13.5 mm) under T1 and lowest in G5 (2.9 mm) under T4 stress. Based on b values, the best performance (highest b value) was observed in genotype G19 (-0.01) followed by G28 (-0.05) and lowest in G5 (-0.44). With the increase of drought stress, root diameter was decreased as shown in linear regression in Figure 15. The minimum reduction% (-35.1%) was observed in G19 under T2 drought stress (Figure 16, Table 9). Maximum reduction% (78.8%) was observed in G5 under T4 stress (Figure 16). The result showed the negative effect of drought stress on root diameter in genotypic dependent manner. Mahmood *et al*. (2022) and Pace *et al*. (1999) showed similar results.

**Table 8. Shoot root length ratio (SRLR) of fifty genotypes at different drought treatments**

| Genotype | SRLR at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 5.4 | 3.1 | 6.1 | 2.2 | 4.2 | 42.2 | -13.2 | 58.5 | 29.1 | -0.18 | 21 |
| G2 | 6.4 | 5.9 | 3.1 | 3.7 | 4.8 | 7.3 | 51.8 | 42.4 | 33.8 | -0.08 | 13 |
| G3 | 4.1 | 4.6 | 7.5 | 3.2 | 4.8 | -12.4 | -84.4 | 22.1 | -24.9 | -0.08 | 13 |
| G4 | 6.4 | 6.0 | 6.3 | 2.1 | 5.2 | 6.4 | 1.0 | 67.2 | 24.8 | -0.19 | 22 |
| G5 | 6.6 | 6.1 | 4.1 | 3.2 | 5.0 | 7.3 | 38.0 | 50.8 | 32.0 | -0.11 | 15 |
| G6 | 6.4 | 5.3 | 8.5 | 2.8 | 5.7 | 17.8 | -32.6 | 56.6 | 13.9 | -0.20 | 23 |
| G7 | 5.4 | 6.6 | 3.5 | 3.1 | 4.7 | -21.0 | 34.9 | 43.3 | 19.1 | -0.06 | 11 |
| G8 | 7.1 | 5.6 | 3.5 | 3.3 | 4.9 | 21.4 | 51.2 | 53.8 | 42.1 | -0.13 | 16 |
| G9 | 5.8 | 7.7 | 3.6 | 5.0 | 5.5 | -33.0 | 37.5 | 13.0 | 5.8 | 0.03 | 3 |
| G10 | 5.2 | 7.9 | 5.8 | 2.4 | 5.3 | -50.8 | -10.5 | 53.7 | -2.5 | -0.09 | 14 |
| G11 | 5.8 | 4.4 | 5.3 | 2.6 | 4.5 | 23.8 | 7.8 | 54.6 | 28.7 | -0.15 | 18 |
| G12 | 3.8 | 9.3 | 4.6 | 2.7 | 5.1 | -141.4 | -20.9 | 28.4 | -44.6 | 0.02 | 4 |
| G13 | 6.0 | 3.7 | 3.4 | 2.6 | 3.9 | 38.8 | 42.4 | 57.1 | 46.1 | -0.14 | 17 |
| G14 | 6.8 | 5.9 | 4.5 | 2.3 | 4.9 | 13.0 | 33.7 | 65.7 | 37.5 | -0.17 | 20 |
| G15 | 4.6 | 5.1 | 4.5 | 2.3 | 4.1 | -9.6 | 3.1 | 49.6 | 14.4 | -0.09 | 14 |
| G16 | 6.2 | 5.3 | 4.6 | 2.5 | 4.6 | 15.0 | 25.3 | 59.6 | 33.3 | -0.15 | 18 |
| G17 | 5.0 | 6.1 | 3.4 | 3.2 | 4.4 | -21.9 | 32.8 | 36.1 | 15.7 | -0.04 | 9 |
| G18 | 6.1 | 5.9 | 9.0 | 2.8 | 6.0 | 4.1 | -47.5 | 53.8 | 3.4 | -0.19 | 22 |
| G19 | 3.4 | 4.6 | 4.9 | 3.3 | 4.1 | -36.4 | -46.2 | 1.6 | -27.0 | -0.01 | 6 |
| G20 | 4.3 | 4.1 | 6.2 | 2.9 | 4.4 | 2.8 | -46.2 | 32.7 | -3.6 | -0.09 | 14 |
| G21 | 3.9 | 5.9 | 6.1 | 2.2 | 4.5 | -51.9 | -55.8 | 43.5 | -21.4 | -0.07 | 12 |
| G22 | 6.1 | 6.8 | 6.1 | 2.7 | 5.4 | -10.2 | -0.2 | 56.0 | 15.2 | -0.14 | 17 |
| G23 | 5.3 | 5.6 | 4.2 | 2.7 | 4.4 | -5.6 | 22.0 | 50.2 | 22.2 | -0.09 | 14 |
| G24 | 4.1 | 5.2 | 4.5 | 2.0 | 3.9 | -27.3 | -10.7 | 52.4 | 4.8 | -0.08 | 13 |
| G25 | 3.2 | 3.7 | 4.1 | 2.2 | 3.3 | -14.4 | -27.8 | 32.7 | -3.2 | -0.05 | 10 |
| G26 | 3.5 | 3.0 | 4.1 | 2.2 | 3.2 | 13.9 | -18.0 | 37.6 | 11.2 | -0.07 | 12 |
| G27 | 6.8 | 4.3 | 6.0 | 2.4 | 4.9 | 36.9 | 11.2 | 65.4 | 37.8 | -0.22 | 24 |
| G28 | 3.6 | 8.7 | 4.1 | 3.5 | 5.0 | -143.8 | -14.2 | 2.3 | -51.9 | 0.06 | 1 |
| G29 | 5.3 | 7.2 | 4.9 | 4.3 | 5.4 | -37.2 | 6.7 | 17.5 | -4.3 | -0.01 | 6 |
| G30 | 4.7 | 4.4 | 3.9 | 3.7 | 4.2 | 5.6 | 15.7 | 20.6 | 14.0 | -0.03 | 8 |
| G31 | 5.1 | 3.7 | 3.6 | 3.1 | 3.9 | 28.5 | 29.4 | 40.3 | 32.7 | -0.09 | 14 |
| G32 | 5.5 | 3.5 | 3.7 | 3.5 | 4.1 | 36.8 | 32.7 | 36.8 | 35.4 | -0.09 | 14 |
| G33 | 4.9 | 4.5 | 3.9 | 4.0 | 4.3 | 6.9 | 20.5 | 18.5 | 15.3 | -0.03 | 8 |
| G34 | 5.3 | 3.6 | 6.3 | 3.2 | 4.6 | 31.9 | -20.5 | 39.9 | 17.1 | -0.13 | 16 |
| G35 | 4.0 | 3.7 | 3.1 | 3.4 | 3.6 | 6.9 | 21.3 | 13.8 | 14.0 | -0.02 | 7 |
| G36 | 4.1 | 6.1 | 3.5 | 4.4 | 4.5 | -47.0 | 14.4 | -6.8 | -13.1 | 0.05 | 2 |
| G37 | 5.7 | 3.4 | 6.7 | 2.9 | 4.7 | 39.3 | -18.8 | 48.5 | 23.0 | -0.16 | 19 |
| G38 | 10.7 | 2.7 | 3.3 | 3.4 | 5.0 | 74.4 | 69.0 | 68.4 | 70.6 | -0.32 | 25 |
| G39 | 5.7 | 3.6 | 4.5 | 2.9 | 4.2 | 36.4 | 21.0 | 49.7 | 35.7 | -0.13 | 16 |
| G40 | 4.6 | 11.7 | 4.3 | 3.2 | 6.0 | -157.6 | 4.7 | 30.3 | -40.9 | 0.05 | 2 |
| G41 | 6.6 | 2.9 | 4.6 | 3.1 | 4.3 | 56.5 | 30.4 | 52.6 | 46.5 | -0.17 | 20 |
| G42 | 4.5 | 3.2 | 3.1 | 4.4 | 3.8 | 28.1 | 29.8 | 1.4 | 19.7 | 0.00 | 5 |
| G43 | 4.8 | 9.8 | 5.0 | 3.5 | 5.8 | -106.5 | -4.6 | 26.4 | -28.2 | 0.02 | 4 |
| G44 | 5.7 | 8.4 | 4.8 | 3.4 | 5.6 | -47.9 | 16.4 | 40.2 | 2.9 | -0.05 | 10 |
| G45 | 4.7 | 6.2 | 3.9 | 3.0 | 4.4 | -31.3 | 17.6 | 35.6 | 7.3 | -0.04 | 9 |
| G46 | 6.3 | 5.6 | 2.7 | 4.4 | 4.8 | 10.7 | 57.0 | 29.7 | 32.5 | -0.04 | 9 |
| G47 | 6.6 | 4.2 | 4.7 | 1.7 | 4.3 | 36.0 | 28.9 | 73.9 | 46.2 | -0.22 | 24 |
| G48 | 5.1 | 6.3 | 3.6 | 2.6 | 4.4 | -22.3 | 30.2 | 48.7 | 18.9 | -0.07 | 12 |
| G49 | 5.8 | 3.8 | 3.6 | 3.6 | 4.2 | 34.0 | 37.3 | 37.5 | 36.3 | -0.09 | 14 |
| G50 | 4.2 | 3.0 | 3.3 | 2.7 | 3.3 | 28.9 | 21.3 | 35.0 | 28.4 | -0.07 | 12 |
| Mean (T) | 5.3 | 5.4 | 4.7 | 3.1 | | | | | | | |

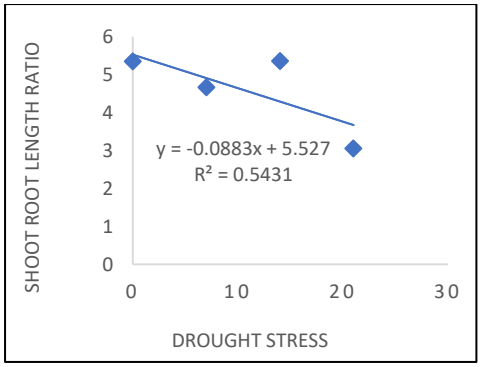



**Figure 13. Relationships between shoot root length ratio of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

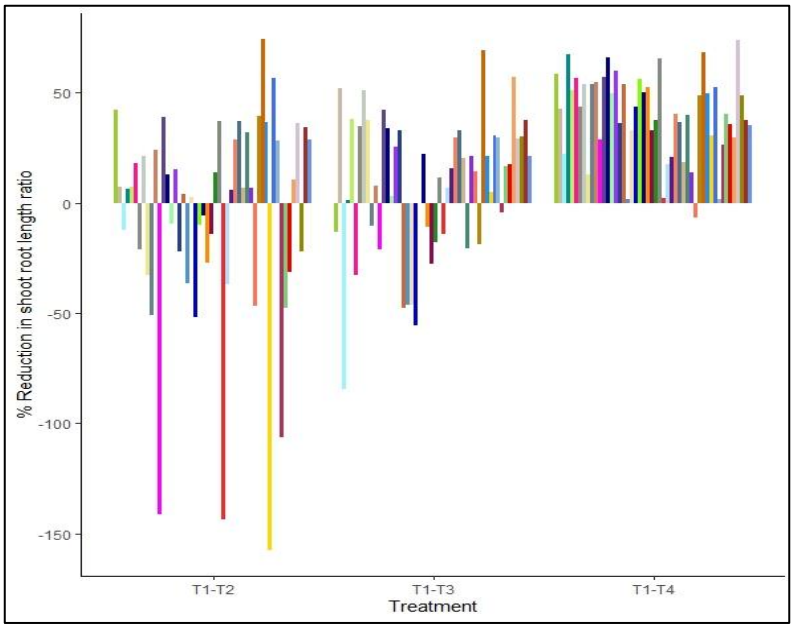
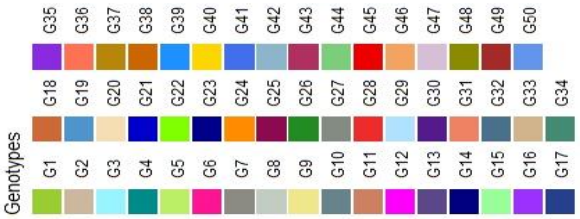



**Figure 14. Reduction percentage of shoot root length ratio of fifty cotton genotypes under different drought stresses compared with control**



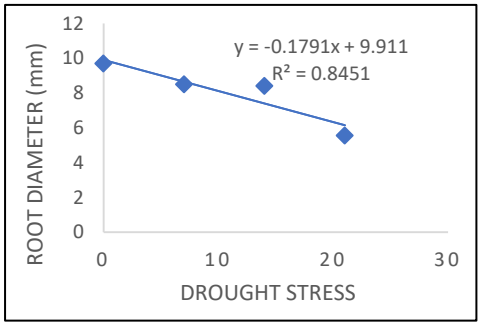




**Figure 15. Relationships between root diameter of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

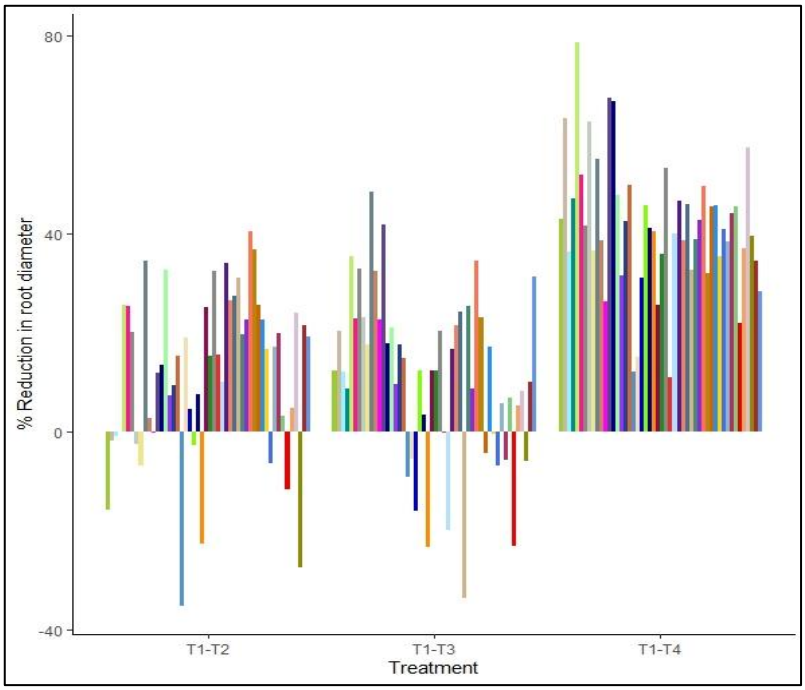



**Figure 16. Reduction percentage of root diameter of fifty cotton genotypes under different drought stresses compared with control**

## Table 9. Root diameter (mm) of fifty genotypes at different drought treatments

| Genotype | Root diameter at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 8.5 | 9.8 | 7.5 | 4.9 | 7.7 | -15.6 | 12.4 | 43.1 | 13.3 | -0.12 | 7 |
| G2 | 10.5 | 10.7 | 8.4 | 3.8 | 8.4 | -1.8 | 20.3 | 63.5 | 27.3 | -0.25 | 20 |
| G3 | 9.5 | 9.6 | 8.3 | 6.0 | 8.4 | -0.9 | 12.3 | 36.5 | 16.0 | -0.13 | 8 |
| G4 | 8.8 | 8.8 | 8.0 | 4.7 | 7.6 | 0.1 | 8.9 | 47.2 | 18.7 | -0.17 | 12 |
| G5 | 13.5 | 10.1 | 8.7 | 2.9 | 8.8 | 25.6 | 35.5 | 78.8 | 46.6 | -0.44 | 24 |
| G6 | 10.6 | 7.9 | 8.1 | 5.1 | 7.9 | 25.5 | 23.1 | 52.0 | 33.5 | -0.24 | 18 |
| G7 | 10.4 | 8.3 | 6.9 | 6.0 | 7.9 | 20.3 | 33.0 | 41.7 | 31.7 | -0.17 | 12 |
| G8 | 10.8 | 11.0 | 8.3 | 4.0 | 8.5 | -2.3 | 23.2 | 62.7 | 27.8 | -0.25 | 19 |
| G9 | 8.6 | 9.1 | 7.0 | 5.4 | 7.5 | -6.7 | 17.8 | 36.6 | 15.9 | -0.10 | 5 |
| G10 | 13.3 | 8.7 | 6.9 | 6.0 | 8.7 | 34.5 | 48.5 | 55.3 | 46.1 | -0.29 | 23 |
| G11 | 9.4 | 9.1 | 6.3 | 5.8 | 7.6 | 3.0 | 32.5 | 38.7 | 24.7 | -0.12 | 7 |
| G12 | 8.3 | 8.3 | 6.4 | 6.1 | 7.3 | -0.2 | 22.8 | 26.4 | 16.3 | -0.07 | 3 |
| G13 | 11.8 | 10.4 | 6.9 | 3.8 | 8.2 | 12.0 | 41.9 | 67.5 | 40.5 | -0.29 | 23 |
| G14 | 9.5 | 8.2 | 7.8 | 3.2 | 7.2 | 13.5 | 17.9 | 66.7 | 32.7 | -0.27 | 22 |
| G15 | 10.3 | 6.9 | 8.1 | 5.4 | 7.6 | 32.8 | 21.1 | 47.8 | 33.9 | -0.23 | 17 |
| G16 | 8.9 | 8.2 | 8.0 | 6.1 | 7.8 | 7.5 | 9.8 | 31.6 | 16.3 | -0.12 | 7 |
| G17 | 9.6 | 8.7 | 7.9 | 5.5 | 7.9 | 9.4 | 17.7 | 42.5 | 23.2 | -0.16 | 11 |
| G18 | 10.1 | 8.5 | 8.6 | 5.1 | 8.1 | 15.3 | 15.0 | 49.8 | 26.7 | -0.22 | 16 |
| G19 | 7.6 | 10.2 | 8.2 | 6.6 | 8.2 | -35.1 | -8.9 | 12.3 | -10.6 | -0.01 | 1 |
| G20 | 10.0 | 8.1 | 10.6 | 8.5 | 9.3 | 19.0 | -5.3 | 15.1 | 9.6 | -0.10 | 5 |
| G21 | 8.2 | 7.8 | 9.5 | 5.6 | 7.8 | 4.7 | -15.9 | 31.2 | 6.7 | -0.13 | 8 |
| G22 | 9.4 | 9.7 | 8.3 | 5.1 | 8.1 | -2.6 | 12.4 | 45.8 | 18.5 | -0.16 | 11 |
| G23 | 10.0 | 9.3 | 9.7 | 5.9 | 8.7 | 7.7 | 3.5 | 41.3 | 17.5 | -0.18 | 13 |
| G24 | 8.4 | 10.3 | 10.4 | 5.0 | 8.5 | -22.6 | -23.3 | 40.5 | -1.8 | -0.15 | 10 |
| G25 | 9.0 | 6.8 | 7.9 | 6.7 | 7.6 | 25.3 | 12.5 | 25.7 | 21.2 | -0.12 | 7 |
| G26 | 8.9 | 7.5 | 7.8 | 5.7 | 7.5 | 15.3 | 12.5 | 36.1 | 21.3 | -0.14 | 9 |
| G27 | 10.4 | 7.0 | 8.3 | 4.9 | 7.6 | 32.6 | 20.3 | 53.3 | 35.4 | -0.26 | 21 |
| G28 | 7.7 | 6.5 | 7.7 | 6.9 | 7.2 | 15.6 | -0.2 | 11.1 | 8.8 | -0.05 | 2 |
| G29 | 9.0 | 8.0 | 10.7 | 5.4 | 8.3 | 10.3 | -19.7 | 40.2 | 10.3 | -0.19 | 14 |
| G30 | 10.4 | 6.8 | 8.6 | 5.5 | 7.8 | 34.1 | 16.9 | 46.7 | 32.5 | -0.23 | 17 |
| G31 | 9.6 | 7.1 | 7.6 | 5.9 | 7.5 | 26.6 | 21.5 | 38.7 | 28.9 | -0.17 | 12 |
| G32 | 9.9 | 7.2 | 7.5 | 5.4 | 7.5 | 27.4 | 24.4 | 46.1 | 32.6 | -0.20 | 15 |
| G33 | 9.9 | 6.8 | 13.2 | 6.7 | 9.2 | 31.2 | -33.5 | 32.9 | 10.2 | -0.23 | 17 |
| G34 | 9.9 | 8.0 | 7.4 | 6.1 | 7.8 | 19.7 | 25.4 | 38.8 | 28.0 | -0.16 | 11 |
| G35 | 10.6 | 8.2 | 9.7 | 6.0 | 8.6 | 22.7 | 8.7 | 42.8 | 24.7 | -0.22 | 16 |
| G36 | 10.3 | 6.1 | 6.7 | 5.2 | 7.1 | 40.7 | 34.6 | 49.8 | 41.7 | -0.23 | 17 |
| G37 | 9.4 | 5.9 | 7.2 | 6.4 | 7.2 | 36.9 | 23.3 | 32.1 | 30.7 | -0.15 | 10 |
| G38 | 10.7 | 8.0 | 11.2 | 5.9 | 8.9 | 25.6 | -4.3 | 45.5 | 22.3 | -0.26 | 21 |
| G39 | 9.6 | 7.4 | 7.9 | 5.2 | 7.6 | 22.7 | 17.3 | 45.7 | 28.6 | -0.20 | 15 |
| G40 | 8.6 | 7.2 | 8.6 | 5.5 | 7.5 | 16.9 | -0.3 | 35.6 | 17.4 | -0.15 | 10 |
| G41 | 8.9 | 9.5 | 9.5 | 5.3 | 8.3 | -6.4 | -6.7 | 40.9 | 9.3 | -0.16 | 11 |
| G42 | 9.0 | 7.5 | 8.5 | 5.5 | 7.6 | 17.1 | 5.9 | 38.4 | 20.5 | -0.16 | 11 |
| G43 | 9.7 | 7.8 | 10.2 | 5.4 | 8.3 | 19.9 | -5.7 | 44.1 | 19.4 | -0.22 | 16 |
| G44 | 9.5 | 9.2 | 8.8 | 5.1 | 8.1 | 3.3 | 6.9 | 45.7 | 18.6 | -0.18 | 13 |
| G45 | 8.2 | 9.1 | 10.0 | 6.4 | 8.4 | -11.6 | -22.9 | 22.1 | -4.1 | -0.09 | 4 |
| G46 | 9.1 | 8.7 | 8.6 | 5.7 | 8.0 | 5.0 | 5.4 | 37.2 | 15.9 | -0.15 | 10 |
| G47 | 10.9 | 8.3 | 10.0 | 4.7 | 8.5 | 24.1 | 8.3 | 57.4 | 29.9 | -0.29 | 23 |
| G48 | 9.2 | 11.7 | 9.8 | 5.6 | 9.1 | -27.3 | -5.9 | 39.6 | 2.1 | -0.13 | 8 |
| G49 | 9.7 | 7.6 | 8.7 | 6.3 | 8.1 | 21.5 | 10.1 | 34.7 | 22.1 | -0.16 | 11 |
| G50 | 10.8 | 8.7 | 7.4 | 7.7 | 8.6 | 19.3 | 31.4 | 28.3 | 26.4 | -0.11 | 6 |
| Mean (T) | 9.7 | 8.4 | 8.5 | 5.5 | | | | | | | |

#### 4.1.1.5 Total biomass of root

Genotype, treatment, and their interaction significantly affected the total biomass of root. The highest mean biomass of root (4.7 g) was observed in T1 drought stress whereas the lowest total biomass of root (1.5 g) was observed in T4 drought stress (Table 10). Among the genotypes, highest mean biomass of root (5.3 g) was observed in G3 whereas lowest (1.9 g) in G36. Based on the genotype stress interaction, highest total biomass of root was observed in G33 (11.9 g) under T3 and lowest in G5 (0.3 g) under T4 stress. On the basis of b values, the best performance (highest b value) was observed in genotype G19 (-0.01) followed by G12 (-0.05) and lowest in G5 (-0.34). With the increase of drought stress, total biomass of root was decreased as shown in linear regression in Figure 17. The minimum reduction% (-133.3%) was observed in G33 under T3 drought stress (Figure 18, Table 10). Maximum reduction% (96.2%) was observed in G5 under T4 stress (Figure 18). The result showed the negative effect of drought stress on total biomass of root in genotypic dependent manner. Similar result has been observed in Zhou and Oosterhuis (2012). The underlying reasons behind the reduction in biomass of root under severe drought stress is due to the suppression of cell growth, division, and elongation (Liu *et al*., 2004).

#### 4.1.1.6 No. of lateral root

Genotype, treatment and their interaction significantly affected the no. of lateral root. The highest mean no. of lateral root (31.2) was observed in T1 drought stress whereas the lowest no. of lateral root (28.3) was observed in T4 drought stress (Table 11). Among the genotypes, highest no. of lateral root (38.4) was observed in G8 whereas lowest (22.6) in G25. Based on the genotype stress interaction, highest no. of lateral root was observed in G50 (51.3) under T4 and lowest in G2 (5.0) under T4 stress. On the basis of b values, the best performance (highest b value) was observed in genotype G43 (0.93) followed by G50 (0.79) and lowest in G26 (-1.24). With the increase of drought stress, no. of lateral root was decreased as shown in linear regression in Figure 19. The minimum reduction% (-103.0%) was observed in G43 under T4 drought stress (Figure 20, Table 11). Maximum reduction% (80.7%) was observed in G5 under T4 stress (Figure 20). The result showed the negative effect of drought stress on no. of lateral root in genotypic dependent manner. No genotypes showed increase in total biomass of root under the severe drought stress. Ahmad *et al*. (2020) observed water stress adversely reduced the values of number of lateral roots.

**Table 10. Total biomass of root (TBMOR) (g) of fifty genotypes at different drought treatments**

| Genotype | TBMOR at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 4.27 | 6.6 | 2.97 | 0.77 | 3.7 | -54.7 | 30.5 | 82.0 | 19.3 | -0.10 | 6 |
| G2 | 5.8 | 7.57 | 3.83 | 0.6 | 4.5 | -30.5 | 33.9 | 89.7 | 31.0 | -0.17 | 13 |
| G3 | 6.87 | 8.07 | 3.73 | 2.4 | 5.3 | -17.5 | 45.6 | 65.0 | 31.1 | -0.13 | 9 |
| G4 | 5.8 | 3.57 | 4.53 | 1.07 | 3.7 | 38.5 | 21.8 | 81.6 | 47.3 | -0.22 | 16 |
| G5 | 7.97 | 3.23 | 3.9 | 0.3 | 3.9 | 59.4 | 51.0 | 96.2 | 68.9 | -0.34 | 21 |
| G6 | 6.47 | 1.7 | 3.97 | 0.83 | 3.2 | 73.7 | 38.7 | 87.1 | 66.5 | -0.27 | 18 |
| G7 | 6.47 | 4.47 | 3.43 | 1.63 | 4.0 | 30.9 | 46.9 | 74.7 | 50.9 | -0.19 | 15 |
| G8 | 8.07 | 6.6 | 3.97 | 0.67 | 4.8 | 18.2 | 50.8 | 91.7 | 53.6 | -0.28 | 19 |
| G9 | 4.43 | 3.97 | 2.87 | 1.77 | 3.3 | 10.5 | 35.3 | 60.2 | 35.3 | -0.10 | 6 |
| G10 | 6.4 | 4.37 | 2.73 | 2.27 | 3.9 | 31.8 | 57.3 | 64.6 | 51.2 | -0.15 | 11 |
| G11 | 3.63 | 5.23 | 4.53 | 1.6 | 3.7 | -44.0 | -24.8 | 56.0 | -4.3 | -0.08 | 4 |
| G12 | 3.87 | 4.53 | 2.2 | 2.03 | 3.2 | -17.2 | 43.1 | 47.4 | 24.4 | -0.05 | 2 |
| G13 | 6.4 | 6.93 | 2.83 | 0.57 | 4.2 | -8.3 | 55.7 | 91.1 | 46.2 | -0.19 | 15 |
| G14 | 4.27 | 2.57 | 3.43 | 0.63 | 2.7 | 39.8 | 19.5 | 85.2 | 48.2 | -0.17 | 13 |
| G15 | 4.33 | 2.7 | 5.7 | 1.43 | 3.5 | 37.7 | -31.5 | 66.9 | 24.4 | -0.17 | 13 |
| G16 | 4.87 | 2.47 | 4.37 | 2.03 | 3.4 | 49.3 | 10.3 | 58.2 | 39.3 | -0.15 | 11 |
| G17 | 5.53 | 3.93 | 3.33 | 1.3 | 3.5 | 28.9 | 39.8 | 76.5 | 48.4 | -0.17 | 13 |
| G18 | 4.3 | 3.33 | 3.73 | 1.13 | 3.1 | 22.5 | 13.2 | 73.6 | 36.4 | -0.14 | 10 |
| G19 | 2.9 | 6.23 | 3.83 | 1.87 | 3.7 | -114.9 | -32.2 | 35.6 | -37.2 | -0.01 | 1 |
| G20 | 4.8 | 2.93 | 3.73 | 2.38 | 3.5 | 38.9 | 22.2 | 50.3 | 37.2 | -0.12 | 8 |
| G21 | 4.13 | 3.33 | 5.87 | 1.87 | 3.8 | 19.4 | -41.9 | 54.8 | 10.8 | -0.13 | 9 |
| G22 | 4.23 | 3.37 | 2.67 | 1.43 | 2.9 | 20.5 | 37.0 | 66.1 | 41.2 | -0.11 | 7 |
| G23 | 3 | 3.1 | 4.93 | 1.53 | 3.1 | -3.3 | -64.4 | 48.9 | -6.3 | -0.09 | 5 |
| G24 | 4.57 | 6.57 | 6.97 | 1.27 | 4.8 | -43.8 | -52.6 | 72.3 | -8.0 | -0.15 | 11 |
| G25 | 3.2 | 2.13 | 3.3 | 1.73 | 2.6 | 33.3 | -3.1 | 45.8 | 25.3 | -0.08 | 4 |
| G26 | 3.37 | 2.97 | 4.27 | 1.27 | 3.0 | 11.9 | -26.7 | 62.4 | 15.8 | -0.11 | 7 |
| G27 | 3.63 | 2.1 | 3.43 | 1.13 | 2.6 | 42.2 | 5.5 | 68.8 | 38.8 | -0.13 | 9 |
| G28 | 3.3 | 1.6 | 3.13 | 1.27 | 2.3 | 51.5 | 5.1 | 61.6 | 39.4 | -0.11 | 7 |
| G29 | 2.37 | 1.93 | 5.33 | 1.33 | 2.7 | 18.3 | -125.4 | 43.7 | -21.1 | -0.09 | 5 |
| G30 | 6.1 | 2.33 | 4.7 | 1.27 | 3.6 | 61.7 | 23.0 | 79.2 | 54.6 | -0.24 | 17 |
| G31 | 3.23 | 2.47 | 3.37 | 1.47 | 2.6 | 23.7 | -4.1 | 54.6 | 24.7 | -0.09 | 5 |
| G32 | 6.33 | 2.1 | 2.5 | 1.43 | 3.1 | 66.8 | 60.5 | 77.4 | 68.2 | -0.22 | 16 |
| G33 | 5.1 | 2.1 | 11.9 | 1.33 | 5.1 | 58.8 | -133.3 | 73.9 | -0.2 | -0.30 | 20 |
| G34 | 3.07 | 2.8 | 6.6 | 2.13 | 3.7 | 8.7 | -115.2 | 30.4 | -25.4 | -0.09 | 5 |
| G35 | 5.87 | 3.17 | 6.13 | 2.33 | 4.4 | 46.0 | -4.5 | 60.2 | 33.9 | -0.19 | 15 |
| G36 | 3.33 | 1.47 | 1.7 | 1.03 | 1.9 | 56.0 | 49.0 | 69.0 | 58.0 | -0.10 | 6 |
| G37 | 4.6 | 1.67 | 3.33 | 1.47 | 2.8 | 63.8 | 27.5 | 68.1 | 53.1 | -0.16 | 12 |
| G38 | 6.17 | 2.17 | 4.27 | 1.77 | 3.6 | 64.9 | 30.8 | 71.4 | 55.7 | -0.22 | 16 |
| G39 | 5.97 | 3.07 | 3.4 | 1.03 | 3.4 | 48.6 | 43.0 | 82.7 | 58.1 | -0.22 | 16 |
| G40 | 4.57 | 2.3 | 2.73 | 1.43 | 2.8 | 49.6 | 40.1 | 68.6 | 52.8 | -0.14 | 10 |
| G41 | 5.73 | 4.57 | 4.33 | 1.47 | 4.0 | 20.3 | 24.4 | 74.4 | 39.7 | -0.18 | 14 |
| G42 | 4.4 | 1.67 | 2.87 | 1.6 | 2.6 | 62.1 | 34.8 | 63.6 | 53.5 | -0.14 | 10 |
| G43 | 2.47 | 3.07 | 4.7 | 1.3 | 2.9 | -24.3 | -90.5 | 47.3 | -22.5 | -0.07 | 3 |
| G44 | 3.83 | 2.77 | 4 | 1.43 | 3.0 | 27.8 | -4.3 | 62.6 | 28.7 | -0.12 | 8 |
| G45 | 4.8 | 4.27 | 5.93 | 1.5 | 4.1 | 11.1 | -23.6 | 68.8 | 18.8 | -0.17 | 13 |
| G46 | 4.63 | 2.8 | 2.9 | 1.7 | 3.0 | 39.6 | 37.4 | 63.3 | 46.8 | -0.13 | 9 |
| G47 | 3.97 | 2.67 | 4.47 | 0.93 | 3.0 | 32.8 | -12.6 | 76.5 | 32.2 | -0.16 | 12 |
| G48 | 3.73 | 3.8 | 6.57 | 1.47 | 3.9 | -1.8 | -75.9 | 60.7 | -5.7 | -0.14 | 10 |
| G49 | 3.8 | 3.27 | 5.5 | 2.23 | 3.7 | 14.0 | -44.7 | 41.2 | 3.5 | -0.10 | 6 |
| G50 | 5.63 | 2.33 | 3.57 | 2.67 | 3.6 | 58.6 | 36.7 | 52.7 | 49.3 | -0.14 | 10 |
| Mean (T) | 4.7 | 3.5 | 4.2 | 1.5 | | | | | | | |

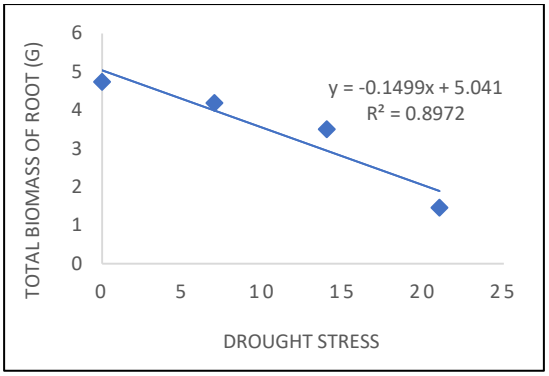



**Figure 17. Relationships between total biomass of root of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

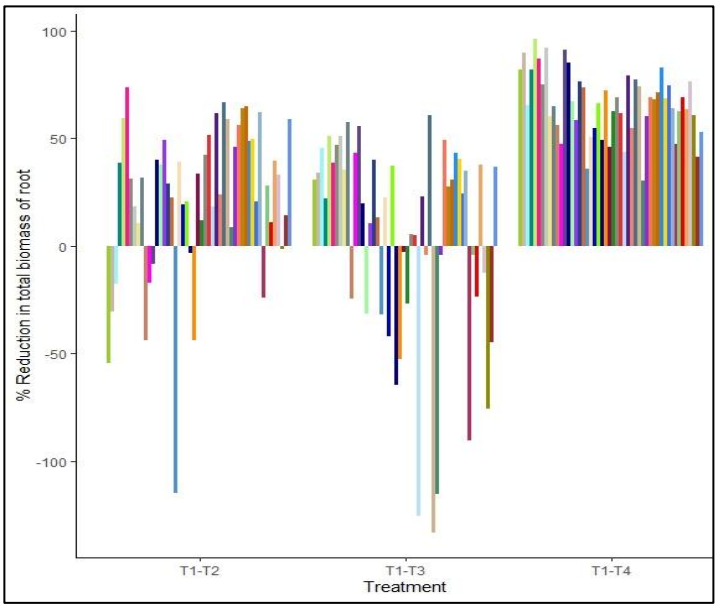
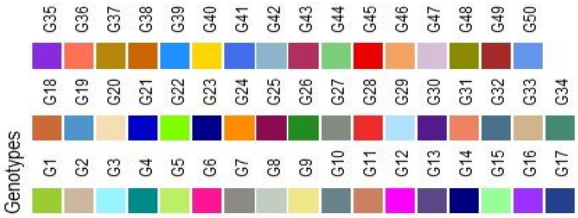



**Figure 18. Reduction percentage of total biomass of root of fifty cotton genotypes under different drought stresses compared with control Figure 17. Relationships between total biomass of root of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**



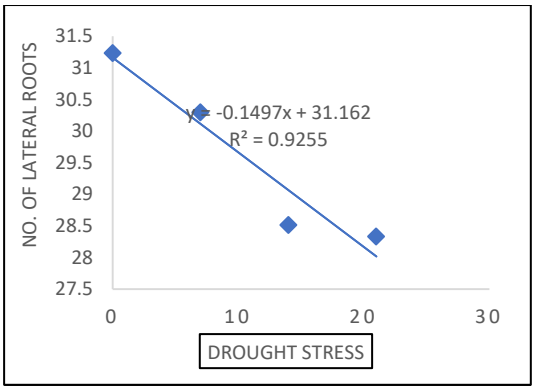




**Figure 19. Relationships between number of lateral roots of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

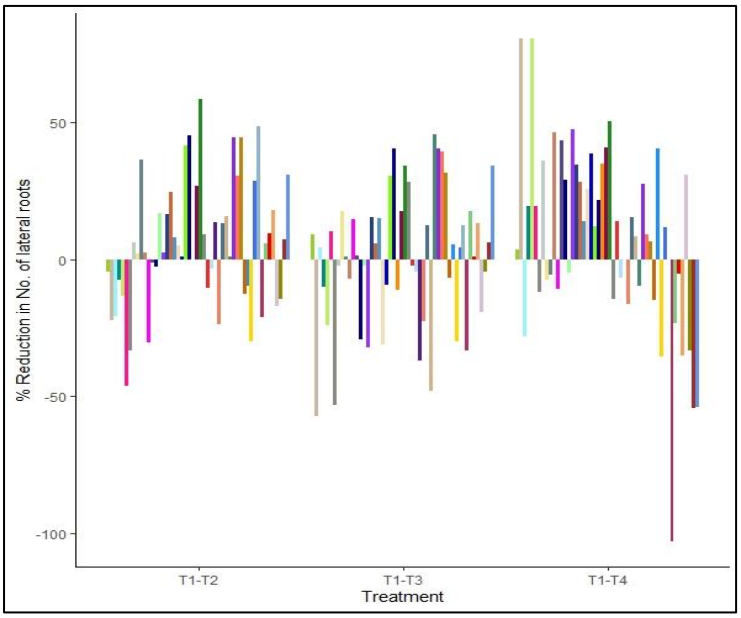



**Figure 20. Reduction percentage of number of lateral roots of fifty cotton genotypes under different drought stresses compared with control**

**Table 11. No. of lateral roots (NOLR) of fifty genotypes at different drought treatments**

| Genotype | NOLR at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 29.7 | 31.0 | 27.0 | 28.7 | 29.1 | -4.5 | 9.0 | 3.4 | 2.6 | 0.01 | 16 |
| G2 | 25.7 | 31.3 | 40.3 | 5.0 | 25.6 | -22.1 | -57.1 | 80.5 | 0.4 | -1.01 | 40 |
| G3 | 30.7 | 37.0 | 29.3 | 39.3 | 34.1 | -20.7 | 4.3 | -28.3 | -14.9 | 0.48 | 4 |
| G4 | 26.0 | 28.0 | 28.7 | 21.0 | 25.9 | -7.7 | -10.3 | 19.2 | 0.4 | -0.22 | 23 |
| G5 | 27.7 | 31.3 | 34.3 | 5.3 | 24.7 | -13.3 | -24.1 | 80.7 | 14.5 | -1.00 | 39 |
| G6 | 26.0 | 38.0 | 23.3 | 21.0 | 27.1 | -46.2 | 10.3 | 19.2 | -5.6 | 0.00 | 17 |
| G7 | 25.0 | 33.3 | 38.3 | 28.0 | 31.2 | -33.3 | -53.3 | -12.0 | -32.9 | 0.06 | 14 |
| G8 | 42.7 | 40.0 | 43.7 | 27.3 | 38.4 | 6.2 | -2.3 | 35.9 | 13.3 | -0.71 | 38 |
| G9 | 30.3 | 29.7 | 25.0 | 32.7 | 29.4 | 2.2 | 17.6 | -7.7 | 4.0 | 0.17 | 12 |
| G10 | 34.7 | 22.0 | 34.3 | 36.7 | 31.9 | 36.5 | 1.0 | -5.8 | 10.6 | -0.09 | 20 |
| G11 | 28.0 | 27.3 | 30.0 | 15.0 | 25.1 | 2.4 | -7.1 | 46.4 | 13.9 | -0.60 | 35 |
| G12 | 27.3 | 35.7 | 23.3 | 30.3 | 29.2 | -30.5 | 14.6 | -11.0 | -8.9 | 0.30 | 8 |
| G13 | 28.3 | 28.7 | 28.0 | 16.0 | 25.3 | -1.2 | 1.2 | 43.5 | 14.5 | -0.52 | 32 |
| G14 | 26.3 | 27.0 | 34.0 | 18.7 | 26.5 | -2.5 | -29.1 | 29.1 | -0.8 | -0.43 | 29 |
| G15 | 27.7 | 23.0 | 28.3 | 29.0 | 27.0 | 16.9 | -2.4 | -4.8 | 3.2 | -0.02 | 18 |
| G16 | 26.0 | 25.3 | 34.3 | 13.7 | 24.8 | 2.6 | -32.1 | 47.4 | 6.0 | -0.66 | 37 |
| G17 | 34.7 | 29.0 | 29.3 | 22.7 | 28.9 | 16.3 | 15.4 | 34.6 | 22.1 | -0.52 | 32 |
| G18 | 29.7 | 22.3 | 28.0 | 21.3 | 25.3 | 24.7 | 5.6 | 28.1 | 19.5 | -0.44 | 30 |
| G19 | 33.3 | 30.7 | 28.3 | 28.7 | 30.3 | 8.0 | 15.0 | 14.0 | 12.3 | -0.17 | 22 |
| G20 | 32.3 | 30.7 | 42.3 | 24.0 | 32.3 | 5.2 | -30.9 | 25.8 | 0.0 | -0.52 | 32 |
| G21 | 32.0 | 31.7 | 35.0 | 19.7 | 29.6 | 1.0 | -9.4 | 38.5 | 10.1 | -0.58 | 34 |
| G22 | 45.0 | 26.3 | 31.3 | 39.7 | 35.6 | 41.5 | 30.4 | 11.9 | 27.9 | -0.30 | 26 |
| G23 | 41.3 | 22.7 | 24.7 | 32.3 | 30.3 | 45.2 | 40.3 | 21.8 | 35.8 | -0.41 | 28 |
| G24 | 32.3 | 32.3 | 36.0 | 21.0 | 30.4 | 0.0 | -11.3 | 35.1 | 7.9 | -0.54 | 33 |
| G25 | 28.7 | 21.0 | 23.7 | 17.0 | 22.6 | 26.7 | 17.4 | 40.7 | 28.3 | -0.54 | 33 |
| G26 | 49.7 | 20.7 | 32.7 | 24.7 | 31.9 | 58.4 | 34.2 | 50.3 | 47.7 | -1.24 | 41 |
| G27 | 29.7 | 27.0 | 21.3 | 34.0 | 28.0 | 9.0 | 28.1 | -14.6 | 7.5 | 0.27 | 9 |
| G28 | 28.7 | 31.7 | 29.3 | 24.7 | 28.6 | -10.5 | -2.3 | 14.0 | 0.4 | -0.14 | 21 |
| G29 | 29.0 | 30.0 | 30.3 | 31.0 | 30.1 | -3.4 | -4.6 | -6.9 | -5.0 | 0.08 | 13 |
| G30 | 34.3 | 29.7 | 47.0 | 34.3 | 36.3 | 13.6 | -36.9 | 0.0 | -7.8 | -0.25 | 24 |
| G31 | 26.7 | 33.0 | 32.7 | 31.0 | 30.8 | -23.8 | -22.5 | -16.3 | -20.8 | 0.19 | 11 |
| G32 | 32.7 | 28.3 | 28.7 | 27.7 | 29.3 | 13.3 | 12.2 | 15.3 | 13.6 | -0.22 | 23 |
| G33 | 32.0 | 27.0 | 47.3 | 29.3 | 33.9 | 15.6 | -47.9 | 8.3 | -8.0 | -0.40 | 27 |
| G34 | 34.3 | 34.0 | 18.7 | 37.7 | 31.2 | 1.0 | 45.6 | -9.7 | 12.3 | 0.36 | 6 |
| G35 | 49.3 | 27.3 | 29.3 | 35.7 | 35.4 | 44.6 | 40.5 | 27.7 | 37.6 | -0.61 | 36 |
| G36 | 29.7 | 20.7 | 18.0 | 27.0 | 23.8 | 30.3 | 39.3 | 9.0 | 26.2 | -0.08 | 19 |
| G37 | 30.7 | 17.0 | 21.0 | 28.7 | 24.3 | 44.6 | 31.5 | 6.5 | 27.5 | -0.14 | 21 |
| G38 | 29.3 | 33.0 | 31.3 | 33.7 | 31.8 | -12.5 | -6.8 | -14.8 | -11.4 | 0.21 | 10 |
| G39 | 31.3 | 34.3 | 29.7 | 18.7 | 28.5 | -9.6 | 5.3 | 40.4 | 12.1 | -0.48 | 31 |
| G40 | 23.3 | 30.3 | 30.3 | 31.7 | 28.9 | -30.0 | -30.0 | -35.7 | -31.9 | 0.36 | 6 |
| G41 | 31.3 | 22.3 | 30.0 | 27.7 | 27.8 | 28.7 | 4.3 | 11.7 | 14.9 | -0.27 | 25 |
| G42 | 32.3 | 16.7 | 28.3 | 32.3 | 27.4 | 48.5 | 12.4 | 0.0 | 20.3 | -0.17 | 22 |
| G43 | 22.0 | 26.7 | 29.3 | 44.7 | 30.7 | -21.2 | -33.3 | -103.0 | -52.5 | 0.93 | 1 |
| G44 | 28.7 | 27.0 | 23.7 | 35.3 | 28.7 | 5.8 | 17.4 | -23.3 | 0.0 | 0.33 | 7 |
| G45 | 31.7 | 28.7 | 31.3 | 33.3 | 31.3 | 9.5 | 1.1 | -5.3 | 1.8 | 0.03 | 15 |
| G46 | 33.3 | 27.3 | 29.0 | 45.0 | 33.7 | 18.0 | 13.0 | -35.0 | -1.3 | 0.48 | 4 |
| G47 | 29.3 | 34.3 | 35.0 | 20.3 | 29.7 | -17.0 | -19.3 | 30.7 | -1.9 | -0.40 | 27 |
| G48 | 30.0 | 34.3 | 31.3 | 40.0 | 33.9 | -14.4 | -4.4 | -33.3 | -17.4 | 0.47 | 5 |
| G49 | 27.7 | 25.7 | 26.0 | 42.7 | 30.5 | 7.2 | 6.0 | -54.2 | -13.7 | 0.64 | 3 |
| G50 | 33.3 | 23.0 | 22.0 | 51.3 | 32.4 | 31.0 | 34.0 | -54.0 | 3.7 | 0.79 | 2 |
| Mean (T) | 31.2 | 28.5 | 30.3 | 28.3 | | | | | | | |

#### 4.1.1.7 No of vegetative branches

Genotype, treatment and their interaction significantly affected the no. of vegetative branch. The highest mean vegetative branches (1.8) were observed in T4 drought stress and the lowest no. of vegetative branches (1.2) was observed in T3 drought stress (Table 12). Highest no. of vegetative branches (2.5) was observed in G45 whereas lowest (0.7) in both G1 and G25. Based on the genotype stress interaction, highest no. of vegetative branches was observed in G3, G35 under T4 and G45 under T3 (3.0) and lowest in G23, G25, G27, G28, G43, G50 (0.3) under T1, G1, G10, G24, G25, G28, G47 (0.3) under T2 and G1, G4, G5, G6, G10, G11, G16, G42 (0.3) under T3 stress. Based on b values, the best performance was observed in genotype G43 (0.11) and lowest in G12 (-0.05). With the increase of drought stress, no. of vegetative branches was increased as shown in linear regression in Figure 21. The minimum reduction% (-700.0%) was observed in G43 under T4 drought stress (Figure 22, Table 12). Maximum reduction% (85.7%) was observed in G5 under T3 stress (Figure 22). The result showed the positive effect of drought on no. of vegetative branch genotypically. Cotton is moderately tolerant to drought stress especially for vegetative growth, but its reproductive growth is highly sensitive to drought (Ui-Allah *et al*., 2021; Niu *et al*., 2018; Iqbal *et al*., 2017 and Wang *et al*., 2016a). Drought affects the source-sink relationship by influencing the source capacity of assimilates production and their assimilation in different fruiting branches (Pilon *et al*., 2019, Zhao *et al*., 2019b).

#### 4.1.1.8 No of reproductive branches

Genotype, treatment and their interaction significantly affected the no. of reproductive branches. The highest mean reproductive branches (7.6) were observed in T4 drought stresses and the lowest no. (5.5) was observed in T3 drought stress (Table 13). Highest no. of reproductive branches (8.4) was observed in G10 whereas lowest (4.7) in G25. Based on the genotype stress interaction, highest no. of reproductive branches was observed in G38 under T1 and G11 under T2 (12.0) and lowest in G36 (0.7) under T3 stress. Based on b values, the best performance was observed in genotype G12 (0.21) and lowest in G5 (-0.25). Increasing no. of reproductive branches was shown as the drought increased (Figure 23). The minimum reduction% (-100.0%) was observed in G45 under T2 and G12 under T4 drought stress (Figure 24, Table 13). Maximum reduction% (92.6%) was observed in G36 under T3 stress (Figure 24). The result

## Table 12. No. of vegetative branches (NOVB) of fifty genotypes at different drought treatments

| Genotype | NOVB at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 1.0 | 0.3 | 0.3 | 1.0 | 0.7 | 66.7 | 66.7 | 0.0 | 44.4 | 0.00 | 11 |
| G2 | 2.0 | 1.7 | 2.0 | 2.0 | 1.9 | 16.7 | 0.0 | 0.0 | 5.6 | 0.00 | 11 |
| G3 | 1.0 | 1.7 | 1.3 | 3.0 | 1.8 | -66.7 | -33.3 | -200.0 | -100.0 | 0.09 | 2 |
| G4 | 2.0 | 2.0 | 0.3 | 2.0 | 1.6 | 0.0 | 83.3 | 0.0 | 27.8 | 0.02 | 9 |
| G5 | 2.3 | 2.0 | 0.3 | 1.7 | 1.6 | 14.3 | 85.7 | 28.6 | 42.9 | 0.00 | 11 |
| G6 | 2.0 | 2.7 | 0.3 | 1.3 | 1.6 | -33.3 | 83.3 | 33.3 | 27.8 | 0.00 | 11 |
| G7 | 2.0 | 1.7 | 1.0 | 1.0 | 1.4 | 16.7 | 50.0 | 50.0 | 38.9 | -0.03 | 14 |
| G8 | 2.0 | 2.3 | 1.0 | 2.0 | 1.8 | -16.7 | 50.0 | 0.0 | 11.1 | 0.02 | 9 |
| G9 | 2.0 | 2.0 | 0.7 | 2.3 | 1.8 | 0.0 | 66.7 | -16.7 | 16.7 | 0.03 | 8 |
| G10 | 1.3 | 0.3 | 0.3 | 1.7 | 0.9 | 75.0 | 75.0 | -25.0 | 41.7 | 0.01 | 10 |
| G11 | 1.7 | 1.7 | 0.3 | 1.3 | 1.3 | 0.0 | 80.0 | 20.0 | 33.3 | 0.00 | 11 |
| G12 | 2.0 | 1.0 | 1.3 | 1.0 | 1.3 | 50.0 | 33.3 | 50.0 | 44.4 | -0.05 | 15 |
| G13 | 2.0 | 1.7 | 1.0 | 1.0 | 1.4 | 16.7 | 50.0 | 50.0 | 38.9 | -0.03 | 1 |
| G14 | 1.3 | 1.3 | 1.7 | 1.3 | 1.4 | 0.0 | -25.0 | 0.0 | -8.3 | 0.00 | 11 |
| G15 | 2.0 | 1.0 | 2.0 | 2.0 | 1.8 | 50.0 | 0.0 | 0.0 | 16.7 | -0.01 | 12 |
| G16 | 1.3 | 1.3 | 0.3 | 1.0 | 1.0 | 0.0 | 75.0 | 25.0 | 33.3 | 0.00 | 11 |
| G17 | 2.3 | 1.7 | 0.7 | 1.7 | 1.6 | 28.6 | 71.4 | 28.6 | 42.9 | -0.01 | 12 |
| G18 | 2.0 | 1.0 | 0.7 | 2.0 | 1.4 | 50.0 | 66.7 | 0.0 | 38.9 | 0.00 | 11 |
| G19 | 0.7 | 0.7 | 1.7 | 2.3 | 1.3 | 0.0 | -150.0 | -250.0 | -133.3 | 0.06 | 5 |
| G20 | 0.7 | 1.3 | 1.7 | 1.3 | 1.3 | -100.0 | -150.0 | -100.0 | -116.7 | 0.02 | 9 |
| G21 | 1.0 | 1.3 | 1.0 | 2.0 | 1.3 | -33.3 | 0.0 | -100.0 | -44.4 | 0.05 | 6 |
| G22 | 1.0 | 1.7 | 1.0 | 2.3 | 1.5 | -66.7 | 0.0 | -133.3 | -66.7 | 0.07 | 4 |
| G23 | 0.3 | 0.7 | 2.0 | 2.3 | 1.3 | -100.0 | -500.0 | -600.0 | -400.0 | 0.07 | 4 |
| G24 | 0.7 | 0.3 | 1.7 | 1.7 | 1.1 | 50.0 | -150.0 | -150.0 | -83.3 | 0.02 | 9 |
| G25 | 0.3 | 0.3 | 1.0 | 1.3 | 0.7 | 0.0 | -200.0 | -300.0 | -166.7 | 0.03 | 8 |
| G26 | 0.7 | 2.0 | 0.7 | 1.3 | 1.2 | -200.0 | 0.0 | -100.0 | -100.0 | 0.05 | 6 |
| G27 | 0.3 | 1.0 | 1.3 | 1.3 | 1.0 | -200.0 | -300.0 | -300.0 | -266.7 | 0.04 | 7 |
| G28 | 0.3 | 0.3 | 1.3 | 1.3 | 0.8 | 0.0 | -300.0 | -300.0 | -200.0 | 0.03 | 8 |
| G29 | 0.7 | 2.3 | 1.0 | 2.0 | 1.5 | -250.0 | -50.0 | -200.0 | -166.7 | 0.08 | 3 |
| G30 | 2.0 | 0.7 | 1.0 | 1.7 | 1.3 | 66.7 | 50.0 | 16.7 | 44.4 | -0.02 | 13 |
| G31 | 1.3 | 1.3 | 1.3 | 2.3 | 1.6 | 0.0 | 0.0 | -75.0 | -25.0 | 0.04 | 7 |
| G32 | 0.7 | 1.7 | 1.7 | 1.3 | 1.3 | -150.0 | -150.0 | -100.0 | -133.3 | 0.03 | 8 |
| G33 | 2.0 | 1.0 | 1.0 | 1.3 | 1.3 | 50.0 | 50.0 | 33.3 | 44.4 | -0.03 | 14 |
| G34 | 1.3 | 0.7 | 2.3 | 2.3 | 1.7 | 50.0 | -75.0 | -75.0 | -33.3 | 0.02 | 9 |
| G35 | 2.0 | 2.7 | 2.0 | 3.0 | 2.4 | -33.3 | 0.0 | -50.0 | -27.8 | 0.05 | 6 |
| G36 | 1.0 | 1.7 | 0.7 | 1.7 | 1.3 | -66.7 | 33.3 | -66.7 | -33.3 | 0.04 | 7 |
| G37 | 1.0 | 2.7 | 1.3 | 2.0 | 1.8 | -166.7 | -33.3 | -100.0 | -100.0 | 0.06 | 5 |
| G38 | 1.0 | 1.0 | 2.0 | 2.0 | 1.5 | 0.0 | -100.0 | -100.0 | -66.7 | 0.03 | 8 |
| G39 | 2.0 | 2.0 | 1.7 | 2.0 | 1.9 | 0.0 | 16.7 | 0.0 | 5.6 | 0.00 | 11 |
| G40 | 0.7 | 1.3 | 2.7 | 1.7 | 1.6 | -100.0 | -300.0 | -150.0 | -183.3 | 0.02 | 9 |
| G41 | 1.7 | 2.0 | 0.7 | 2.3 | 1.7 | -20.0 | 60.0 | -40.0 | 0.0 | 0.05 | 6 |
| G42 | 1.0 | 1.3 | 0.3 | 1.7 | 1.1 | -33.3 | 66.7 | -66.7 | -11.1 | 0.04 | 7 |
| G43 | 0.3 | 2.3 | 1.3 | 2.7 | 1.7 | -600.0 | -300.0 | -700.0 | -533.3 | 0.11 | 1 |
| G44 | 1.7 | 1.7 | 0.7 | 2.0 | 1.5 | 0.0 | 60.0 | -20.0 | 13.3 | 0.03 | 8 |
| G45 | 2.3 | 2.7 | 3.0 | 2.0 | 2.5 | -14.3 | -28.6 | 14.3 | -9.5 | -0.02 | 13 |
| G46 | 0.7 | 0.7 | 1.0 | 1.3 | 0.9 | 0.0 | -50.0 | -100.0 | -50.0 | 0.02 | 9 |
| G47 | 1.3 | 0.3 | 1.7 | 1.7 | 1.3 | 75.0 | -25.0 | -25.0 | 8.3 | 0.00 | 11 |
| G48 | 0.7 | 1.7 | 0.7 | 1.3 | 1.1 | -150.0 | 0.0 | -100.0 | -83.3 | 0.04 | 7 |
| G49 | 1.0 | 1.7 | 1.3 | 1.3 | 1.3 | -66.7 | -33.3 | -33.3 | -44.4 | 0.02 | 9 |
| G50 | 0.3 | 1.3 | 2.0 | 2.0 | 1.4 | -300.0 | -500.0 | -500.0 | -433.3 | 0.06 | 5 |
| Mean (T) | 1.3 | 1.4 | 1.2 | 1.8 | | | | | | | |

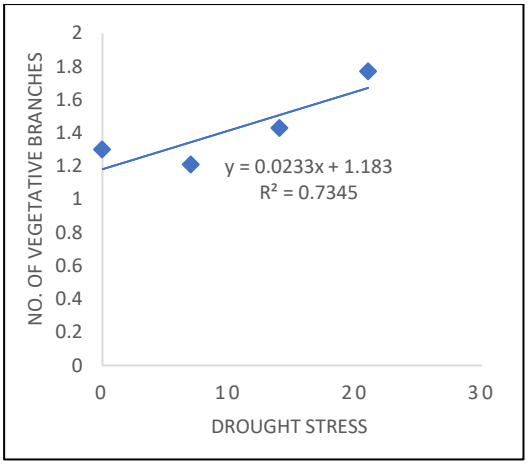



**Figure 21. Relationships between number of vegetative branches of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

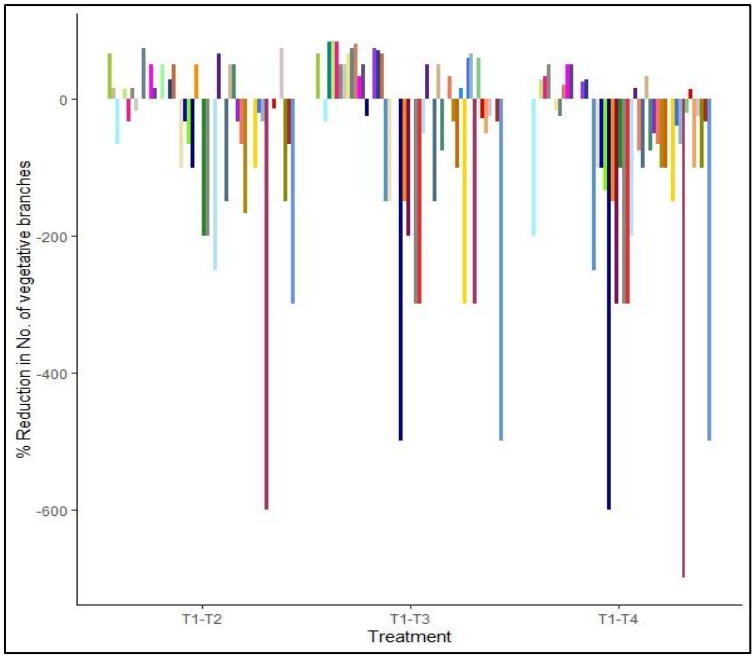
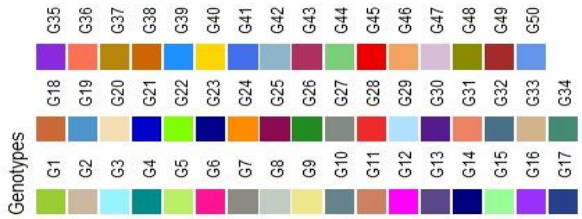



**Figure 22. Reduction percentage of number of vegetative branches of fifty cotton genotypes under different drought stresses compared with control**



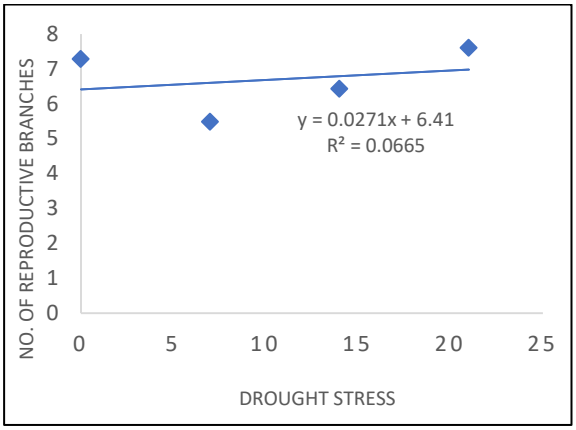




**Figure 23. Relationships between number of reproductive branches of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

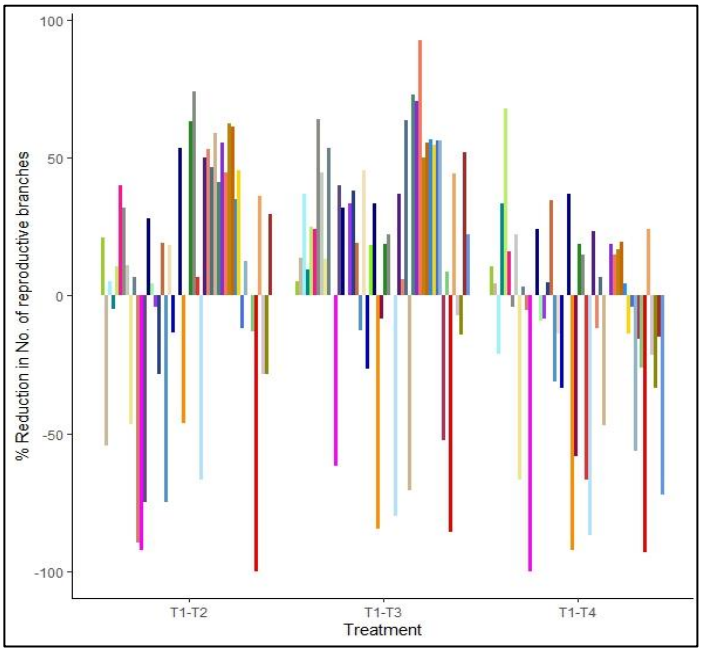



**Figure 24. Reduction percentage of number of reproductive branches of fifty cotton genotypes under different drought stresses compared with control**

**Table 13. No. of reproductive branches (NORB) of fifty genotypes at different drought treatments**

| Genotype | NORB at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 6.3 | 5.0 | 6.0 | 5.7 | 5.8 | 21.1 | 5.3 | 10.5 | 12.3 | -0.04 | 21 |
| G2 | 7.3 | 11.3 | 6.3 | 7.0 | 8.0 | -54.5 | 13.6 | 4.5 | -12.1 | 0.06 | 14 |
| G3 | 6.3 | 6.0 | 4.0 | 7.7 | 6.0 | 5.3 | 36.8 | -21.1 | 7.0 | 0.09 | 11 |
| G4 | 7.0 | 7.3 | 6.3 | 4.7 | 6.3 | -4.8 | 9.5 | 33.3 | 12.7 | -0.09 | 25 |
| G5 | 9.3 | 8.3 | 7.0 | 3.0 | 6.9 | 10.7 | 25.0 | 67.9 | 34.5 | -0.25 | 30 |
| G6 | 8.3 | 5.0 | 6.3 | 7.0 | 6.7 | 40.0 | 24.0 | 16.0 | 26.7 | -0.08 | 24 |
| G7 | 8.3 | 5.7 | 3.0 | 8.7 | 6.4 | 32.0 | 64.0 | -4.0 | 30.7 | 0.05 | 15 |
| G8 | 9.0 | 8.0 | 5.0 | 7.0 | 7.3 | 11.1 | 44.4 | 22.2 | 25.9 | -0.04 | 21 |
| G9 | 5.0 | 7.3 | 4.3 | 8.3 | 6.2 | -46.7 | 13.3 | -66.7 | -33.3 | 0.19 | 3 |
| G10 | 10.0 | 9.3 | 4.7 | 9.7 | 8.4 | 6.7 | 53.3 | 3.3 | 21.1 | 0.05 | 15 |
| G11 | 6.3 | 12.0 | 6.3 | 6.7 | 7.8 | -89.5 | 0.0 | -5.3 | -31.6 | 0.10 | 10 |
| G12 | 4.3 | 8.3 | 7.0 | 8.7 | 7.1 | -92.3 | -61.5 | -100.0 | -84.6 | 0.21 | 1 |
| G13 | 6.7 | 11.7 | 4.0 | 6.7 | 7.3 | -75.0 | 40.0 | 0.0 | -11.7 | 0.11 | 10 |
| G14 | 8.3 | 6.0 | 5.7 | 6.3 | 6.6 | 28.0 | 32.0 | 24.0 | 28.0 | -0.08 | 24 |
| G15 | 7.3 | 7.0 | 7.3 | 8.0 | 7.4 | 4.5 | 0.0 | -9.1 | -1.5 | 0.02 | 17 |
| G16 | 8.0 | 8.3 | 5.3 | 8.7 | 7.6 | -4.2 | 33.3 | -8.3 | 6.9 | 0.07 | 12 |
| G17 | 7.0 | 9.0 | 4.3 | 6.7 | 6.8 | -28.6 | 38.1 | 4.8 | 4.8 | 0.05 | 15 |
| G18 | 8.7 | 7.0 | 7.0 | 5.7 | 7.1 | 19.2 | 19.2 | 34.6 | 24.4 | -0.13 | 28 |
| G19 | 5.3 | 9.3 | 6.0 | 7.0 | 6.9 | -75.0 | -12.5 | -31.3 | -39.6 | 0.12 | 8 |
| G20 | 7.3 | 6.0 | 4.0 | 8.3 | 6.4 | 18.2 | 45.5 | -13.6 | 16.7 | 0.07 | 13 |
| G21 | 5.0 | 5.7 | 6.3 | 6.7 | 5.9 | -13.3 | -26.7 | -33.3 | -24.4 | 0.06 | 14 |
| G22 | 7.3 | 7.3 | 6.0 | 7.3 | 7.0 | 0.0 | 18.2 | 0.0 | 6.1 | 0.02 | 17 |
| G23 | 10.0 | 4.7 | 6.7 | 6.3 | 6.9 | 53.3 | 33.3 | 36.7 | 41.1 | -0.19 | 29 |
| G24 | 4.3 | 6.3 | 8.0 | 8.3 | 6.7 | -46.2 | -84.6 | -92.3 | -74.4 | 0.15 | 6 |
| G25 | 4.0 | 4.0 | 4.3 | 6.3 | 4.7 | 0.0 | -8.3 | -58.3 | -22.2 | 0.10 | 10 |
| G26 | 9.0 | 3.3 | 7.3 | 7.3 | 6.7 | 63.0 | 18.5 | 18.5 | 33.3 | -0.13 | 28 |
| G27 | 9.0 | 2.3 | 7.0 | 7.7 | 6.5 | 74.1 | 22.2 | 14.8 | 37.0 | -0.12 | 27 |
| G28 | 5.0 | 4.7 | 5.0 | 8.3 | 5.8 | 6.7 | 0.0 | -66.7 | -20.0 | 0.14 | 7 |
| G29 | 5.0 | 8.3 | 9.0 | 9.3 | 7.9 | -66.7 | -80.0 | -86.7 | -77.8 | 0.18 | 4 |
| G30 | 10.0 | 5.0 | 6.3 | 7.7 | 7.3 | 50.0 | 36.7 | 23.3 | 36.7 | -0.12 | 27 |
| G31 | 5.7 | 2.7 | 5.3 | 6.3 | 5.0 | 52.9 | 5.9 | -11.8 | 15.7 | -0.01 | 20 |
| G32 | 10.0 | 5.3 | 3.7 | 9.3 | 7.1 | 46.7 | 63.3 | 6.7 | 38.9 | 0.00 | 19 |
| G33 | 5.7 | 2.3 | 9.7 | 8.3 | 6.5 | 58.8 | -70.6 | -47.1 | -19.6 | 0.01 | 18 |
| G34 | 7.3 | 4.3 | 2.0 | 7.3 | 5.2 | 40.9 | 72.7 | 0.0 | 37.9 | 0.03 | 16 |
| G35 | 9.0 | 4.0 | 2.7 | 7.3 | 5.8 | 55.6 | 70.4 | 18.5 | 48.1 | -0.05 | 22 |
| G36 | 9.0 | 5.0 | 0.7 | 7.7 | 5.6 | 44.4 | 92.6 | 14.8 | 50.6 | 0.00 | 19 |
| G37 | 8.0 | 3.0 | 4.0 | 6.7 | 5.4 | 62.5 | 50.0 | 16.7 | 43.1 | -0.07 | 23 |
| G38 | 12.0 | 4.7 | 5.3 | 9.7 | 7.9 | 61.1 | 55.6 | 19.4 | 45.4 | -0.11 | 26 |
| G39 | 7.7 | 5.0 | 3.3 | 7.3 | 5.8 | 34.8 | 56.5 | 4.3 | 31.9 | 0.01 | 18 |
| G40 | 7.3 | 4.0 | 3.3 | 8.3 | 5.7 | 45.5 | 54.5 | -13.6 | 28.8 | 0.05 | 15 |
| G41 | 8.3 | 9.3 | 3.7 | 8.7 | 7.5 | -12.0 | 56.0 | -4.0 | 13.3 | 0.10 | 10 |
| G42 | 5.3 | 4.7 | 2.3 | 8.3 | 5.2 | 12.5 | 56.3 | -56.3 | 4.2 | 0.16 | 5 |
| G43 | 6.3 | 6.3 | 9.7 | 7.3 | 7.4 | 0.0 | -52.6 | -15.8 | -22.8 | 0.00 | 19 |
| G44 | 7.7 | 8.7 | 7.0 | 9.7 | 8.3 | -13.0 | 8.7 | -26.1 | -10.1 | 0.11 | 10 |
| G45 | 4.7 | 9.3 | 8.7 | 9.0 | 7.9 | -100.0 | -85.7 | -92.9 | -92.9 | 0.20 | 2 |
| G46 | 8.3 | 5.3 | 4.7 | 6.3 | 6.2 | 36.0 | 44.0 | 24.0 | 34.7 | -0.08 | 24 |
| G47 | 4.7 | 6.0 | 5.0 | 5.7 | 5.3 | -28.6 | -7.1 | -21.4 | -19.0 | 0.06 | 14 |
| G48 | 7.0 | 9.0 | 8.0 | 9.3 | 8.3 | -28.6 | -14.3 | -33.3 | -25.4 | 0.11 | 9 |
| G49 | 9.0 | 6.3 | 4.3 | 10.3 | 7.5 | 29.6 | 51.9 | -14.8 | 22.2 | 0.09 | 11 |
| G50 | 6.0 | 6.0 | 4.7 | 10.3 | 6.8 | 0.0 | 22.2 | -72.2 | -16.7 | 0.20 | 2 |
| Mean (T) | 7.3 | 6.4 | 5.5 | 7.6 | | | | | | | |

showed the positive effect of drought stress on no. of reproductive branches in genotypic dependent manner. Drought affects the source-sink relationship of cotton by influencing the source capacity of assimilates production and their assimilation in different fruiting branches of cotton (Pilon *et al*., 2019, Zhao *et al*., 2019b).

#### 4.1.1.9 Drought Response Index (DRI)

Drought Response Index (DRI) was calculated from the observed phenotypic value of each character. DRI value represents the relative change for each of the character caused by drought treatment. The DRI value was considered as the indicator drought tolerance. Comparing the DRI value, we have received important information about the drought tolerance in different genotypes of cotton. Finding from this study will provide theoretical bases and practical guidance for distinguishing drought tolerant germplasm resources and breeding for drought tolerant cultivar.

Fifty cotton genotypes showed a wider range of drought tolerance index (Table 14). DRI value for root length showed a wide range having maximum DRI (179.3) and minimum (51.1) in G38 and G36, respectively. The genotypes G6 and G20 showed the minimum (44.9) and maximum (122.9) DRI value for shoot length. The genotypes G38 and G28 showed the minimum (29.4) and maximum (151.7) DRI value. In case of root diameter, the minimum (53.3) and maximum (110.5) DRI value was observed in G5 and G19 respectively. The genotypes G5 and G19 showed the minimum (31.1) and maximum (137.1) DRI value. Minimum (52.4) and maximum (152.5) DRI value for number of lateral roots were observed in genotype G26 and G43, respectively. In case of number of vegetative branches, minimum (55.3) and maximum (639.4) DRI value was observed in G1 and G43, respectively. DRI value for number of vegetive branches showed wider range of value among the genotypes. In case of number of reproductive branches, minimum (49.4) and maximum (192.7) DRI were observed in G36 and G45, respectively. Based on the average DRI value of each genotype for eight agromorphogenic traits, genotypes were classified into four groups such as drought tolerant, moderately tolerant, moderately susceptible and susceptible genotypes (Table 15). Among the 50 genotypes 20 genotypes were tolerant genotypes, 17 genotypes showed moderately tolerant, 10 genotypes showed moderately susceptible and 3 genotypes showed susceptible based on the average DRI values. Majority of the genotypes (37) of cotton showed tolerant to drought stress. Very few genotypes (G5, G6 and G39) showed susceptible to drought stress.

**Table 14. Drought Response Index (DRI) values of fifty cotton genotypes for eight agromorphogenic characters**

| Genotypes | Root length | Shoot length | Shoot root length ratio | Root diameter | Total biomass of root | No. of lateral roots | No. of vegetative branches | No. of reproductive branches | Grouping |
|---|---|---|---|---|---|---|---|---|---|
| **G1** | 83.7 | 92.1 | 70.9 | 86.8 | 80.7 | 97.4 | 55.3 | 87.8 | MT |
| **G2** | 88.7 | 54.6 | 66.1 | 72.7 | 69.0 | 99.5 | 94.5 | 112.1 | MT |
| **G3** | 76.6 | 59.0 | 124.8 | 84.1 | 68.9 | 114.8 | 200.0 | 93.0 | T |
| **G4** | 78.7 | 88.4 | 75.2 | 81.3 | 52.7 | 99.6 | 72.2 | 87.3 | MS |
| **G5** | 64.2 | 60.5 | 68.0 | 53.3 | 31.1 | 85.5 | 57.2 | 65.5 | S |
| **G6** | 66.7 | 44.9 | 86.0 | 66.5 | 33.5 | 105.6 | 72.2 | 73.3 | S |
| **G7** | 76.4 | 54.3 | 80.9 | 68.3 | 49.1 | 132.9 | 61.2 | 69.4 | MS |
| **G8** | 84.4 | 60.0 | 57.9 | 72.2 | 46.4 | 86.7 | 88.8 | 74.1 | MS |
| **G9** | 73.1 | 48.7 | 94.1 | 84.1 | 64.8 | 96.0 | 83.3 | 133.3 | MT |
| **G10** | 72.7 | 67.7 | 102.6 | 53.9 | 48.8 | 89.4 | 58.4 | 78.9 | MS |
| **G11** | 85.0 | 68.3 | 71.3 | 75.3 | 104.3 | 86.1 | 66.5 | 131.6 | MT |
| **G12** | 85.2 | 59.9 | 144.4 | 83.7 | 75.5 | 109.0 | 55.5 | 184.8 | T |
| **G13** | 106.6 | 111.4 | 53.9 | 59.5 | 53.8 | 85.5 | 61.2 | 111.6 | MT |
| **G14** | 97.8 | 59.3 | 62.5 | 67.2 | 51.8 | 100.9 | 108.5 | 72.0 | MS |
| **G15** | 96.5 | 61.5 | 85.6 | 66.1 | 75.7 | 96.8 | 83.3 | 101.5 | MT |
| **G16** | 116.6 | 83.6 | 66.8 | 83.7 | 60.7 | 94.0 | 66.7 | 93.0 | MT |
| **G17** | 79.2 | 79.1 | 84.3 | 76.8 | 51.6 | 77.9 | 57.4 | 95.2 | MS |
| **G18** | 77.5 | 66.9 | 96.5 | 73.3 | 63.5 | 80.5 | 61.2 | 75.6 | MS |
| **G19** | 96.2 | 73.5 | 127.0 | 110.5 | 137.1 | 87.7 | 232.3 | 139.6 | T |
| **G20** | 72.8 | 122.9 | 103.6 | 90.4 | 62.8 | 100.0 | 215.4 | 83.4 | T |
| **G21** | 91.8 | 73.1 | 121.5 | 93.3 | 89.3 | 89.9 | 144.3 | 124.5 | T |
| **G22** | 89.5 | 108.1 | 84.8 | 81.5 | 58.9 | 72.1 | 166.7 | 94.0 | T |
| **G23** | 96.2 | 74.1 | 77.8 | 82.5 | 106.2 | 64.3 | 505.1 | 58.9 | T |
| **G24** | 95.6 | 72.6 | 95.3 | 101.8 | 108.0 | 92.1 | 182.6 | 174.4 | T |
| **G25** | 81.3 | 87.6 | 103.3 | 78.8 | 74.6 | 71.7 | 268.7 | 122.2 | T |
| **G26** | 68.7 | 81.8 | 89.0 | 78.7 | 84.2 | 52.4 | 199.0 | 66.6 | T |
| **G27** | 97.2 | 61.5 | 62.2 | 64.6 | 61.2 | 92.5 | 369.7 | 63.0 | T |
| **G28** | 64.5 | 57.8 | 151.7 | 91.1 | 60.6 | 99.6 | 302.0 | 120.0 | T |
| **G29** | 91.1 | 90.4 | 104.4 | 89.8 | 120.8 | 105.0 | 265.2 | 177.7 | T |
| **G30** | 67.4 | 93.0 | 86.1 | 67.5 | 45.4 | 107.8 | 55.7 | 63.3 | MS |
| **G31** | 106.4 | 57.5 | 67.2 | 71.1 | 75.4 | 120.8 | 125.1 | 84.2 | MT |
| **G32** | 90.2 | 71.7 | 64.6 | 67.4 | 31.8 | 86.4 | 232.3 | 61.1 | MT |
| **G33** | 85.3 | 58.4 | 84.6 | 89.8 | 100.2 | 108.0 | 55.5 | 119.5 | MT |
| **G34** | 83.4 | 71.1 | 82.9 | 72.0 | 125.2 | 87.7 | 133.6 | 62.1 | MT |
| **G35** | 81.2 | 62.3 | 85.9 | 75.3 | 66.0 | 62.4 | 127.8 | 51.9 | MS |
| **G36** | 51.1 | 69.5 | 113.2 | 58.3 | 42.0 | 73.8 | 133.7 | 49.4 | MS |
| **G37** | 74.0 | 57.5 | 77.0 | 69.3 | 46.9 | 72.5 | 200.0 | 57.0 | MT |
| **G38** | 179.3 | 51.9 | 29.4 | 77.7 | 44.4 | 111.4 | 166.7 | 54.6 | MT |
| **G39** | 77.3 | 53.1 | 64.3 | 71.4 | 41.9 | 88.0 | 94.5 | 68.1 | S |
| **G40** | 65.6 | 49.2 | 140.7 | 82.5 | 47.1 | 131.9 | 282.1 | 71.2 | T |
| **G41** | 109.6 | 82.0 | 53.5 | 90.7 | 60.3 | 85.1 | 99.8 | 86.7 | MT |
| **G42** | 95.3 | 57.5 | 80.3 | 79.5 | 46.5 | 79.7 | 111.0 | 95.9 | MT |
| **G43** | 81.4 | 74.9 | 128.1 | 80.5 | 122.4 | 152.5 | 639.4 | 122.9 | T |
| **G44** | 81.2 | 93.0 | 97.1 | 81.4 | 71.4 | 100.0 | 86.6 | 110.1 | T |
| **G45** | 99.8 | 73.1 | 92.6 | 104.2 | 81.3 | 98.2 | 109.7 | 192.7 | T |
| **G46** | 94.6 | 90.1 | 67.5 | 84.1 | 53.3 | 101.3 | 149.3 | 65.3 | MT |
| **G47** | 130.6 | 58.7 | 53.8 | 70.1 | 67.8 | 101.9 | 92.0 | 119.0 | MT |
| **G48** | 113.8 | 71.2 | 81.1 | 97.9 | 105.8 | 117.4 | 182.6 | 125.4 | T |
| **G49** | 83.0 | 90.0 | 63.6 | 77.9 | 96.5 | 113.6 | 144.3 | 77.7 | T |
| **G50** | 92.1 | 52.9 | 71.6 | 73.6 | 50.7 | 96.3 | 538.4 | 116.7 | T |

**Table 15. Grouping of 50 genotypes based on DRI values under drought stress**

| Sl No. | Scale | % DRI values | Drought tolerant group | Name of genotypes |
|---|---|---|---|---|
| **1** | I | >90 | Tolerant (T) | G3, G12, G19, G20, G21, G22, G23, G24, G25, G26, G27, G28, G29, G40, G43, G44, G45, G48, G49, G50 |
| **2** | II | 80-90 | Moderately tolerant (MT) | G1, G2, G9, G11, G13, G15, G16, G31, G32, G33, G34, G37, G38, G41, G42, G46, G47. |
| **3** | III | 70-80 | Moderately susceptible (MS) | G4, G7, G8, G10, G14, G17, G18, G30, G35, G36 |
| **4** | IV | <70 | Susceptible (S) | G5, G6, G39 |

### 4.1.2 Genetic variability analysis

The extent of variation among the genotypes in respect of eight characters was studied and mean sum of square, phenotypic variance ($\sigma^2p$), genotypic variance ($\sigma^2g$), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ($h^2b$), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) presented in Table 16.

#### 4.1.2.1 Root length

Minimum and Maximum value of root length were 10.13 cm and 19.87 cm respectively which showed the presence of variation in toot length among the genotypes (Table 16). The genotypic and phenotypic variance for this trait was 2.58 and 2.83 respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were medium (11.06 and 10.56 respectively). PCV was higher than GCV which suggested that the variation was not only due to the genotypes but also due to the influences of environment. However, narrow gap between the PCV and GCV was very low indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates were very high (91%) with low genetic advance (3.16) and genetic advance in mean % (20.78). High heritability coupled with low genetic advance indicated the non-additive gene action. High heritability was due to the influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability for root length in cotton was also observed in Riaz *et al*. (2019). They found medium genetic advance which contradict to ours.

#### 4.1.2.2 Shoot length

Minimum and Maximum value of shoot length were 44.5 cm and 86.0 cm respectively which showed the presence of variation in shoot length among the genotypes (Table 16). The genotypic and phenotypic variance for this trait was 59.49 and 63.34, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of

**Table 16. Estimation of genetic parameters of eight characters of fifty genotypes in cotton**

| Genetic parameters | Root length | Shoot length | Shoot root length ratio | Root diameter | Total biomass of root | No. of lateral roots | No. of vegetative branches | No. of reproductive branches |
|---|---|---|---|---|---|---|---|---|
| Minimum | 10.13 | 44.5 | 3.02 | 6.55 | 1.70 | 22.50 | 0.25 | 4.25 |
| Maximum | 19.87 | 86.00 | 6.33 | 9.68 | 5.40 | 39.25 | 2.75 | 8.75 |
| GM | 15.22 | 67.72 | 4.60 | 8.03 | 3.47 | 29.59 | 1.43 | 6.69 |
| σ2g | 2.58 | 59.49 | 0.43 | 0.27 | 0.49 | 11.81 | 0.09 | 0.82 |
| σ2e | 0.25 | 4.13 | 0.04 | 0.09 | 0.06 | 0.86 | 0.11 | 0.16 |
| σ2p | 2.83 | 63.54 | 0.47 | 0.37 | 0.55 | 12.67 | 0.20 | 0.98 |
| GCV | 10.56 | 11.38 | 14.27 | 6.53 | 22.18 | 11.61 | 21.50 | 13.51 |
| ECV | 3.28 | 3.00 | 4.56 | 3.83 | 6.97 | 3.13 | 23.36 | 5.97 |
| PCV | 11.06 | 11.77 | 14.98 | 7.57 | 21.35 | 12.03 | 31.75 | 14.77 |
| Heritability | 0.91 | 0.94 | 0.91 | 0.74 | 0.89 | 0.93 | 0.46 | 0.84 |
| GA (5%) | 3.16 | 15.35 | 1.29 | 0.93 | 1.36 | 6.84 | 0.43 | 1.70 |
| GA (% mean) | 20.78 | 22.67 | 28.01 | 11.60 | 39.30 | 23.10 | 29.99 | 25.45 |
| SEM | 0.29 | 1.17 | 0.12 | 0.18 | 0.14 | 0.53 | 0.19 | 0.23 |
| CD 5% | 0.81 | 3.29 | 0.34 | 0.50 | 0.39 | 1.50 | 0.54 | 0.65 |
| CD1% | 1.07 | 4.36 | 0.45 | 0.66 | 0.52 | 1.99 | 0.71 | 0.86 |

Here, GM= Grand mean; $\sigma^2$g= Genotypic variance; σ2e= environmental variance; σ2p= phenotypic variance; GCV= genotypic coefficient of variation; ECV=Environmental coefficient of variation, PCV= Phenotypic coefficient of variation, GA= genetic advance; SEM=Standard error of mean, CD= Critical differences.

genes controlling this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were medium (11.77 and 11.38, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (94%) with medium genetic advance (15.35) and genetic advance in mean (22.67%). The high heritability coupled with medium genetic advance indicates the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and medium phenotypic coefficient of variation for cotton shoot length had been also reported in Shar *et al*. (2017).

#### 4.1.2.3 Shoot root length ratio

Minimum and Maximum value of root length ratio were 3.02 and 6.33, respectively which showed the presence of variation in shoot root length ratio among the genotypes (Table 16). The genotypic and phenotypic variance for this trait was 0.43 and 0.47, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were medium (14.98 and 14.27, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (91%) with low genetic advance (1.29) and genetic advance in mean (28.01%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding.

#### 4.1.2.4 Root diameter

Minimum and Maximum value of root diameter were 6.55 mm and 9.68 mm respectively which showed the presence of variation in root diameter among the genotypes (Table 16). The genotypic and phenotypic variance for this trait was 0.27 and 0.37 respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (7.57 and 6.53, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were high (74%) with low genetic advance (0.93) and genetic advance in mean (11.60%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. Similar result for heritability, genetic advance and phenotypic coefficient of variation has been observed in Dhivya *et al*. (2014).

#### 4.1.2.5 Total biomass of root

Minimum and Maximum value of biomass of root were 1.70 gm and 5.40 gm respectively which showed the presence of variation in total biomass of root among the genotypes (Table 16). The genotypic and phenotypic variance for this trait was 0.49 and 0.55, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high (21.35 and 22.18 respectively). GCV was higher than PCV which suggested that there was little influence of the environment on the expression of character. However, the differences between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection

for the improvement of the crop will be rewarding. The heritability estimates for this trait were very high (89%) with low genetic advance (1.36) and genetic advance in mean (39.30%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. Khan *et al*. (2017) found that cotton genotypes showed higher heritability and environmental coefficient of variation under drought stress conditions.

#### 4.1.2.6 No. of lateral root

Minimum and Maximum value of number of lateral roots were 22.50 and 39.25, respectively which showed the presence of variation in no. of lateral root among the genotypes (Table 16). The genotypic and phenotypic variance for this trait was 11.81 and 12.67, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (12.03 and 11.61, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (93%) with low genetic advance (6.84) and genetic advance in mean (23.10%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability, high phenotypic coefficient of variation and genetic advance has been found in Nawaz *et al*. (2019).

#### 4.1.2.7 No. of vegetative branches

Minimum and Maximum value of number of vegetative branches were 0.25 and 2.75, respectively which showed the presence of variation in no. of vegetative branch among the genotypes (Table 16). The genotypic and phenotypic variance for this trait was 0.09 and 0.20 respectively. The phenotypic and environmental variance appeared

to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV) and genotypic coefficient of variation (GCV) were high (31.75, 23.36 and 21.50, respectively). PCV and ECV were higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was high which indicated that environmental influence was major on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be misleading for the improvement of the crop. The heritability estimates for this trait were very low (46%) with low genetic advance (0.43) and genetic advance in mean (29.99%). The low heritability coupled with low genetic advance indicated that the character was highly influence of environment rather than the genotypes and selection based on this trait would be ineffective. Similar findings have been reported in Shakeel *et al*. (2015). However, Adeela *et al*. (2021) showed higher of phenotypic, genotypic, and environmental coefficient variation for number of vegetative branches in cotton genotypes with higher heritability and genetic advances.

#### 4.1.2.8 No. of reproductive branches

Minimum and Maximum value of number of reproductive branches were 4.25 and 8.75, respectively which showed the presence of variation in no. of reproductive branches among the genotypes (Table 16). The genotypic and phenotypic variance for this trait was 0.82 and 0.98, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (14.77 and 13.51, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (84%) with low genetic advance (1.70) and genetic advance in mean (25.45%). The high heritability coupled with low genetic advance indicated

the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. Similar results have been reported in Shakeel *et al*. (2015) and Khan *et al*. (2017) for environmental coefficient of variation and heritability.

### 4.1.3 Correlation coefficient

Correlation studies along with path analysis provide a better understanding of the association of different characters with yield related traits. Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components as suggested by Sing and Chaudhary 1985. Phenotypic and genotypic correlation coefficients among the different pairs for different genotypes of cotton are given in Table 17 and Table 18, respectively.

In case of genotypic correlation coefficient, root length showed significant positive correlation with root diameter (0.33), total biomass of root (0.43), number of lateral roots (0.46), significant negative correlation with shoot root length ratio (-0.56) and non-significant correlation with shoot length (0.26), number of vegetative branches (0.22) and number of reproductive branches (0.21) (Table 17). Shoot length showed statistical positive significant correlation with shoot root length ration (0.61), total biomass of root (0.28), number of vegetative branches (0.45) and number of reproductive branches (0.56), and non-significant correlation with root diameter (0.26) and number of lateral roots (0.28). Shoot root length ratio showed significant positive correlation with number of reproductive branches (0.29) and non-significant relation with root diameter (-0.04), total biomass of root (-0.16), number of lateral roots (-0.08) and number of vegetative branches (0.16). Root diameter showed significant positive correlation with total biomass of root (0.62), number of lateral roots (0.50) and number of reproductive branches (0.44) and non-significant correlation with number of vegetative branches (0.19). Total biomass of root showed significant positive correlation with number of lateral roots (0.41), number of vegetative branches (0.38) and number of reproductive branches (0.33). Number of lateral roots showed non-significant correlation with number of vegetative branches (0.21) and number of reproductive branches (0.15). Number of vegetative branches showed non-significant correlation with number of reproductive branches (0.11). Number of reproductive branches showed significant positive correlation with shoot length (0.56),

**Table 17. Genotypic correlation coefficient among different pairs of agromorphogenic characters of fifty genotypes of cotton**

| Characters | Root length | Shoot length | Shoot root length ratio | Root diameter | Total biomass of root | No. of lateral roots | No. of vegetative branches | No. of reproductive branches |
|---|---|---|---|---|---|---|---|---|
| **Root length** | | $0.26^{NS}$ | $-0.56^{**}$ | $0.33^{*}$ | $0.43^{**}$ | $0.46^{**}$ | $0.22^{NS}$ | $0.21^{NS}$ |
| **Shoot length** | | | $0.61^{**}$ | $0.26^{NS}$ | $0.28^{*}$ | $0.28^{NS}$ | $0.45^{**}$ | $0.56^{**}$ |
| **Shoot root length ratio** | | | | $-0.04^{NS}$ | $-0.16^{NS}$ | $-0.08^{NS}$ | $0.16^{NS}$ | $0.29^{*}$ |
| **Root diameter** | | | | | $0.62^{**}$ | $0.50^{**}$ | $0.19^{NS}$ | $0.44^{**}$ |
| **Total biomass of root** | | | | | | $0.41^{**}$ | $0.38^{**}$ | $0.33^{*}$ |
| **No. of lateral roots** | | | | | | | $0.21^{NS}$ | $0.15^{NS}$ |
| **No. of vegetative branches** | | | | | | | | $0.11^{NS}$ |
| **No. of reproductive branches** | | | | | | | | |

$^{*}$Significant at 5% level
$^{**}$Significant at 1% level
$^{NS}$ Non-significant

**Table 18. Phenotypic correlation coefficient among different pairs of agromorphogenic characters of fifty genotypes of cotton**

| Characters | Root length | Shoot length | Shoot root length ratio | Root diameter | Total biomass of root | No. of lateral roots | No. of vegetative branches | No. of reproductive branches |
|---|---|---|---|---|---|---|---|---|
| **Root length** | | 0.25** | -0.57** | 0.27** | 0.38** | 0.43** | 0.17* | 0.19* |
| **Shoot length** | | | 0.61** | 0.23** | 0.27** | 0.26** | 0.28** | 0.51** |
| **Shoot root length ratio** | | | | -0.25NS | -0.14NS | -0.08NS | 0.09NS | 0.27** |
| **Root diameter** | | | | | 0.55** | 0.43** | 0.07NS | 0.40** |
| **Total biomass of root** | | | | | | 0.38** | 0.27** | 0.30** |
| **No. of lateral roots** | | | | | | | 0.12NS | 0.12** |
| **No. of vegetative branches** | | | | | | | | 0.13NS |
| **No. of reproductive branches** | | | | | | | | |

*Significant at 5% level
**Significant at 1% level
NS Non-significant

shoot root length ratio (0.29), root diameter (0.44), total biomass of root (0.33), non-significant correlation with root length (0.21), number of lateral roots (0.15) and number for vegetative branches (0.11). At the genotypic level, Adeela *et al*. (2021) showed that plant height showed significant positive correlation with number of reproductive branches, number of vegetative branches and root diameter. He also showed that vegetative branches per plant showed non-significant positive correlation with number of reproductive branches which have been observed in our experiment as well.

In case of phenotypic correlation coefficient**,** root length showed significant positive correlation with shoot length (0.25), root diameter (0.27), total biomass of root (0.38), number of lateral roots (0.43), number of vegetative branch (0.17), number of reproductive branch (0.19) and significant negative correlation with shoot root length ratio (-0.57) (Table 18). Shoot length showed statistical positive significant correlation with shoot root length ration (0.61), root diameter (0.23), total biomass of root (0.27), number of lateral root (0.26), number of vegetative branches (0.28) and number of reproductive branches (0.51). Shoot root length ratio showed significant positive correlation with number of reproductive branches (0.27) and non-significant relation with root diameter (-0.25), total biomass of root (-0.14), number of lateral roots (-0.08) and number of vegetative branches (0.09). Root diameter showed significant positive correlation with total biomass of root (0.55), number of lateral roots (0.43) and number of reproductive branches (0.40) and non-significant correlation with number of vegetative branches (0.07). Total biomass of root showed significant positive correlation with number of lateral roots (0.38), number of vegetative branches (0.27) and number of reproductive branches (0.30). Number of lateral roots showed significant positive correlation with number of reproductive branches (0.12) and non-significant correlation with number of vegetative branches (0.12). Number of vegetative branches showed non-significant correlation with number of reproductive branches (0.13). Number of reproductive branches showed significant positive correlation with root length (0.19), shoot length (0.51), shoot root length ratio (0.27), root diameter (0.40), total biomass of root (0.30), number of lateral roots (0.12) and non-significant correlation with number for vegetative branches (0.13). At the phenotypic level, similar result has been observed in Adeela *et al*. (2021), Reddy *et al*. (2019) and Kumbhar *et al*. (2020). They reported a significantly positive association

of plant height with sympodial branches. Salahuddin *et al*. (2010) found that at the phenotypic level, yield was positively associated with sympodial and bolls. Pujer *et al*. (2014), Joshi *et al*. (2006), Anandan (2009) indicated that sympodial branches/plant positively correlated with plant height and number of vegetative branches. Mvula *et al*. (2018) also reported that the association between growth parameters and total biomass had positive correlation coefficients implying that selection for taproot length, lateral root number, shoot fresh weight, shoot dry weight, root fresh weight, root dry weight, shoot length, root volume, stem diameter and number of leaves might improve total biomass under water stressed conditions.

### 4.1.4 Path coefficient analysis

Path coefficient is a means of measuring the direct and indirect effects of one variable through the other variables on the end-product. Here number of reproductive branches was considered as effect (dependent variable) and root length, shoot diameter, shot root length ratio, root diameter, total biomass of root, number of lateral roots, number of vegetative branches and numbers of reproductive branches were considered as independent variables. Wright (1921) developed the path coefficient analysis technique and later demonstrated by Deway and Lu (1959) facilitates the partitioning of correlation coefficients into direct and indirect contribution of various characters on number of reproductive branches. It is standardized partial regression coefficient analysis. As such, it measures the direct influence if one variable upon other. Estimation of direct and indirect effect of path coefficient analysis is presented in Table 19 and Table 20.

In case of genotypic path coefficient analysis, root length had positive direct effect on number of reproductive branches (0.09) which was contributed to result non-significant positive genotypic correlation (0.21) (Table 19). Root length had positive indirect effect on shoot length (0.14), root diameter (0.12), total biomass of root (0.04), and negative indirect effect on shoor root length ratio (-0.14), number of lateral root (-0.09) and number of vegetative branches (-0.05) (Table 19). Shoot length showed positive direct effect (0.53) on number of reproductive branches with significant positive genotypic correlation (0.56). Shoot length had positive indirect effect on root length (0.03), shoot root length ratio (0.04), root diameter (0.09), total biomass of root (0.03) and negative indirect effect on number of lateral roots (-0.06)

**Table 19. Genotypic path coefficient analysis showing the direct (bold) and indirect effect of different characters on No. of reproductive branches of cotton**

| Characters | Root length | Shoot length | Shoot root length ratio | Root diameter | Total biomass of root | No. of lateral roots | No. of vegetative branches | Genotypic correlation with No. of reproductive branches |
|---|---|---|---|---|---|---|---|---|
| **Root length** | **0.09** | 0.14 | -0.04 | 0.12 | 0.04 | -0.09 | -0.05 | $0.21^{NS}$ |
| **Shoot length** | 0.03 | **0.53** | 0.04 | 0.09 | 0.03 | -0.06 | -0.09 | $0.56^{**}$ |
| **Shoot root length ratio** | -0.06 | 0.32 | **0.07** | -0.01 | -0.01 | 0.02 | -0.03 | $0.29^{*}$ |
| **Root diameter** | 0.03 | 0.14 | -0.00 | **0.36** | 0.06 | -0.10 | -0.04 | $0.44^{**}$ |
| **Total biomass of root** | 0.04 | 0.15 | -0.01 | 0.22 | **0.09** | -0.08 | -0.08 | $0.33^{*}$ |
| **No. of lateral roots** | 0.05 | 0.15 | -0.00 | 0.18 | 0.04 | **-0.21** | -0.05 | $0.15^{NS}$ |
| **No. of vegetative branches** | 0.02 | 0.24 | 0.01 | 0.07 | 0.03 | -0.04 | **-0.22** | $0.11^{NS}$ |

**Table 20. Phenotypic path coefficient analysis showing the direct (bold) and indirect effect of different characters on No. of reproductive branches of cotton**

| Characters | Root length | Shoot length | Shoot root length ratio | Root diameter | Total biomass of root | No. of lateral roots | No. of vegetative branches | Phenotypic correlation with No. of reproductive branches |
|---|---|---|---|---|---|---|---|---|
| **Root length** | **0.18** | 0.08 | -0.10 | 0.09 | 0.02 | -0.08 | -0.00 | 0.19* |
| **Shoot length** | 0.04 | **0.33** | 0.11 | 0.78 | 0.02 | -0.05 | -0.01 | 0.51** |
| **Shoot root length ratio** | -0.10 | 0.20 | **0.17** | -01 | -0.01 | 0.01 | -0.00 | 0.27** |
| **Root diameter** | 0.05 | 0.08 | -0.00 | **0.33** | 0.04 | -0.08 | -0.00 | 0.40** |
| **Total biomass of root** | 0.07 | 0.09 | -0.02 | 0.18 | **0.06** | -0.07 | -0.01 | 0.30** |
| **No. of lateral roots** | 0.08 | 0.08 | -0.01 | 0.14 | 0.02 | **-0.19** | -0.00 | 0.12** |
| **No. of vegetative branches** | 0.03 | 0.09 | 0.02 | 0.02 | 0.07 | -0.02 | **-0.03** | 0.13NS |

and number of vegetative branches (-0.09). Shoot root length ratio had positive direct effect on number of reproductive branches (0.07) which was contributed to result on significant positive genotypic correlation (0.29). Shoot root length ratio had negative indirect effect on root length (-0.06, root diameter (-0.01), total biomass of root (-0.01) and number of vegetative branches (-0.03) and positive indirect effect on shoot length (0.32) and number of lateral roots (0.02). Root diameter had positive direct effect on number of reproductive branches (0.36) which was contributed to result in significant positive genotypic correlation (0.44). Root diameter had positive indirect effect on root length (0.03), shoot length (0.14), total biomass of root (0.06) and negative indirect effect on shoot root length ratio (-0.00), number of lateral roots (-0.10) and number of vegetative branches (-0.04). Total biomass of root had direct positive effect on number of reproductive branches (0.09) which was contributed significant positive genotypic correlation (0.33). Total biomass of root had positive indirect effect on root length (0.04), shoot length (0.15), root diameter (0.22) and indirect negative effect on shoot root length ratio (-0.01), number of lateral roots (-0.08) and number of vegetative branches (-0.08). Number of lateral roots had negative direct effect on number of reproductive branches (-0.21) which was contributed non-significant genotypic correlation (0.15). Number of lateral roots had positive indirect effect on root length (0.05), shoot length (0.15), root diameter (0.18), total biomass of root (0.04) and negative indirect effect on shoot root length ratio (-0.00) and number of vegetative branches (-0.05). Number of vegetative branches had negative direct effect on number of reproductive branches (-0.22) which was contributed non-significant genotypic correlation (0.11). Number of vegetative branches had positive indirect effect on root length (0.02), shoot length (0.24), shoot root length ratio (0.01), root diameter (0.07), total biomass of root (0.03) and negative indirect effect number of lateral roots (-0.04). Genotypic path coefficient analysis carried out by Chapepa *et al*. (2020) showed that plant height and number of lateral roots have the highest direct effect on cotton yield and number of reproductive branches which had also observed in this study. In this study showed the negative direct effect on number of reproductive branches which had been also observed in Rauf *et al*. (2004).

In case of phenotypic path coefficient, root length had positive direct effect on number of reproductive branches (0.18) which was contributed to result significant positive phenotypic correlation (0.19) (Table 20). Root length had positive indirect effect on

shoot length (0.08), root diameter (0.09), total biomass of root (0.02), and negative indirect effect on shoot root length ratio (-0.10), number of lateral root (-0.08) and number of vegetative branches (-0.00) (Table 20). Shoot length showed positive direct effect (0.33) on number of reproductive branches with significant positive phenotypic correlation (0.51). Shoot length had positive indirect effect on root length (0.04), shoot root length ratio (0.11), root diameter (0.78), total biomass of root (0.02) and negative indirect effect on number of lateral roots (-0.05) and number of vegetative branches (-0.01). Shoot root length ratio had positive direct effect on number of reproductive branches (0.17) which was contributed to result on significant positive phenotypic correlation (0.27). Shoot root length ratio had negative indirect effect on root length (-0.10), root diameter (-0.01), total biomass of root (-0.01) and number of vegetative branches (-0.00) and positive indirect effect on shoot length (0.20) and number of lateral roots (0.01). Root diameter had positive direct effect on number of reproductive branches (0.33) which was contributed to result in significant positive phenotypic correlation (0.40). Root diameter had positive indirect effect on root length (0.05), shoot length (0.08), total biomass of root (0.04) and negative indirect effect on shoot root length ratio (-0.00), number of lateral roots (-0.08) and number of vegetative branches (-0.00). Total biomass of root had direct positive effect on number of reproductive branches (0.06) which was contributed significant positive phenotypic correlation (0.30). Total biomass of root had positive indirect effect on root length (0.07), shoot length (0.09), root diameter (0.18) and indirect negative effect on shoot root length ratio (-0.02), number of lateral roots (-0.07) and number of vegetative branches (-0.01). Number of lateral roots had negative direct effect on number of reproductive branches (-0.19) which was contributed significant phenotypic correlation (0.12). Number of lateral roots had positive indirect effect on root length (0.08), shoot length (0.08), root diameter (0.14), total biomass of root (0.02) and negative indirect effect on shoot root length ratio (-0.01) and number of vegetative branches (-0.00). Number of vegetative branches had negative direct effect on number of reproductive branches (-0.03) which was contributed non-significant phenotypic correlation (0.13). Number of vegetative branches had positive indirect effect on root length (0.03), shoot length (0.09), shoot root length ratio (0.02), root diameter (0.02), total biomass of root (0.07) and negative indirect effect number of lateral roots (-0.02).

### 4.1.5 Multivariate analysis

#### 4.1.5.1 Principal component analysis (PCA)

Principal component analysis was calculated with fifty genotypes of cotton which provides the information Eigen values, contribution of each eight variables for each component and the relationship among the genotypes and treatments based on their similarity or dissimilarity of their performance.

PCA for fifty genotypes of cotton provides eight components (Table 21). The highest Eigen value was observed in PC1 (3.27) followed by PC2 (1.59) and PC3 (1.05). PC1 showed the highest % variance (40.88) followed by PC2 (19.85) and PC3 (13.07). Scree plot showed the percentage of explained variances by each PCs (Figure 25). First two PCs explained 60.745 of observed variation (Table 21). First five PCs explained 93.12% variances. Adeela *et al*., (2021) showed the similar results for eigen value for cotton genotypes under drought stress conditions. However, the first six components showed eigne value above 1 whereas in the study showed the first three PCs with an eigne value above 1.

Based on the two highest principal components (PC1 and PC2) along with the contributions of each response variables of fifty genotypes, two-dimensional scatter diagram has been prepared using X axis as first component and Y axis as second component (Figure 26 and Figure 27). The color denotes the contributions of each response variables to explain the variation among the genotypes. In case of PC1, the most important response variables having the highest explained variances were observed for shoot length followed by root diameter, total biomass of root, shoot root length ratio and number of lateral roots (Figure 26, Figure 27). The most important variables for PC2 having the highest percent of explained variance was observed in root length followed by shoot root length ratio and number of lateral roots. From this scatter diagram, the most important variables were related to shoot and root characters. Isong *et al*. (2017) reported that characters related to shoot and root contributed most to explain the observed variation. Adeela *et al*. (2021) showed that shoot length, root diameter, and number vegetative branches contributed mostly to explain the observed variations among the cotton genotypes under drought stress.

**Table 21. List of components with their eigen values, percent varaince and cumulative percent varaince**

| Components | Eigen value | % variance | % Cumulative varaince |
|---|---|---|---|
| **PC1** | 3.27 | 40.88 | 40.88 |
| **PC2** | 1.59 | 19.85 | 60.74 |
| **PC3** | 1.05 | 13.07 | 73.81 |
| **PC4** | 0.82 | 10.31 | 84.12 |
| **PC5** | 0.72 | 8.99 | 93.12 |
| **PC6** | 0.33 | 4.18 | 97.30 |
| **PC7** | 0.19 | 2.35 | 99.65 |
| **PC8** | 0.03 | 0.35 | 100 |

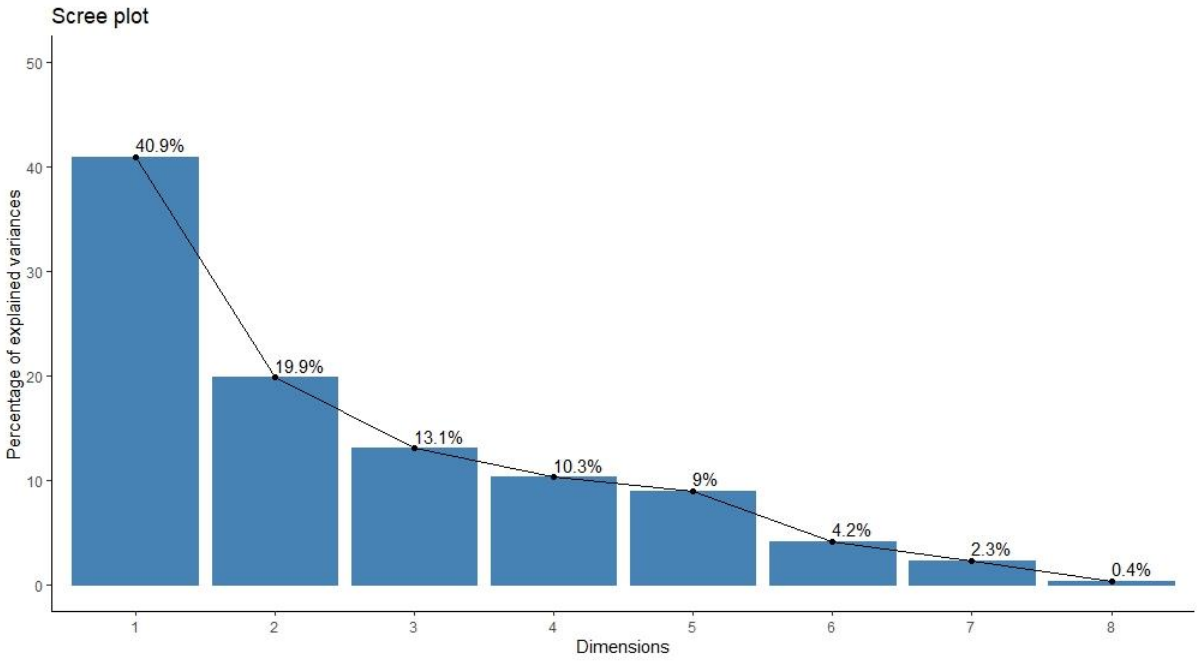



**Figure 25. Scree plot showing the percentage of explained variance by each of the eight Principal components**

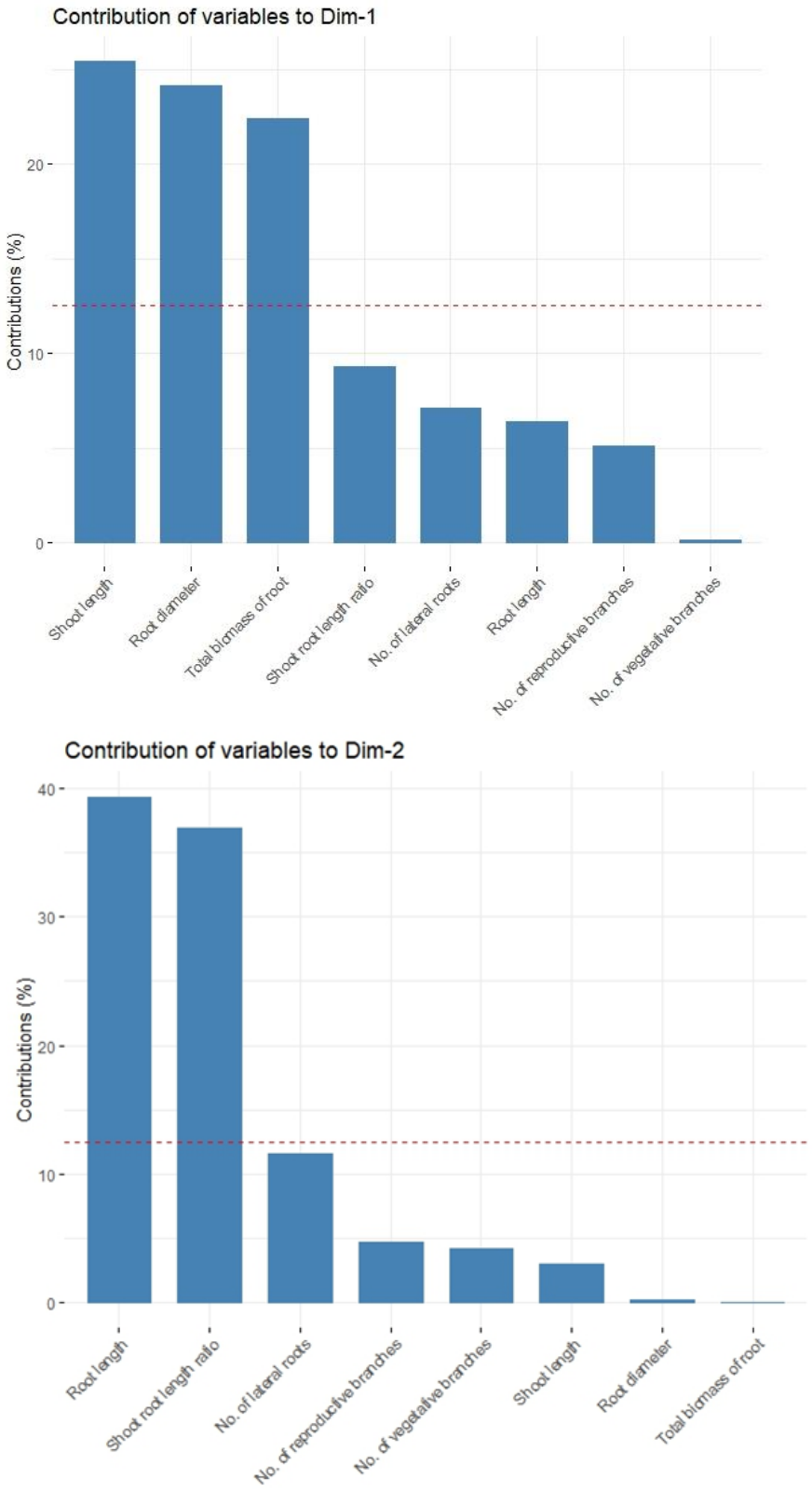



**Figure 26. Contribution of each eight agromorphogenic characters of fifty genotypes for PC1 (top) and PC2 (bottom)**

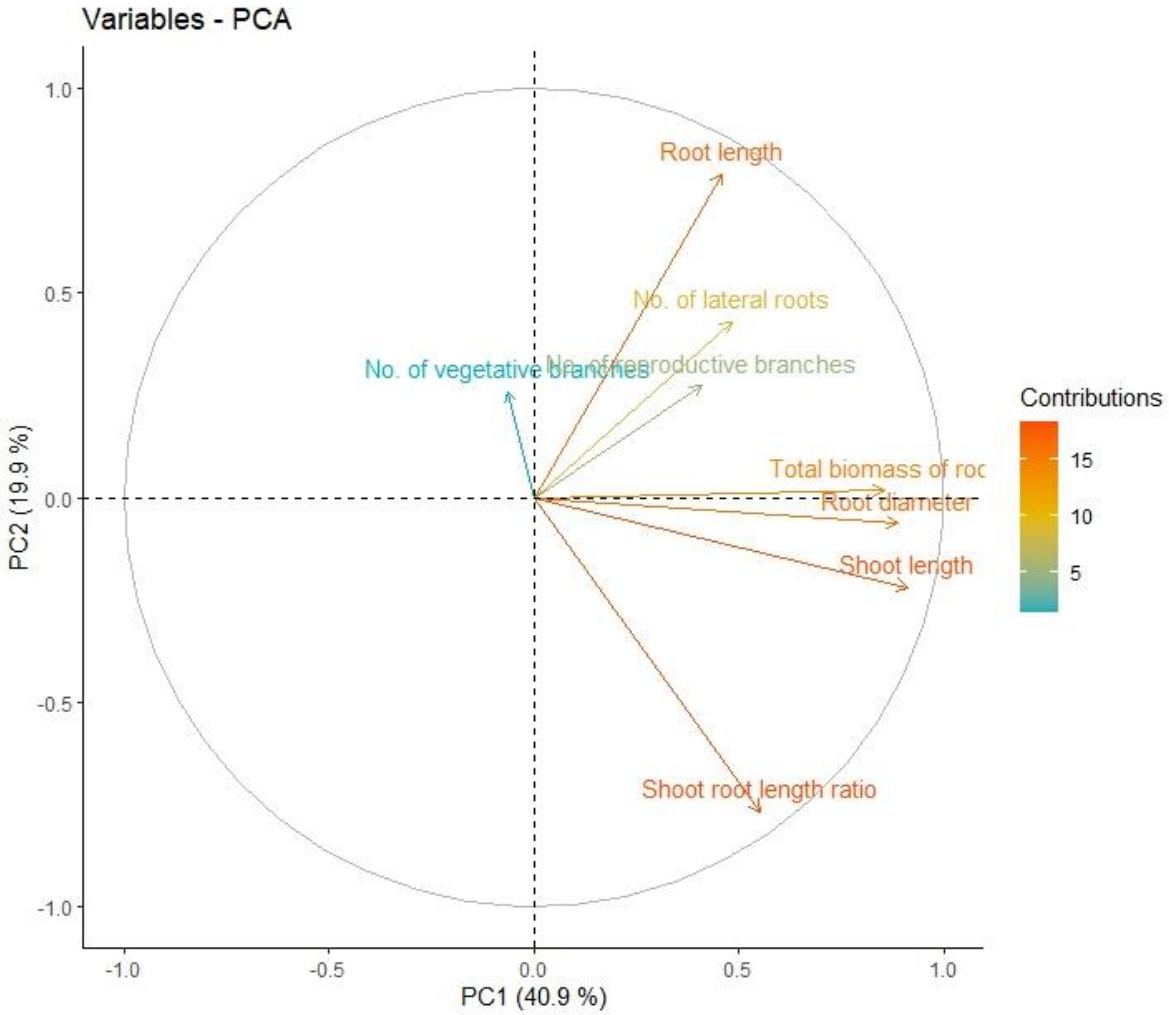



**Figure 27. Principal Component Analysis (PCA) showing the contributions of each variable for the first two major PCs of fifty genotypes under four different drought treatments**

To find out the relationship among the treatments based on their similarity and dissimilarity in their effects, PCA biplot was prepared (Figure 28). The biplot revealed that the effect of T4 was highly dissimilar from rest of the treatments (T1, T2 and T3) as it clustered separately from others. The highly similarity was observed between T1 with T2 and T2 with T4. Similar observation has been reported by Mahmood *et al*. (2022). The similar observation showing the higher similarity between the moderate and mild drought stress has been observed in Singh *et al*. (2018).

### 4.1.6 Divergence analysis

It is one of the potent techniques to measure the genetic diversity, which measures the forces of differentiation at two levels namely intra and inter cluster levels, and thus helps in the selection of genetically divergent genotypes which is a prerequisite for any plant breeding program.

#### 4.1.6.1 Cluster analysis

In this study, k means hierarchical cluster analysis of fifty cotton genotypes was carried out taking eight agromorphogenic characters (root length, shoot length, shoot root length ratio, root diameter, total biomass of root, number of lateral roots, number of vegetative branches and number of reproductive branches) using the R software (version 4.2). The Dendogram revealed the clustering and position of genotypes based on their D2 value (Figure 29) and summarized in Table 22. The wards method of clustering was adopted using the Euclidean distances, genotypes were grouped into eight clusters (Table 22 and Figure 29). Form the result, the largest cluster V with 12 cotton genotypes followed by cluster II with 10 genotypes and cluster III with 10 genotypes (Figure 29 and Table 22). The smallest cluster was observed in cluster I, cluster IV, and cluster VII with 2 genotypes in each cluster. The clustering pattern of the genotypes indicated that developing from the same location; common eco-geographic origin did not form a single cluster. The genotypes belonging from different locations were included in the same cluster. This result indicated that there were no relationships between genotypic distribution and genetic divergence. However, genotypes developed at the same place had different genetic make-up.

#### 4.1.6.2 Cluster distance (Canonical variate analysis)

The averages of intra and inter cluster distance were shown in Table 23. It was

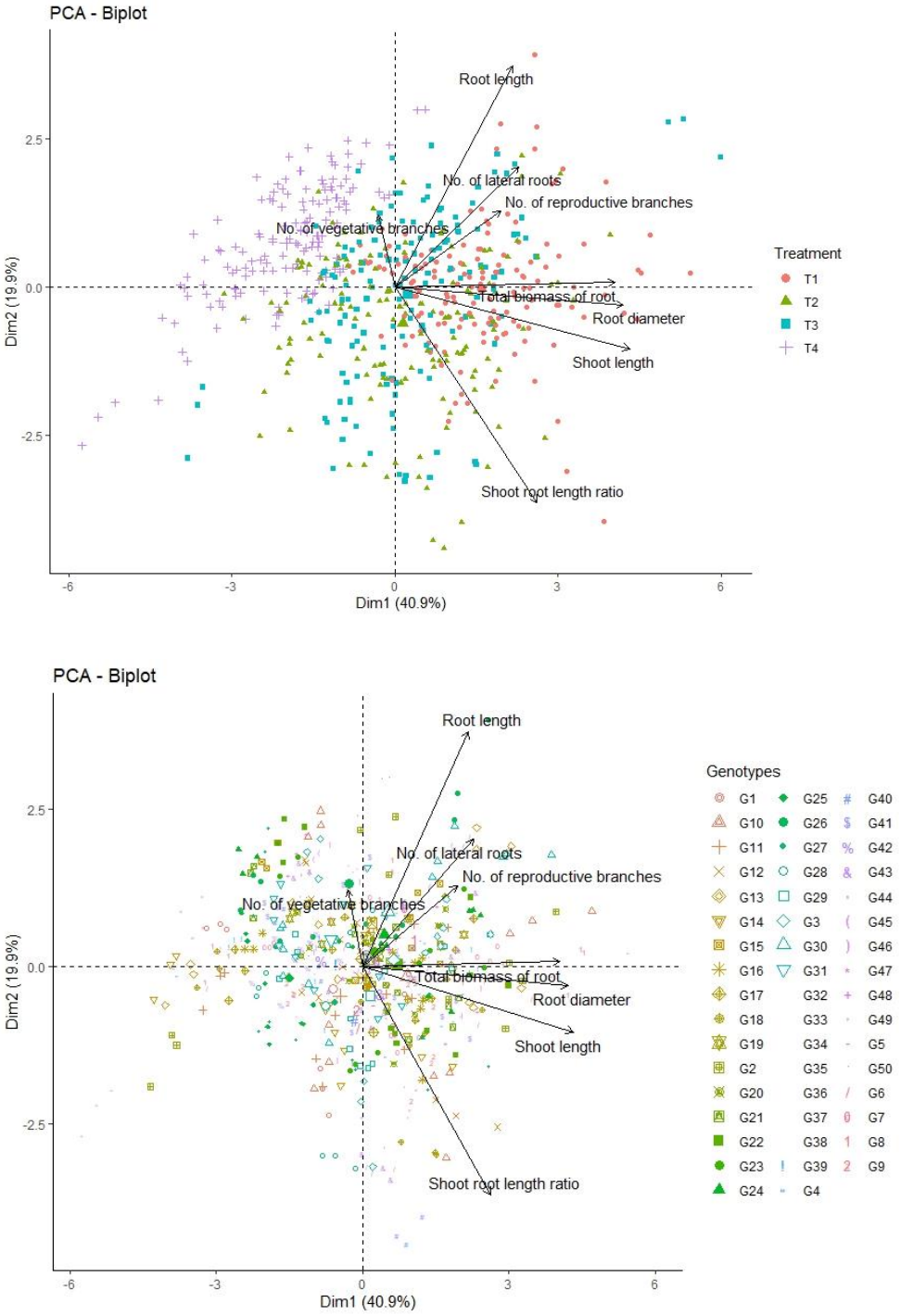



**Figure 28. Biplot showing the 600 observations of fifty genotypes under four drought treatments with the contributions of each of eight agromorphogenic traits**

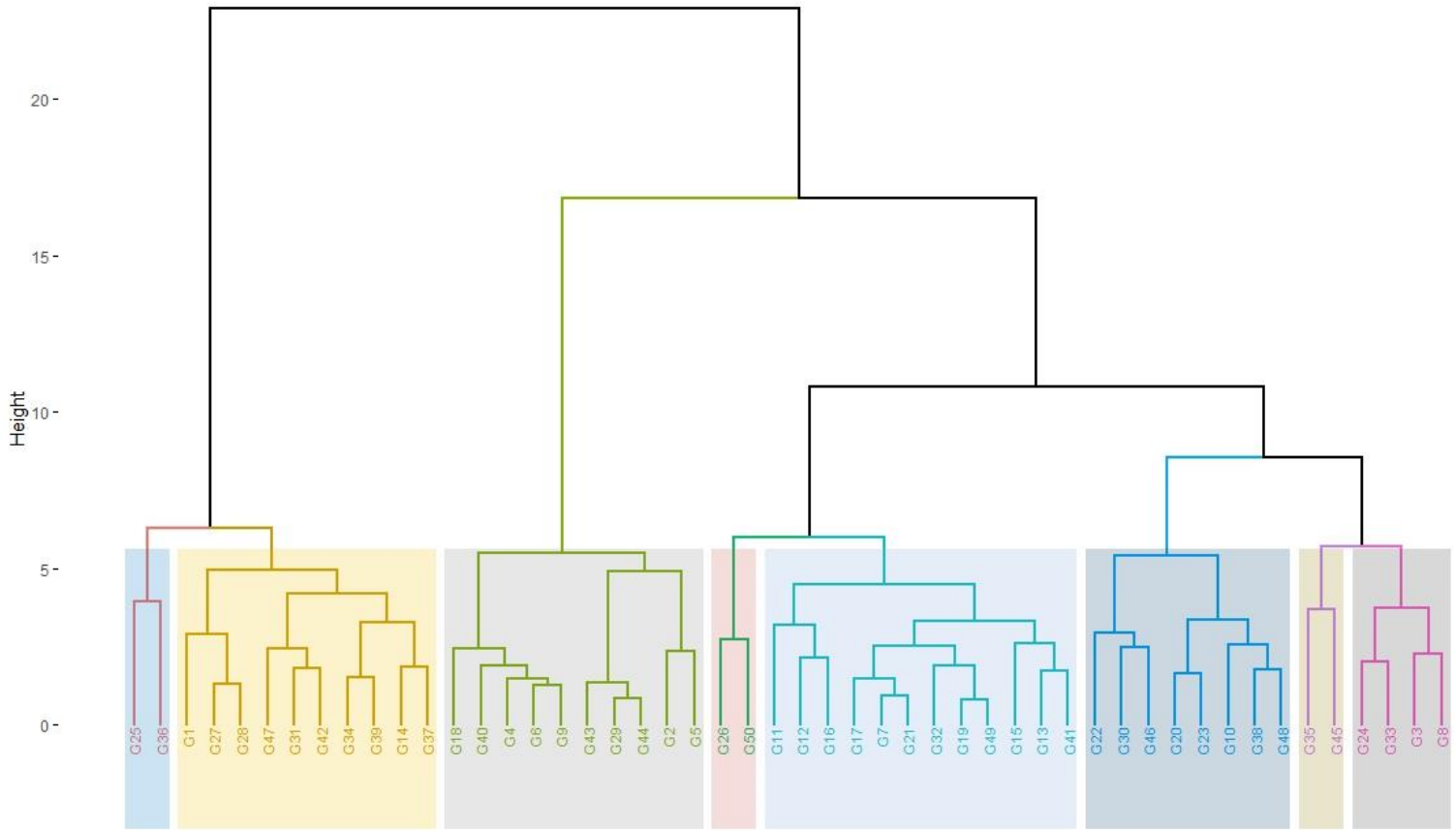



**Figure 29. Dendogram showing hierarchical clustring (K means) based on eight agromorphogenic traits treated of fifty genotypes under four drought treatments**

**Table 22. Distrubution of genotypes in different clusters**

| Cluster number | Number of genotypes | Genotypes |
|---|---|---|
| **I** | 2 | G25, G36 |
| **II** | 10 | G1, G27, G28, G47, G31, G42, G34, G39, G14, G37 |
| **III** | 10 | G18, G40, G4, G6, G9, G43, G29, G44, G2, G5 |
| **IV** | 2 | G26, G50 |
| **V** | 12 | G11, G12, G16, G17, G7, G21, G32, G19, G49, G15, G13, G41 |
| **VI** | 8 | G22, G30, G46, G20, G23, G10, G38, G48 |
| **VII** | 2 | G35, G45 |
| **VIII** | 4 | G24, G33, G3, G8 |

**Table 23. Intra (bold) and Inter cluster distance for fifty genotypes of cotton**

| Cluster | I | II | III | IV | V | VI | VII | VIII |
|---|---|---|---|---|---|---|---|---|
| **I** | **3.30** | 5.47 | 5.47 | 6.22 | 7.66 | 5.08 | 4.66 | 4.32 |
| **II** | | **4.13** | 6.30 | 6.16 | 7.07 | 5.44 | 5.10 | 5.23 |
| **III** | | | **3.63** | 6.79 | 7.00 | 5.58 | 5.92 | 4.92 |
| **IV** | | | | **3.86** | 8.47 | 4.85 | 4.49 | 5.64 |
| **V** | | | | | **3.19** | 8.91 | 8.17 | 7.69 |
| **VI** | | | | | | **2.77** | 4.77 | 5.45 |
| **VII** | | | | | | | **3.34** | 5.08 |
| **VIII** | | | | | | | | **3.29** |

observed that inter group distance was always higher than those of intra group distance (Table 23). Highest intra cluster distance was estimated for cluster II (4.13) which consisted of ten genotypes followed by the cluster IV (3.86) with 2 genotypes. The lowest intra cluster distance was estimated for cluster VI (2.77) with eight genotypes only followed by cluster V (3.19) with twelve genotypes. The cluster analysis showed that the inter cluster distance ranged from 4.32 to 8.91. The highest inter cluster distance was observed between cluster V and VI (8.91). This indicated maximum genetic diversity between those two clusters. The minimum inter cluster distance was observed between cluster I and cluster VIII (4.32) which indicated that the genotypes included those two clusters had relatively closer ancestry. The second highest inter cluster distance was observed between cluster IV and cluster V (8.47) followed by cluster V and cluster VII (8.17) and cluster V and cluster VIII (7.69). Maximum amount of heterosis will be obtained in hybrids involving genotypes belonging to the more divergent cluster. However, in practice, plant breeder's objective is to achieve high level of production by improving the yield contributing traits so that it could be adjusted in various types of purpose rather than getting only high heterosis.

#### 4.1.6.3 Characterization of individual characters

The cluster mean value for eight agromorphogenic traits is presented in Table 24. Difference cluster means existed for almost all the characters. From the cluster mean values, it was found that cluster IV had the highest mean value for shoot length (76.85) and number reproductive branches (7.80). Highest cluster mean value for shoot root length ratio (5.57) was observed in cluster VI. Cluster VII showed the highest cluster mean value for root diameter (8.61), total biomass of root (4.74), number of lateral roots (34.62) and number of vegetative branches (1.97) (Table 24). Highest mean value of cluster for root length was observed in cluster VIII (16.63). Based on the cluster mean value, cluster VII had highest mean for traits related to drought stress tolerant, which indicated the presence of drought tolerant genotypes in cluster VII. However, the cluster mean value for number of reproductive branches was observed in cluster IV, which indicated the presence of high yield cotton genotypes in cluster IV. Rauf *et al*. (2004) observed the similar cluster mean analysis for root length, shoot length and number of vegetative branches for cotton genotypes under drought stress.

**Table 24. Cluster mean values of eight different characters of fifty genotypes of cotton**

| Parameters | I | II | III | IV | V | VI | VII | VIII |
|---|---|---|---|---|---|---|---|---|
| **Root length** | 14.66 | 14.73 | 16.01 | 14.75 | 12.70 | 13.54 | 16.48 | 16.63 |
| **Shoot length** | 53.75 | 61.95 | 66.22 | 76.85 | 58.63 | 74.21 | 70.94 | 70.93 |
| **Shoot root length ratio** | 3.77 | 4.33 | 4.25 | 5.49 | 4.75 | 5.57 | 4.40 | 4.37 |
| **Root diameter** | 7.63 | 7.73 | 8.57 | 8.30 | 7.34 | 7.89 | 8.61 | 7.71 |
| **Total biomass of root** | 2.96 | 3.09 | 3.87 | 3.10 | 2.65 | 3.33 | 4.74 | 3.41 |
| **No. of lateral roots** | 26.36 | 28.92 | 30.05 | 31.38 | 26.40 | 26.89 | 34.62 | 30.19 |
| **No. of vegetative branches** | 0.83 | 1.63 | 1.39 | 1.42 | 1.15 | 1.58 | 1.97 | 1.32 |
| **No. of reproductive branches** | 5.20 | 5.37 | 7.30 | 7.80 | 6.45 | 6.50 | 6.68 | 6.84 |

### 4.1.7 Selection of genotypes based on selection index

The importance of selection index lies in evaluating the merits of individuals in terms of several traits. Selection based on indices permits maximizing the response to selection for one or a group of traits. Screening of cotton genotypes for tolerance to drought stress was undertaken at flowering stage at Sher e Bangla Agricultural University, Shere Bangla nagar, Dhaka. There was very much little rain from March to May during growing season. After 32 days of seed sowing, drought builds up to 7, 14, 21 days interval by irrigation. After 74 days of seed sowing, the plant characters were count the final plant survival and growth rate was noted. So selection based either shoot or root characters may not be as effective for population improvement as it would be effective on the basis of selection indices for which some more agromorphogenic characters are given relative weightage. Discriminant functions is a biometrical technique which provides information about the relative contribution of the eight traits to morphology and aids in the isolation from populations of superior genotypes by providing information for indirect selection for drought tolerance. On the basis of fitted discriminate functions, selection scores were computed for all the 50 genotypes and ranked (Table 25). Genotypes were selected acceding to top ranking, 4 cultivars and 2 descending genotypes compare with experiment-2 based on selection scores for Experiment 3 at Barind tract. These 50 genotypes having good plant morphology at flowering stage and growth rate which may generate primary information regarding suitability of deferent genotypes for drought tolerance. These 50 genotypes were used as a plant material for the next experiments of physiological characters (Experiment 2) and selection suitable genotypes under drought condition for Barind tract.

**Table 25. Relative selection index scores and ranking of fifty cotton genotypes based on morphological characters**

| Sl. No. | Genotypes | Variety / line | Selection Index score | Rank |
|---|---|---|---|---|
| 1 | G1 | CB-1 | 108.57 | 48 |
| 2 | G2 | CB-2 | 132.29 | 8 |
| 3 | G3 | CB-3 | 129.79 | 14 |
| 4 | G4 | CB-4 | 124.30 | 31 |
| 5 | G5 | CB-5 | 125.29 | 29 |
| 6 | G6 | CB-6 | 124.20 | 33 |
| 7 | G7 | CB-7 | 131.69 | 10 |
| 8 | G8 | CB-8 | 142.78 | 2 |
| 9 | G9 | CB-9 | 127.36 | 20 |
| 10 | G10 | CB-10 | 137.53 | 5 |
| 11 | G11 | CB-11 | 110.10 | 47 |
| 12 | G12 | CB-12 | 127.94 | 18 |
| 13 | G13 | CB-13 | 122.24 | 34 |
| 14 | G14 | CB-14 | 113.77 | 44 |
| 15 | G15 | CB-15 | 131.30 | 11 |
| 16 | G16 | Ra-2 | 126.08 | 24 |
| 17 | G17 | Ra-3 | 125.48 | 28 |
| 18 | G18 | Ra-4 | 132.04 | 9 |
| 19 | G19 | Ra-5 | 124.70 | 30 |
| 20 | G20 | Ra-9 | 125.60 | 27 |
| 21 | G21 | Ra-15 | 129.01 | 15 |
| 22 | G22 | Ra-16 | 147.16 | 1 |
| 23 | G23 | JA-08/9 | 128.30 | 17 |
| 24 | G24 | JA-11/M | 124.30 | 32 |
| 25 | G25 | JA-10/55 | 94.08 | 49 |
| 26 | G26 | JA-08/B | 121.54 | 35 |
| 27 | G27 | JA-11/L | 115.93 | 40 |
| 28 | G28 | JA-09/H | 114.49 | 43 |
| 29 | G29 | JA-13/R | 128.99 | 16 |
| 30 | G30 | SR-15 | 137.86 | 4 |
| 31 | G31 | SR-16 | 118.09 | 37 |
| 32 | G32 | SR-17 | 125.81 | 25 |
| 33 | G33 | BC-272 | 132.96 | 7 |
| 34 | G34 | BC-385 | 117.91 | 39 |
| 35 | G35 | BC-394 | 126.92 | 21 |
| 36 | G36 | BC-397 | 91.04 | 50 |
| 37 | G37 | BC-410 | 112.13 | 45 |
| 38 | G38 | BC-413 | 126.56 | 22 |
| 39 | G39 | BC-415 | 115.88 | 41 |
| 40 | G40 | BC-419 | 127.91 | 19 |
| 41 | G41 | BC-423 | 120.74 | 36 |
| 42 | G42 | BC-430 | 111.32 | 46 |
| 43 | G43 | BC-433 | 133.95 | 6 |
| 44 | G44 | BC-435 | 130.66 | 12 |
| 45 | G45 | BC-442 | 141.31 | 3 |
| 46 | G46 | BC-462 | 130.25 | 13 |
| 47 | G47 | BC-509 | 115.86 | 42 |
| 48 | G48 | BC-510 | 126.23 | 23 |
| 49 | G49 | BC-511 | 125.68 | 26 |
| 50 | G50 | BC-512 | 117.95 | 38 |

## 4.2 Experiment 2. Physiological study and genetic diversity of cotton genotypes against drought at early flowering stage

This investigation was conducted to evaluate the fifty cotton genotypes under drought stresses based on ten physiological characters and to assess the genetic variation among the genotypes for drought tolerance. Ten physiological traits of fifty cotton genotypes were observed under four drought stress conditions. The physiologic traits included soil moisture content, relative water content, water saturation deficit, water retention capacity, water uptake capacity, total chlorophyll, nitrogen content, membrane stability index, pollen viability and proline content. Data are presented in Tables and Figures for better understanding.

### 4.2.1 Physiological performance of cotton genotypes under drought stress

Ten physiologic responses of fifty genotypes were observed under four different drought stress conditions. ANOVA showed the significant effect of genotypes, treatment and interaction on all ten physiologic characters (Appendix V).

#### 4.2.1.1 Soil moisture content

Genotype, treatment, and their interaction significantly affected the soil moisture content. The highest means of soil moisture content (33.11%) was observed in T1 drought stress whereas the lowest soil moisture content (14.29 %) was observed in T4 drought stress (Table 26). Among the genotypes, highest soil moisture content (25.46%) was observed in G40 and lowest (18.68%) in G50. Based on the genotype stress interaction, highest soil moisture content (34.50%) and lowest (10.27%) was observed in G46 under T1 and G49 under T4 stress respectively. On the basis of b values, the best performance (highest b value) was observed in genotype G38 (-0.61) followed by G13 (-0.64) and lowest in G28 (-1.16). With the increase of drought stress, soil moisture content was decreased as shown in linear regression in Figure 30. The minimum reduction% (9.10 %) was observed in G10 under T2 drought stress (Figure 31, Table 26). Maximum reduction% (68.47%) was observed in G49 under T4 stress (Figure 31). The result showed the negative effect of drought stress on soil moisture content in genotypic dependent manner. Under drought stress conditions, soil moisture content showed both an increase and decrease depending on the genetic

**Table 26. Soil moisture content (SMC) of fifty genotypes at different drought treatments**

| Genotype | SMC (%) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | Mean | | |
| G1 | 32.37 | 28.13 | 21.17 | 13.77 | 23.86 | 13.08 | 34.60 | 57.47 | 35.05 | -0.90 | 19 |
| G2 | 30.13 | 27.27 | 20.53 | 15.37 | 23.33 | 9.51 | 31.86 | 49.00 | 30.13 | -0.73 | 6 |
| G3 | 31.73 | 26.67 | 15.00 | 12.50 | 21.48 | 15.97 | 52.73 | 60.61 | 43.10 | -0.99 | 25 |
| G4 | 34.03 | 26.70 | 20.27 | 15.93 | 24.23 | 21.55 | 40.45 | 53.18 | 38.39 | -0.87 | 16 |
| G5 | 33.80 | 28.07 | 22.53 | 14.83 | 24.81 | 16.96 | 33.33 | 56.11 | 35.47 | -0.89 | 18 |
| G6 | 33.57 | 26.70 | 18.17 | 13.23 | 22.92 | 20.46 | 45.88 | 60.58 | 42.30 | -0.99 | 25 |
| G7 | 33.47 | 27.73 | 17.93 | 13.57 | 23.18 | 17.13 | 46.41 | 59.46 | 41.00 | -0.99 | 25 |
| G8 | 33.40 | 26.53 | 22.57 | 15.30 | 24.45 | 20.56 | 32.44 | 54.19 | 35.73 | -0.83 | 12 |
| G9 | 34.27 | 27.00 | 19.40 | 13.27 | 23.48 | 21.21 | 43.39 | 61.28 | 41.96 | -1.01 | 27 |
| G10 | 30.40 | 27.63 | 22.70 | 14.93 | 23.92 | 9.10 | 25.33 | 50.88 | 28.44 | -0.73 | 6 |
| G11 | 32.70 | 24.33 | 22.43 | 14.80 | 23.57 | 25.59 | 31.40 | 54.74 | 37.24 | -0.79 | 9 |
| G12 | 30.67 | 25.93 | 22.17 | 15.50 | 23.57 | 15.43 | 27.72 | 49.46 | 30.87 | -0.70 | 5 |
| G13 | 30.70 | 24.97 | 22.17 | 16.70 | 23.63 | 18.68 | 27.80 | 45.60 | 30.69 | -0.64 | 2 |
| G14 | 32.63 | 23.13 | 14.73 | 11.97 | 20.62 | 29.11 | 54.85 | 63.33 | 49.10 | -1.01 | 27 |
| G15 | 34.13 | 24.47 | 20.80 | 15.37 | 23.69 | 28.32 | 39.06 | 54.98 | 40.79 | -0.86 | 15 |
| G16 | 34.33 | 24.97 | 20.50 | 15.27 | 23.77 | 27.28 | 40.29 | 55.53 | 41.04 | -0.88 | 17 |
| G17 | 33.20 | 26.00 | 20.57 | 15.13 | 23.73 | 21.69 | 38.05 | 54.42 | 38.05 | -0.85 | 14 |
| G18 | 33.87 | 22.30 | 19.77 | 14.90 | 22.71 | 34.15 | 41.63 | 56.00 | 43.93 | -0.85 | 14 |
| G19 | 34.30 | 22.17 | 21.23 | 16.47 | 23.54 | 35.37 | 38.10 | 51.99 | 41.82 | -0.78 | 8 |
| G20 | 34.07 | 25.50 | 18.13 | 14.83 | 23.13 | 25.15 | 46.77 | 56.46 | 42.79 | -0.93 | 21 |
| G21 | 33.93 | 27.83 | 18.50 | 14.07 | 23.58 | 17.98 | 45.48 | 58.55 | 40.67 | -0.98 | 24 |
| G22 | 33.73 | 24.37 | 17.70 | 13.53 | 22.33 | 27.77 | 47.53 | 59.88 | 45.06 | -0.96 | 22 |
| G23 | 34.20 | 28.27 | 18.90 | 14.97 | 24.08 | 17.35 | 44.74 | 56.24 | 39.44 | -0.96 | 22 |
| G24 | 33.60 | 24.30 | 22.07 | 15.10 | 23.77 | 27.68 | 34.33 | 55.06 | 39.02 | -0.82 | 11 |
| G25 | 33.80 | 19.50 | 15.67 | 12.17 | 20.28 | 42.31 | 53.65 | 64.00 | 53.32 | -0.98 | 24 |
| G26 | 33.20 | 27.20 | 18.90 | 14.70 | 23.50 | 18.07 | 43.07 | 55.72 | 38.96 | -0.91 | 20 |
| G27 | 33.57 | 27.27 | 15.27 | 11.47 | 21.89 | 18.77 | 54.52 | 65.84 | 46.38 | -1.12 | 35 |
| G28 | 33.73 | 27.03 | 14.10 | 10.87 | 21.43 | 19.86 | 58.20 | 67.79 | 48.62 | -1.16 | 36 |
| G29 | 33.53 | 24.80 | 15.13 | 12.50 | 21.49 | 26.04 | 54.87 | 62.72 | 47.88 | -1.04 | 29 |
| G30 | 34.37 | 26.23 | 14.97 | 13.10 | 22.17 | 23.67 | 56.45 | 61.88 | 47.33 | -1.07 | 32 |
| G31 | 34.20 | 24.73 | 22.33 | 16.90 | 24.54 | 27.68 | 34.70 | 50.58 | 37.65 | -0.78 | 8 |
| G32 | 34.40 | 25.50 | 21.70 | 15.37 | 24.24 | 25.87 | 36.92 | 55.33 | 39.37 | -0.87 | 16 |
| G33 | 30.43 | 25.10 | 14.33 | 10.93 | 20.20 | 17.52 | 52.90 | 64.07 | 44.83 | -0.99 | 25 |
| G34 | 32.23 | 26.83 | 15.00 | 11.47 | 21.38 | 16.75 | 53.46 | 64.43 | 44.88 | -1.06 | 31 |
| G35 | 32.03 | 26.83 | 15.67 | 12.33 | 21.72 | 16.23 | 51.09 | 61.50 | 42.94 | -1.00 | 26 |
| G36 | 33.30 | 27.33 | 22.13 | 15.60 | 24.59 | 17.92 | 33.53 | 53.15 | 34.87 | -0.83 | 12 |
| G37 | 32.87 | 27.73 | 16.00 | 12.27 | 22.22 | 15.62 | 51.32 | 62.68 | 43.20 | -1.05 | 30 |
| G38 | 32.50 | 22.67 | 21.60 | 18.73 | 23.88 | 30.26 | 33.54 | 42.36 | 35.38 | -0.61 | 1 |
| G39 | 34.47 | 28.80 | 21.33 | 16.50 | 25.28 | 16.44 | 38.10 | 52.13 | 35.56 | -0.88 | 17 |
| G40 | 34.47 | 28.63 | 22.23 | 16.50 | 25.46 | 16.92 | 35.49 | 52.13 | 34.85 | -0.86 | 15 |
| G41 | 30.37 | 27.10 | 22.60 | 16.10 | 24.04 | 10.76 | 25.58 | 46.98 | 27.77 | -0.68 | 3 |
| G42 | 33.80 | 25.40 | 17.47 | 12.37 | 22.26 | 24.85 | 48.32 | 63.41 | 45.53 | -1.03 | 28 |
| G43 | 33.80 | 26.37 | 15.27 | 11.53 | 21.74 | 21.99 | 54.83 | 65.88 | 47.57 | -1.11 | 34 |
| G44 | 33.43 | 22.27 | 21.83 | 16.30 | 23.46 | 33.40 | 34.70 | 51.25 | 39.78 | -0.74 | 7 |
| G45 | 33.30 | 24.47 | 19.17 | 15.60 | 23.13 | 26.53 | 42.44 | 53.15 | 40.71 | -0.83 | 12 |
| G46 | 34.50 | 25.90 | 22.30 | 16.10 | 24.70 | 24.93 | 35.36 | 53.33 | 37.87 | -0.84 | 13 |
| G47 | 33.57 | 26.47 | 20.63 | 16.63 | 24.33 | 21.15 | 38.53 | 50.45 | 36.71 | -0.81 | 10 |
| G48 | 30.30 | 25.73 | 22.37 | 15.43 | 23.46 | 15.07 | 26.18 | 49.06 | 30.11 | -0.69 | 4 |
| G49 | 32.57 | 22.10 | 13.33 | 10.27 | 19.57 | 32.14 | 59.06 | 68.47 | 53.22 | -1.08 | 33 |
| G50 | 33.77 | 15.13 | 14.43 | 11.40 | 18.68 | 55.18 | 57.26 | 66.24 | 59.56 | -0.97 | 23 |
| Mean(T) | 33.11 | 25.56 | 19.11 | 14.29 | | | | | | | |

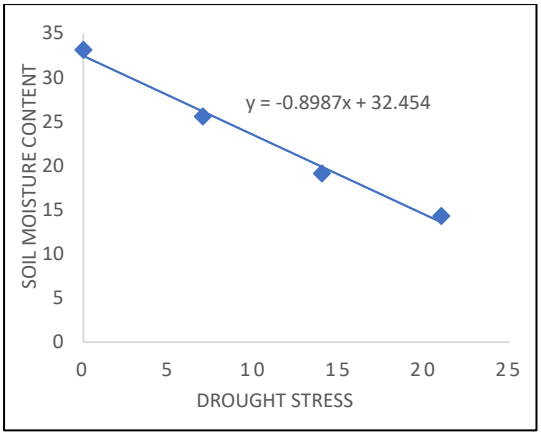



**Figure 30. Relationships between soil moisture content of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

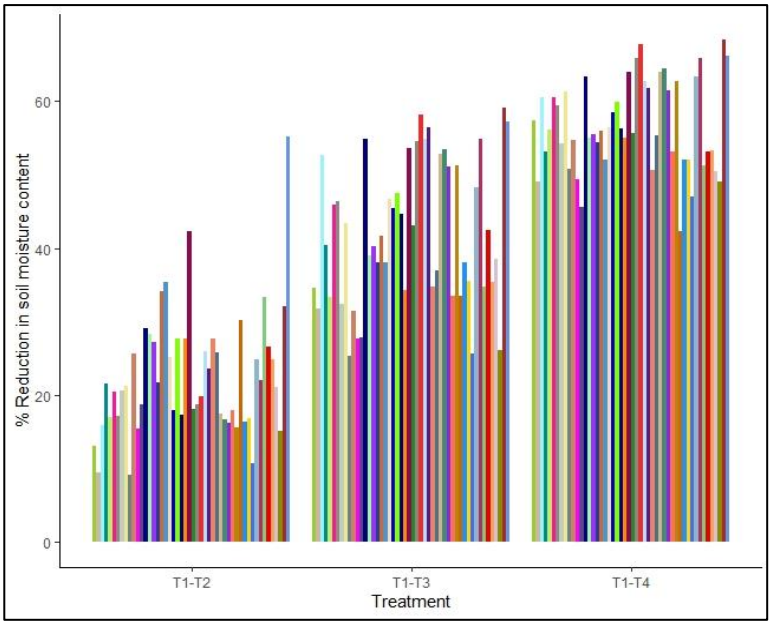
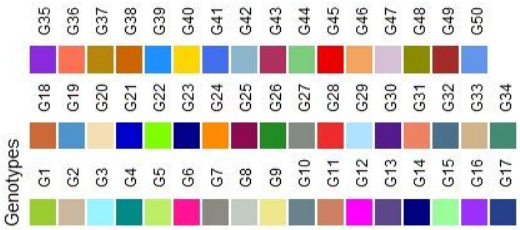



**Figure 31. Reduction percentage of soil moisture content of fifty cotton genotypes under different drought stresses compared with control**



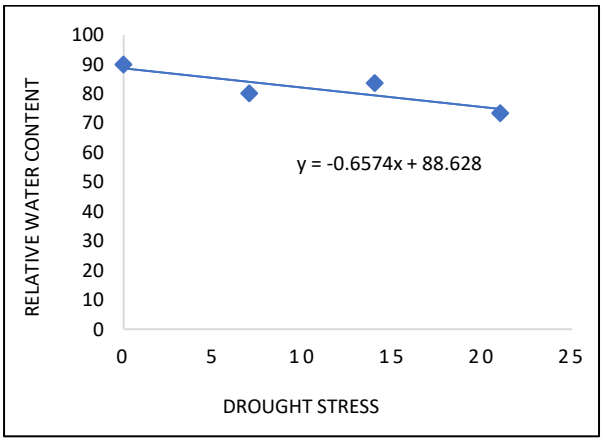




**Figure 32. Relationships between relative water content of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

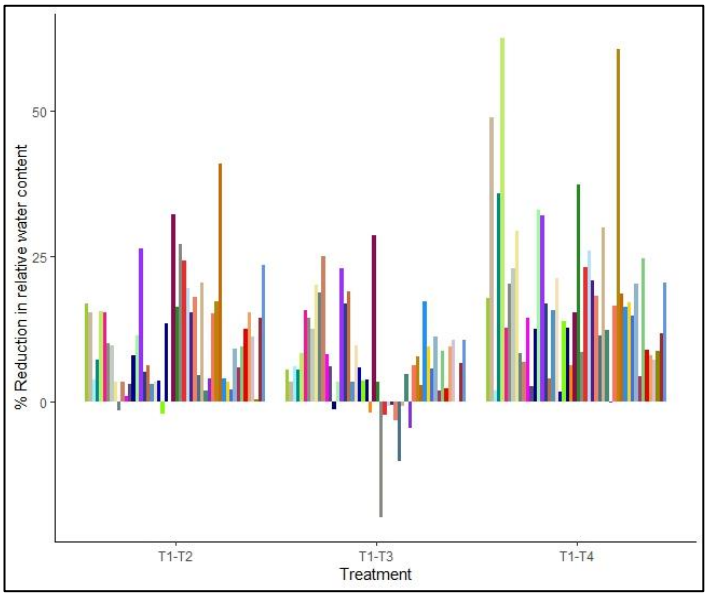



**Figure 33. Reduction percentage of relative water content of fifty cotton genotypes under different drought stresses compared with control**

structure of cotton genotypes (Mahmood *et al*., 2022; Xiao *et al*., 2020). However, the tolerance mechanisms against the drought stress in cotton depends on the genotypes as described in Mahmood *et al*., 2022). Tolerant genotypes have a mechanism to increase the cell division at the root apical meristem to extend their root system in purpose of water uptake (Polania *et al*., 2017). On the other hand, drought susceptible showed less root development.

#### 4.2.1.2 Relative water content

Genotype, treatment and their interaction significantly affected the relative water content. The highest mean relative water content (89.85%) was observed in T1 drought stress whereas the lowest relative water content (73.34%) was observed in T4 drought stress (Table 27). Among the genotypes, highest relative water content (93.28%) was observed in G3 and lowest (70.01%) in G37. Based on the genotype stress interaction, highest relative water content (96.67%) and lowest (35.16%) was observed in G5 under T1 and G37 under T4 stress. On the basis of b values, the best performance (highest b value) was observed in genotype G27 (0.24) followed by G35 (0.11) and lowest in G5 (-2.49). With the increase of drought stress, relative water content was decreased as shown in linear regression in Figure 32. The minimum reduction% (-20.03%) was observed in G27 under T3 drought stress (Figure 33, Table 27). Maximum reduction% (62.55%) was observed in G5 under T4 stress (Figure 33). The result showed the negative effect of drought stress on relative water content in genotypic dependent manner. Some of the genotypes showed an increase in relative water content at mild and moderate drought stress. However, all the genotypes showed a decrease of relative water content under the severe drought stress. Similar result has been observed in (Veesar *et al*., 2020; Khan *et al*., 2018; Nezhadahmadi *et al*., 2013; Nayyar and Gupta, 2006; Siddique *et al*., 2001). Relative water content represents plant water status including water uptake by the roots and water loss by transpiration through plant canopy, as a result reflect the biochemical activities of plant tissue, hence used as a most important trait index for drought tolerance. Kader *et al*. (2015) also reported that all genotypes were significantly affected by drought but some genotypes by maintaining the highest values of relative water content under drought stress. Reduction in RWC was detected in the leaf, which was recovered. It may be due to higher contents of sugars, polyphenols, proline, and amino acids, which are compatible solutes (Parida *et al*., 2007).

## Table 27. Relative Water Content (RWC) of fifty genotypes at different drought treatments

| Genotype | RWC (%) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 88.64 | 73.85 | 83.77 | 72.85 | 79.78 | 16.69 | 5.50 | 17.81 | 13.33 | -0.53 | 19 |
| G2 | 91.24 | 77.33 | 88.24 | 46.70 | 75.88 | 15.25 | 3.28 | 48.82 | 22.45 | -1.75 | 43 |
| G3 | 96.02 | 92.56 | 90.32 | 94.21 | 93.28 | 3.61 | 5.93 | 1.89 | 3.81 | -0.11 | 5 |
| G4 | 93.93 | 87.18 | 88.84 | 60.42 | 82.59 | 7.19 | 5.42 | 35.67 | 16.09 | -1.41 | 42 |
| G5 | 96.67 | 81.68 | 88.72 | 36.20 | 75.82 | 15.50 | 8.22 | 62.55 | 28.76 | -2.49 | 45 |
| G6 | 93.76 | 79.51 | 79.05 | 81.86 | 83.54 | 15.19 | 15.68 | 12.69 | 14.52 | -0.52 | 18 |
| G7 | 93.70 | 84.41 | 80.21 | 74.74 | 83.27 | 9.91 | 14.40 | 20.23 | 14.85 | -0.87 | 34 |
| G8 | 94.79 | 85.65 | 82.96 | 73.15 | 84.14 | 9.65 | 12.48 | 22.83 | 14.98 | -0.97 | 37 |
| G9 | 92.56 | 89.49 | 74.12 | 65.44 | 80.40 | 3.32 | 19.92 | 29.30 | 17.51 | -1.38 | 41 |
| G10 | 89.81 | 91.28 | 73.12 | 82.43 | 84.16 | -1.64 | 18.58 | 8.22 | 8.39 | -0.58 | 22 |
| G11 | 95.05 | 91.85 | 71.28 | 88.58 | 86.69 | 3.36 | 25.00 | 6.81 | 11.72 | -0.57 | 21 |
| G12 | 92.66 | 91.94 | 85.21 | 79.45 | 87.32 | 0.77 | 8.04 | 14.26 | 7.69 | -0.66 | 27 |
| G13 | 93.33 | 90.51 | 87.81 | 90.86 | 90.63 | 3.02 | 5.91 | 2.64 | 3.86 | -0.14 | 6 |
| G14 | 85.51 | 78.85 | 86.75 | 74.88 | 81.50 | 7.78 | -1.45 | 12.43 | 6.25 | -0.34 | 14 |
| G15 | 90.86 | 80.56 | 87.89 | 61.03 | 80.08 | 11.34 | 3.27 | 32.83 | 15.81 | -1.17 | 38 |
| G16 | 91.94 | 67.80 | 70.87 | 62.58 | 73.30 | 26.26 | 22.92 | 31.93 | 27.03 | -1.21 | 39 |
| G17 | 95.12 | 90.39 | 79.21 | 79.07 | 85.95 | 4.96 | 16.72 | 16.87 | 12.85 | -0.85 | 32 |
| G18 | 93.03 | 87.34 | 75.46 | 89.48 | 86.33 | 6.12 | 18.89 | 3.82 | 9.61 | -0.32 | 13 |
| G19 | 88.56 | 85.93 | 85.62 | 74.70 | 83.70 | 2.97 | 3.33 | 15.66 | 7.32 | -0.60 | 24 |
| G20 | 95.79 | 92.68 | 86.65 | 75.48 | 87.65 | 3.24 | 9.54 | 21.20 | 11.33 | -0.96 | 35 |
| G21 | 91.99 | 88.74 | 86.66 | 90.52 | 89.48 | 3.53 | 5.80 | 1.60 | 3.64 | -0.09 | 3 |
| G22 | 88.59 | 90.52 | 85.49 | 76.41 | 85.25 | -2.18 | 3.50 | 13.75 | 5.03 | -0.59 | 23 |
| G23 | 92.01 | 79.65 | 88.63 | 80.39 | 85.17 | 13.43 | 3.68 | 12.63 | 9.91 | -0.37 | 15 |
| G24 | 88.74 | 88.82 | 90.50 | 83.26 | 87.83 | -0.08 | -1.99 | 6.18 | 1.37 | -0.21 | 8 |
| G25 | 87.59 | 59.49 | 62.53 | 74.20 | 70.95 | 32.08 | 28.61 | 15.29 | 25.32 | -0.53 | 19 |
| G26 | 91.74 | 76.78 | 88.67 | 57.51 | 78.68 | 16.30 | 3.34 | 37.31 | 18.98 | -1.30 | 40 |
| G27 | 76.50 | 55.89 | 91.82 | 70.04 | 73.56 | 26.94 | -20.03 | 8.44 | 5.11 | 0.24 | 1 |
| G28 | 91.86 | 69.73 | 93.95 | 70.65 | 81.54 | 24.09 | -2.28 | 23.09 | 14.97 | -0.56 | 20 |
| G29 | 89.96 | 72.56 | 90.68 | 66.64 | 79.96 | 19.34 | -0.80 | 25.92 | 14.82 | -0.74 | 29 |
| G30 | 89.27 | 75.59 | 89.87 | 70.68 | 81.35 | 15.32 | -0.67 | 20.83 | 11.83 | -0.59 | 23 |
| G31 | 84.43 | 69.25 | 87.19 | 69.07 | 77.48 | 17.98 | -3.26 | 18.19 | 10.97 | -0.40 | 16 |
| G32 | 75.79 | 72.44 | 83.69 | 67.27 | 74.80 | 4.41 | -10.42 | 11.24 | 1.74 | -0.20 | 7 |
| G33 | 87.57 | 69.76 | 88.33 | 61.36 | 76.75 | 20.34 | -0.86 | 29.93 | 16.47 | -0.86 | 33 |
| G34 | 85.27 | 83.68 | 81.27 | 74.86 | 81.27 | 1.87 | 4.69 | 12.22 | 6.26 | -0.48 | 17 |
| G35 | 84.56 | 81.22 | 88.55 | 84.80 | 84.78 | 3.95 | -4.71 | -0.28 | -0.34 | 0.11 | 2 |
| G36 | 83.77 | 71.07 | 78.57 | 70.11 | 75.88 | 15.17 | 6.21 | 16.32 | 12.57 | -0.48 | 17 |
| G37 | 89.00 | 73.66 | 82.23 | 35.16 | 70.01 | 17.23 | 7.61 | 60.50 | 28.44 | -2.19 | 44 |
| G38 | 89.66 | 52.94 | 87.28 | 73.03 | 75.73 | 40.95 | 2.66 | 18.55 | 20.72 | -0.22 | 9 |
| G39 | 88.32 | 84.85 | 73.19 | 74.03 | 80.10 | 3.93 | 17.13 | 16.18 | 12.41 | -0.78 | 30 |
| G40 | 82.82 | 80.03 | 75.00 | 68.77 | 76.66 | 3.36 | 9.45 | 16.96 | 9.93 | -0.67 | 28 |
| G41 | 93.27 | 91.47 | 88.07 | 79.58 | 88.10 | 1.93 | 5.57 | 14.68 | 7.39 | -0.64 | 26 |
| G42 | 87.84 | 79.96 | 78.13 | 70.05 | 78.99 | 8.97 | 11.05 | 20.26 | 13.42 | -0.79 | 31 |
| G43 | 86.06 | 81.08 | 84.52 | 82.45 | 83.53 | 5.79 | 1.79 | 4.19 | 3.92 | -0.11 | 4 |
| G44 | 92.27 | 83.65 | 84.33 | 69.56 | 82.45 | 9.34 | 8.60 | 24.62 | 14.19 | -0.96 | 36 |
| G45 | 91.44 | 80.09 | 89.40 | 83.32 | 86.06 | 12.41 | 2.24 | 8.88 | 7.84 | -0.22 | 9 |
| G46 | 92.06 | 78.01 | 83.43 | 84.78 | 84.57 | 15.26 | 9.37 | 7.91 | 10.85 | -0.23 | 10 |
| G47 | 92.25 | 82.06 | 82.56 | 85.75 | 85.65 | 11.04 | 10.50 | 7.04 | 9.53 | -0.27 | 11 |
| G48 | 86.96 | 86.77 | 87.03 | 79.52 | 85.07 | 0.22 | -0.09 | 8.55 | 2.89 | -0.31 | 12 |
| G49 | 88.24 | 75.57 | 82.38 | 77.99 | 81.05 | 14.36 | 6.64 | 11.61 | 10.87 | -0.34 | 14 |
| G50 | 89.64 | 68.68 | 80.25 | 71.34 | 77.48 | 23.38 | 10.47 | 20.41 | 18.09 | -0.62 | 25 |
| Mean (T) | 89.85 | 80.10 | 83.61 | 73.34 | | | | | | | |

#### 4.2.1.3 Water saturation deficit

Genotype, treatment and their interaction significantly affected the water saturation deficit. The highest mean water saturation deficit (26.7%) was observed in T4 drought stress whereas the lowest water saturation deficit (10.2 %) was observed in T1 drought stress (Table 28). Among the genotypes, highest water saturation deficit (30.0%) was observed in G37 and lowest (6.7%) in G3. Based on the genotype stress interaction, highest water saturation deficit (64.8%) and lowest (3.30%) was observed in G37 under T4 and G5 under T1 stress respectively. On the basis of b values, the best performance (highest b value) was observed in genotype G27 (-0.24) followed by G35 (-0.11) and lowest in G5 (-2.49). With the increase of drought stress, water saturation deficit was increased as shown in linear regression in Figure 34. The minimum reduction% (-1814 %) was observed in G5 under T4 drought stress (Figure 35, Table 28). Maximum reduction% (65.2%) was observed in G27 under T3 stress (Figure 35). The result showed the positive effect of drought stress on water saturation deficit in genotypic dependent manner. Similar results were found in the study of Veesar *et al*. (2020). Water saturation deficit has decreased in some of the cotton genotypes according to the findings of Xiao *et al*. (2020). However, the tolerance mechanisms against the drought stress in cotton depends on the genotypes as described in Mahmood *et al*., 2022). Tolerant genotypes have a mechanism to increase the cell division at the root apical meristem to extend their root system in purpose of water uptake (Polania *et al*. 2017). In contrast, drought susceptible produces fewer roots.

#### 4.2.1.4 Water retention capacity

Genotype, treatment and their interaction significantly affected the water retention capacity. The highest mean water retention capacity (4.73) was observed in T1 drought stress whereas the lowest water retention capacity (3.09) was observed in T4 drought stress (Table 29). Among the genotypes, highest water retention capacity (5.85) was observed in G41 and lowest (3.04) in G16. Based on the genotype stress interaction, highest water retention capacity (8.76) and lowest (1.92) was observed in G6 under T1 and G25 under T2 stress. On the basis of b values, the best performance (highest b value) was observed in genotype G6 (0.12) followed by G15 (0.06) and lowest in G7 (-0.26). With the increase of drought stress, water retention capacity was decreased as shown in linear regression in Figure 36. The minimum reduction% (-

## Table 28. Water Saturation Deficit (WSD) of fifty genotypes at different drought treatments

| Genotype | WSD (%) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 11.4 | 26.2 | 16.2 | 27.1 | 20.2 | -130.2 | -42.9 | -139.0 | -104.0 | 0.53 | 19 |
| G2 | 8.8 | 22.7 | 11.8 | 53.3 | 24.1 | -158.7 | -34.1 | -508.2 | -233.7 | 1.75 | 43 |
| G3 | 4.0 | 7.4 | 9.7 | 5.8 | 6.7 | -87.0 | -143.1 | -45.6 | -91.9 | 0.11 | 5 |
| G4 | 6.1 | 12.8 | 11.2 | 39.6 | 17.4 | -111.1 | -83.8 | -551.6 | -248.8 | 1.41 | 42 |
| G5 | 3.3 | 18.3 | 11.3 | 63.8 | 24.2 | -449.6 | -238.3 | -1814 | -834.0 | 2.49 | 45 |
| G6 | 6.2 | 20.5 | 20.9 | 18.1 | 16.5 | -228.1 | -235.4 | -190.5 | -218.0 | 0.52 | 18 |
| G7 | 6.3 | 15.6 | 19.8 | 25.3 | 16.7 | -147.5 | -214.2 | -300.9 | -220.9 | 0.87 | 34 |
| G8 | 5.2 | 14.4 | 17.0 | 26.8 | 15.9 | -175.5 | -227.1 | -415.5 | -272.7 | 0.97 | 37 |
| G9 | 7.4 | 10.5 | 25.9 | 34.6 | 19.6 | -41.3 | -248.0 | -364.6 | -218.0 | 1.38 | 41 |
| G10 | 10.2 | 8.7 | 26.9 | 17.6 | 15.8 | 14.5 | -163.7 | -72.4 | -73.9 | 0.58 | 22 |
| G11 | 5.0 | 8.1 | 28.7 | 11.4 | 13.3 | -64.6 | -480.0 | -130.7 | -225.1 | 0.57 | 21 |
| G12 | 7.3 | 8.1 | 14.8 | 20.6 | 12.7 | -9.8 | -101.5 | -180.1 | -97.1 | 0.66 | 27 |
| G13 | 6.7 | 9.5 | 12.2 | 9.1 | 9.4 | -42.2 | -82.7 | -37.0 | -54.0 | 0.14 | 6 |
| G14 | 14.5 | 21.1 | 13.2 | 25.1 | 18.5 | -45.9 | 8.6 | -73.3 | -36.9 | 0.34 | 14 |
| G15 | 9.1 | 19.4 | 12.1 | 39.0 | 19.9 | -112.7 | -32.5 | -326.3 | -157.2 | 1.17 | 38 |
| G16 | 8.1 | 32.2 | 29.1 | 37.4 | 26.7 | -299.5 | -261.4 | -364.2 | -308.4 | 1.21 | 39 |
| G17 | 4.9 | 9.6 | 20.8 | 20.9 | 14.1 | -96.7 | -325.6 | -328.6 | -250.3 | 0.85 | 32 |
| G18 | 7.0 | 12.7 | 24.5 | 10.5 | 13.7 | -81.6 | -252.1 | -50.9 | -128.2 | 0.32 | 13 |
| G19 | 11.4 | 14.1 | 14.4 | 25.3 | 16.3 | -23.0 | -25.8 | -121.2 | -56.7 | 0.60 | 24 |
| G20 | 4.2 | 7.3 | 13.4 | 24.5 | 12.4 | -73.6 | -216.9 | -481.8 | -257.4 | 0.96 | 35 |
| G21 | 8.0 | 11.3 | 13.3 | 9.5 | 10.5 | -40.6 | -66.6 | -18.4 | -41.9 | 0.09 | 3 |
| G22 | 11.4 | 9.5 | 14.5 | 23.6 | 14.7 | 16.9 | -27.2 | -106.8 | -39.0 | 0.59 | 23 |
| G23 | 8.0 | 20.3 | 11.4 | 19.6 | 14.8 | -154.8 | -42.4 | -145.5 | -114.2 | 0.37 | 15 |
| G24 | 11.3 | 11.2 | 9.5 | 16.7 | 12.2 | 0.7 | 15.7 | -48.7 | -10.8 | 0.21 | 8 |
| G25 | 12.4 | 40.5 | 37.5 | 25.8 | 29.0 | -226.4 | -201.9 | -107.9 | -178.7 | 0.53 | 19 |
| G26 | 8.3 | 23.2 | 11.3 | 42.5 | 21.3 | -181.0 | -37.1 | -414.2 | -210.8 | 1.30 | 40 |
| G27 | 23.5 | 44.1 | 8.2 | 30.0 | 26.4 | -87.7 | 65.2 | -27.5 | -16.6 | -0.24 | 1 |
| G28 | 8.1 | 30.3 | 6.1 | 29.4 | 18.5 | -271.8 | 25.7 | -260.5 | -168.9 | 0.56 | 20 |
| G29 | 10.0 | 27.4 | 9.3 | 33.4 | 20.0 | -173.2 | 7.2 | -232.1 | -132.7 | 0.74 | 29 |
| G30 | 10.7 | 24.4 | 10.1 | 29.3 | 18.6 | -127.5 | 5.6 | -173.3 | -98.4 | 0.59 | 23 |
| G31 | 15.6 | 30.8 | 12.8 | 30.9 | 22.5 | -97.5 | 17.7 | -98.7 | -59.5 | 0.40 | 16 |
| G32 | 24.2 | 27.6 | 16.3 | 32.7 | 25.2 | -13.8 | 32.6 | -35.2 | -5.4 | 0.20 | 7 |
| G33 | 12.4 | 30.2 | 11.7 | 38.6 | 23.2 | -143.3 | 6.1 | -210.9 | -116.0 | 0.86 | 33 |
| G34 | 14.7 | 16.3 | 18.7 | 25.1 | 18.7 | -10.8 | -27.2 | -70.7 | -36.2 | 0.48 | 17 |
| G35 | 15.4 | 18.8 | 11.5 | 15.2 | 15.2 | -21.7 | 25.8 | 1.5 | 1.9 | -0.11 | 2 |
| G36 | 16.2 | 28.9 | 21.4 | 29.9 | 24.1 | -78.3 | -32.1 | -84.2 | -64.9 | 0.48 | 17 |
| G37 | 11.0 | 26.3 | 17.8 | 64.8 | 30.0 | -139.4 | -61.5 | -489.4 | -230.1 | 2.19 | 44 |
| G38 | 10.3 | 47.1 | 12.7 | 27.0 | 24.3 | -355.1 | -23.0 | -160.8 | -179.7 | 0.22 | 9 |
| G39 | 11.7 | 15.2 | 26.8 | 26.0 | 19.9 | -29.7 | -129.4 | -122.3 | -93.8 | 0.78 | 30 |
| G40 | 17.2 | 20.0 | 25.0 | 31.2 | 23.3 | -16.2 | -45.5 | -81.8 | -47.9 | 0.67 | 28 |
| G41 | 6.7 | 8.5 | 11.9 | 20.4 | 11.9 | -26.8 | -77.3 | -203.5 | -102.5 | 0.64 | 26 |
| G42 | 12.2 | 20.0 | 21.9 | 30.0 | 21.0 | -64.8 | -79.8 | -146.3 | -97.0 | 0.79 | 31 |
| G43 | 13.9 | 18.9 | 15.5 | 17.5 | 16.5 | -35.7 | -11.1 | -25.9 | -24.2 | 0.11 | 4 |
| G44 | 7.7 | 16.3 | 15.7 | 30.4 | 17.5 | -111.6 | -102.7 | -294.0 | -169.4 | 0.96 | 36 |
| G45 | 8.6 | 19.9 | 10.6 | 16.7 | 13.9 | -132.7 | -23.9 | -94.9 | -83.8 | 0.22 | 9 |
| G46 | 7.9 | 22.0 | 16.6 | 15.2 | 15.4 | -176.9 | -108.7 | -91.7 | -125.7 | 0.23 | 10 |
| G47 | 7.8 | 17.9 | 17.4 | 14.3 | 14.3 | -131.3 | -124.9 | -83.8 | -113.3 | 0.27 | 11 |
| G48 | 13.0 | 13.2 | 13.0 | 20.5 | 14.9 | -1.4 | 0.6 | -57.0 | -19.3 | 0.31 | 12 |
| G49 | 11.8 | 24.4 | 17.6 | 22.0 | 19.0 | -107.7 | -49.8 | -87.1 | -81.5 | 0.34 | 14 |
| G50 | 10.4 | 31.3 | 19.8 | 28.7 | 22.5 | -202.2 | -90.6 | -176.5 | -156.4 | 0.62 | 25 |
| Mean (T) | 10.2 | 19.9 | 16.4 | 26.7 | | | | | | | |

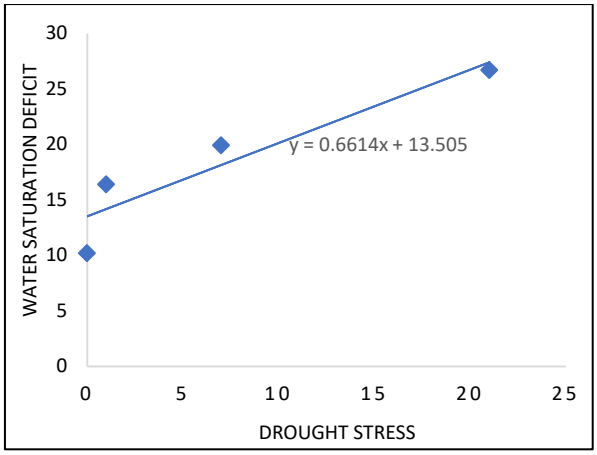



**Figure 34. Relationships between water saturation deficit of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

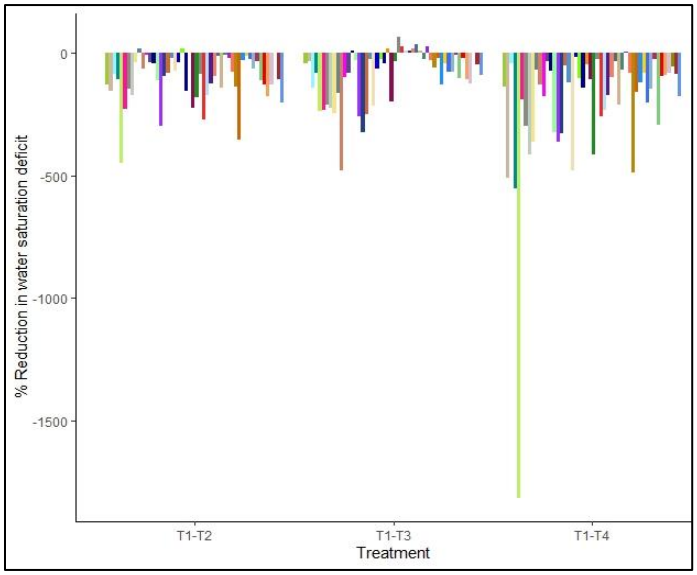
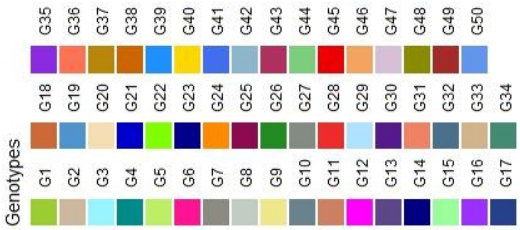



**Figure 35. Reduction percentage of water saturation deficit of fifty cotton genotypes under different drought stresses compared with control**



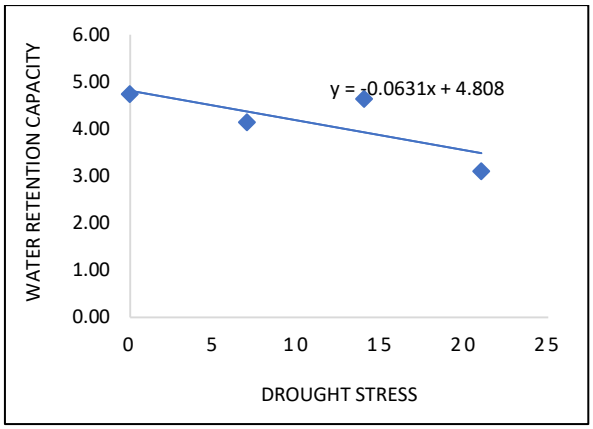




**Figure 36. Relationships between water retention capacity of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

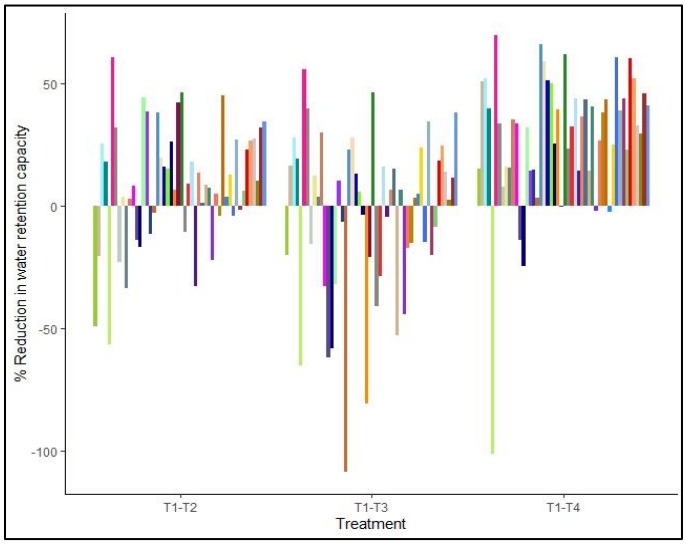



**Figure 37. Reduction percentage of water retention capacity of fifty cotton genotypes under different drought stresses compared with control**

## Table 29. Water Retention Capacity (WRC) of fifty genotypes at different drought treatments

| Genotype | WRC at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 4.27 | 6.37 | 5.13 | 3.63 | 4.85 | -49.20 | -20.32 | 14.94 | -18.20 | wrc | rank |
| G2 | 5.52 | 6.66 | 4.63 | 2.73 | 4.88 | -20.63 | 16.14 | 50.52 | 15.34 | -0.04 | 11 |
| G3 | 6.95 | 5.18 | 5.02 | 3.35 | 5.12 | 25.44 | 27.71 | 51.80 | 34.98 | -0.15 | 20 |
| G4 | 6.65 | 5.47 | 5.37 | 4.01 | 5.38 | 17.85 | 19.26 | 39.74 | 25.62 | -0.16 | 21 |
| G5 | 2.65 | 4.15 | 4.38 | 5.33 | 4.13 | -56.79 | -65.31 | -101.1 | -74.40 | -0.11 | 18 |
| G6 | 8.76 | 3.45 | 3.89 | 2.66 | 4.69 | 60.68 | 55.59 | 69.69 | 61.99 | 0.12 | 1 |
| G7 | 4.99 | 3.41 | 3.01 | 3.33 | 3.68 | 31.68 | 39.61 | 33.31 | 34.87 | -0.26 | 24 |
| G8 | 3.32 | 4.08 | 3.84 | 3.07 | 3.58 | -22.98 | -15.60 | 7.68 | -10.30 | -0.08 | 15 |
| G9 | 3.35 | 3.24 | 2.94 | 2.82 | 3.09 | 3.40 | 12.24 | 15.75 | 10.47 | -0.01 | 8 |
| G10 | 3.20 | 4.27 | 3.08 | 2.70 | 3.31 | -33.55 | 3.63 | 15.49 | -4.81 | -0.03 | 10 |
| G11 | 4.46 | 4.34 | 3.13 | 2.90 | 3.71 | 2.61 | 29.79 | 35.04 | 22.48 | -0.04 | 11 |
| G12 | 4.22 | 3.87 | 5.61 | 2.81 | 4.13 | 8.18 | -32.95 | 33.31 | 2.85 | -0.08 | 15 |
| G13 | 3.16 | 3.61 | 5.12 | 3.61 | 3.88 | -14.09 | -61.76 | -14.12 | -29.99 | -0.04 | 11 |
| G14 | 3.51 | 4.10 | 5.55 | 4.37 | 4.38 | -16.91 | -58.42 | -24.77 | -33.37 | 0.04 | 3 |
| G15 | 4.33 | 2.42 | 5.72 | 2.95 | 3.86 | 44.05 | -32.17 | 31.94 | 14.61 | 0.06 | 2 |
| G16 | 3.61 | 2.22 | 3.24 | 3.09 | 3.04 | 38.41 | 10.08 | 14.21 | 20.90 | -0.01 | 8 |
| G17 | 3.85 | 4.30 | 4.11 | 3.30 | 3.89 | -11.49 | -6.59 | 14.44 | -1.22 | -0.01 | 8 |
| G18 | 2.75 | 2.84 | 5.74 | 2.66 | 3.50 | -3.09 | -108.7 | 3.34 | -36.16 | -0.03 | 10 |
| G19 | 8.03 | 4.99 | 6.19 | 2.74 | 5.49 | 37.79 | 22.89 | 65.88 | 42.19 | 0.04 | 3 |
| G20 | 6.13 | 4.94 | 4.43 | 2.53 | 4.51 | 19.42 | 27.68 | 58.67 | 35.26 | -0.21 | 22 |
| G21 | 5.79 | 4.87 | 5.03 | 2.83 | 4.63 | 15.90 | 13.10 | 51.17 | 26.72 | -0.16 | 21 |
| G22 | 5.29 | 4.49 | 4.99 | 2.66 | 4.36 | 15.07 | 5.59 | 49.67 | 23.44 | -0.12 | 19 |
| G23 | 3.83 | 2.82 | 3.97 | 2.86 | 3.37 | 26.25 | -3.82 | 25.41 | 15.95 | -0.11 | 18 |
| G24 | 3.89 | 3.64 | 7.02 | 2.36 | 4.23 | 6.43 | -80.64 | 39.28 | -11.64 | -0.03 | 10 |
| G25 | 3.33 | 1.92 | 4.02 | 3.34 | 3.15 | 42.13 | -20.89 | -0.51 | 6.91 | -0.02 | 9 |
| G26 | 8.64 | 4.64 | 4.67 | 3.30 | 5.31 | 46.30 | 45.98 | 61.77 | 51.35 | 0.03 | 4 |
| G27 | 3.61 | 3.99 | 5.08 | 2.77 | 3.86 | -10.74 | -40.95 | 23.26 | -9.47 | -0.23 | 23 |
| G28 | 4.56 | 4.16 | 5.87 | 3.08 | 4.42 | 8.83 | -28.78 | 32.40 | 4.15 | -0.02 | 9 |
| G29 | 5.45 | 4.48 | 4.59 | 3.07 | 4.40 | 17.77 | 15.90 | 43.61 | 25.76 | -0.04 | 11 |
| G30 | 3.87 | 5.14 | 4.05 | 3.32 | 4.09 | -32.74 | -4.48 | 14.40 | -7.61 | -0.10 | 17 |
| G31 | 4.83 | 4.19 | 4.52 | 3.08 | 4.16 | 13.26 | 6.53 | 36.19 | 18.66 | -0.04 | 11 |
| G32 | 4.74 | 4.68 | 4.03 | 2.69 | 4.04 | 1.24 | 14.89 | 43.16 | 19.76 | -0.07 | 14 |
| G33 | 4.22 | 3.86 | 6.45 | 3.62 | 4.54 | 8.57 | -52.83 | 14.20 | -10.02 | -0.10 | 17 |
| G34 | 4.46 | 4.14 | 4.17 | 2.66 | 3.86 | 7.29 | 6.44 | 40.37 | 18.03 | 0.01 | 6 |
| G35 | 3.93 | 4.81 | 5.67 | 4.01 | 4.60 | -22.41 | -44.35 | -2.14 | -22.97 | -0.08 | 15 |
| G36 | 4.01 | 3.83 | 4.71 | 2.94 | 3.87 | 4.61 | -17.27 | 26.65 | 4.67 | 0.02 | 5 |
| G37 | 4.39 | 4.58 | 5.06 | 2.72 | 4.19 | -4.35 | -15.26 | 38.03 | 6.14 | -0.03 | 10 |
| G38 | 4.52 | 2.48 | 4.39 | 2.56 | 3.49 | 45.06 | 2.99 | 43.47 | 30.51 | -0.06 | 13 |
| G39 | 3.89 | 3.75 | 3.69 | 3.99 | 3.83 | 3.45 | 4.96 | -2.72 | 1.89 | -0.06 | 13 |
| G40 | 4.99 | 4.36 | 3.81 | 3.75 | 4.23 | 12.50 | 23.53 | 24.84 | 20.29 | 0.00 | 7 |
| G41 | 6.54 | 6.80 | 7.50 | 2.58 | 5.85 | -4.12 | -14.77 | 60.57 | 13.89 | -0.06 | 13 |
| G42 | 4.85 | 3.54 | 3.19 | 2.97 | 3.64 | 27.09 | 34.39 | 38.91 | 33.46 | -0.16 | 21 |
| G43 | 4.55 | 4.62 | 5.46 | 2.56 | 4.30 | -1.58 | -20.03 | 43.70 | 7.36 | -0.09 | 16 |
| G44 | 3.78 | 3.55 | 4.11 | 2.92 | 3.59 | 6.09 | -8.74 | 22.76 | 6.70 | -0.07 | 14 |
| G45 | 6.40 | 4.94 | 5.22 | 2.54 | 4.78 | 22.70 | 18.32 | 60.25 | 33.76 | -0.03 | 10 |
| G46 | 5.26 | 3.87 | 3.97 | 2.52 | 3.90 | 26.45 | 24.58 | 52.09 | 34.37 | -0.16 | 21 |
| G47 | 6.09 | 4.42 | 5.26 | 4.12 | 4.97 | 27.48 | 13.68 | 32.46 | 24.54 | -0.12 | 19 |
| G48 | 4.10 | 3.68 | 4.01 | 2.90 | 3.67 | 10.21 | 2.24 | 29.21 | 13.89 | -0.07 | 14 |
| G49 | 4.68 | 3.19 | 4.16 | 2.53 | 3.64 | 31.92 | 11.20 | 45.95 | 29.69 | -0.05 | 12 |
| G50 | 4.55 | 2.99 | 2.82 | 2.68 | 3.26 | 34.12 | 38.00 | 41.00 | 37.71 | -0.08 | 15 |
| Mean (T) | 4.73 | 4.13 | 4.63 | 3.09 | | | | | | | |

108.7%) was observed in G18 under T3 drought stress (Figure 37, Table 29). Maximum reduction% (69.69%) was observed in G6 under T4 stress (Figure 37). The result showed the negative effect of drought stress on water retention capacity in genotypic dependent manner. Water availability and retention capacity affect the growth and physiological processes of all plants, since water is the major component of actively growing plants, ranging from 70-90% of plant fresh mass (Loka *et al*., 2011). Rabadia *et al*. (1999) also observed that a strong correlation exists between plant water retention and accumulation of dry matter of the developing fiber and seed which implies that quick water uptake is required in order to hold up seed development.

#### 4.2.1.5 Water uptake capacity

Genotype, treatment and their interaction significantly affected the water uptake capacity. The highest mean water uptake capacity (0.6) was observed in T2, T3 and T4 drought stress whereas the lowest water uptake capacity (0.4) was observed in T1 drought stress (Table 30). Among the genotypes, highest water uptake capacity (1.0) was observed in G5 whereas lowest (0.3) in G3, G10, G11, G13, G20 and G23. Based on the genotype stress interaction, highest water uptake capacity (2.80) was observed in G5 under T4 whereas lowest (0.1) G5, G8, G13, G17, G18 under T1 and G3 under T4 stress respectively. On the basis of b values, the best performance (highest b value) was observed in genotype G5 (0.11) followed by G4 (0.04) whereas lowest (-0.02) in G27 and G32. With the increase of drought stress, water uptake capacity was increased as shown in linear regression in Figure 38. The minimum reduction% (-5125.0 %) was observed in G5 under T4 drought stress (Figure 39, Table 30). Maximum reduction% (53.8%) was observed in G21 under T4 stress (Figure 39). The result showed the positive effect of drought stress on water uptake capacity in genotypic dependent manner. Tolerant genotypes have a mechanism to increase the cell division at the root apical meristem to extend their root system in purpose of water uptake (Polania *et al*., 2017). On the other hand, drought susceptible showed less root development. However, the tolerance mechanisms against the drought stress in cotton depends on the genotypes as described in Mahmood *et al*. (2022). Rabadia *et al*. (1999) also observed that a strong correlation exists between plant water retention and accumulation of dry matter of the developing fiber and seed which implies that quick water uptake is required in order to hold up seed development.

## Table 30. Water Uptake Capacity (WUC)) of fifty genotypes at different drought treatments

| Genotype | WUC at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 0.4 | 1.4 | 0.7 | 0.7 | 0.8 | -280.1 | -79.9 | -93.3 | -151.1 | 0.00 | 6 |
| G2 | 0.4 | 1.3 | 0.4 | 0.9 | 0.8 | -224.0 | -6.8 | -132.6 | -121.1 | 0.01 | 5 |
| G3 | 0.2 | 0.3 | 0.4 | 0.1 | 0.3 | -31.4 | -65.9 | 42.8 | -18.2 | 0.00 | 6 |
| G4 | 0.3 | 0.6 | 0.5 | 1.2 | 0.6 | -69.9 | -45.9 | -257.7 | -124.5 | 0.04 | 2 |
| G5 | 0.1 | 0.6 | 0.4 | 2.8 | 1.0 | -981.4 | -610.2 | -5125.0 | -2238.9 | 0.11 | 1 |
| G6 | 0.5 | 0.5 | 0.6 | 0.3 | 0.5 | -3.9 | -27.9 | 37.6 | 1.9 | -0.01 | 7 |
| G7 | 0.2 | 0.4 | 0.4 | 0.6 | 0.4 | -51.8 | -60.5 | -139.9 | -84.1 | 0.01 | 5 |
| G8 | 0.1 | 0.4 | 0.5 | 0.6 | 0.4 | -266.8 | -311.0 | -359.3 | -312.4 | 0.02 | 4 |
| G9 | 0.2 | 0.2 | 0.5 | 0.6 | 0.4 | -33.8 | -184.8 | -259.9 | -159.5 | 0.02 | 4 |
| G10 | 0.2 | 0.3 | 0.6 | 0.3 | 0.3 | -27.4 | -151.1 | -33.6 | -70.7 | 0.01 | 5 |
| G11 | 0.2 | 0.3 | 0.6 | 0.2 | 0.3 | -60.2 | -258.4 | -28.5 | -115.7 | 0.01 | 5 |
| G12 | 0.2 | 0.2 | 0.7 | 0.4 | 0.4 | 2.3 | -186.4 | -57.4 | -80.5 | 0.01 | 5 |
| G13 | 0.1 | 0.2 | 0.5 | 0.2 | 0.3 | -71.5 | -247.4 | -62.7 | -127.2 | 0.01 | 5 |
| G14 | 0.4 | 0.7 | 0.6 | 0.8 | 0.6 | -82.1 | -66.2 | -134.6 | -94.3 | 0.02 | 4 |
| G15 | 0.3 | 0.3 | 0.6 | 0.8 | 0.5 | 8.6 | -87.3 | -150.6 | -76.4 | 0.02 | 4 |
| G16 | 0.2 | 0.4 | 0.6 | 0.8 | 0.5 | -100.3 | -203.7 | -278.5 | -194.2 | 0.03 | 3 |
| G17 | 0.1 | 0.3 | 0.6 | 0.5 | 0.4 | -125.3 | -360.3 | -241.3 | -242.3 | 0.02 | 4 |
| G18 | 0.1 | 0.2 | 1.2 | 0.2 | 0.4 | -85.2 | -816.3 | -39.5 | -313.7 | 0.02 | 4 |
| G19 | 0.8 | 0.6 | 0.7 | 0.4 | 0.6 | 27.7 | 7.8 | 45.5 | 27.0 | -0.01 | 7 |
| G20 | 0.2 | 0.3 | 0.5 | 0.4 | 0.3 | -34.4 | -111.7 | -75.8 | -74.0 | 0.01 | 5 |
| G21 | 0.4 | 0.4 | 0.5 | 0.2 | 0.4 | -15.0 | -42.0 | 53.8 | -1.1 | -0.01 | 7 |
| G22 | 0.5 | 0.3 | 0.6 | 0.4 | 0.4 | 32.3 | -19.0 | 19.4 | 10.9 | 0.00 | 6 |
| G23 | 0.2 | 0.4 | 0.3 | 0.4 | 0.3 | -68.4 | -49.6 | -62.2 | -60.1 | 0.01 | 5 |
| G24 | 0.3 | 0.3 | 0.6 | 0.2 | 0.4 | 10.3 | -77.1 | 29.7 | -12.4 | 0.00 | 6 |
| G25 | 0.3 | 0.4 | 1.1 | 0.6 | 0.6 | -26.9 | -286.3 | -107.2 | -140.1 | 0.02 | 4 |
| G26 | 0.6 | 0.8 | 0.4 | 1.0 | 0.7 | -33.9 | 33.2 | -56.4 | -19.0 | 0.01 | 5 |
| G27 | 0.6 | 1.4 | 0.3 | 0.5 | 0.7 | -126.9 | 46.0 | 13.4 | -22.5 | -0.02 | 8 |
| G28 | 0.3 | 1.0 | 0.3 | 0.6 | 0.5 | -231.9 | -1.6 | -114.8 | -116.1 | 0.00 | 6 |
| G29 | 0.4 | 1.0 | 0.3 | 0.7 | 0.6 | -114.0 | 25.2 | -55.2 | -48.0 | 0.00 | 6 |
| G30 | 0.3 | 1.0 | 0.3 | 0.7 | 0.6 | -225.0 | -2.9 | -126.5 | -118.1 | 0.01 | 5 |
| G31 | 0.6 | 1.0 | 0.5 | 0.6 | 0.7 | -63.9 | 24.6 | -8.4 | -15.9 | -0.01 | 7 |
| G32 | 0.9 | 1.0 | 0.5 | 0.6 | 0.7 | -11.7 | 47.7 | 38.5 | 24.9 | -0.02 | 8 |
| G33 | 0.4 | 0.9 | 0.6 | 1.0 | 0.7 | -114.8 | -57.3 | -151.2 | -107.7 | 0.02 | 4 |
| G34 | 0.5 | 0.5 | 0.6 | 0.4 | 0.5 | -2.2 | -15.6 | 18.1 | 0.1 | 0.00 | 6 |
| G35 | 0.5 | 0.7 | 0.5 | 0.5 | 0.5 | -57.9 | -17.5 | -1.1 | -25.5 | 0.00 | 6 |
| G36 | 0.5 | 0.8 | 0.8 | 0.6 | 0.7 | -66.6 | -62.1 | -19.1 | -49.2 | 0.00 | 6 |
| G37 | 0.4 | 0.9 | 0.7 | 1.1 | 0.8 | -143.5 | -91.5 | -195.1 | -143.4 | 0.03 | 3 |
| G38 | 0.4 | 0.7 | 0.4 | 0.4 | 0.5 | -88.7 | -16.2 | -14.4 | -39.8 | 0.00 | 6 |
| G39 | 0.3 | 0.4 | 0.7 | 0.8 | 0.6 | -24.3 | -112.0 | -133.5 | -89.9 | 0.02 | 4 |
| G40 | 0.7 | 0.7 | 0.7 | 0.9 | 0.7 | 1.5 | -0.2 | -26.0 | -8.2 | 0.01 | 5 |
| G41 | 0.4 | 0.5 | 0.8 | 0.3 | 0.5 | -33.1 | -108.7 | 13.7 | -42.7 | 0.00 | 6 |
| G42 | 0.5 | 0.5 | 0.5 | 0.6 | 0.5 | -8.3 | -1.8 | -25.7 | -11.9 | 0.00 | 6 |
| G43 | 0.5 | 0.7 | 0.7 | 0.3 | 0.5 | -38.7 | -41.2 | 43.8 | -12.0 | -0.01 | 7 |
| G44 | 0.2 | 0.4 | 0.5 | 0.6 | 0.4 | -93.4 | -126.1 | -171.8 | -130.4 | 0.02 | 4 |
| G45 | 0.5 | 0.8 | 0.4 | 0.3 | 0.5 | -70.3 | 3.2 | 44.2 | -7.6 | -0.01 | 7 |
| G46 | 0.3 | 0.6 | 0.5 | 0.2 | 0.4 | -90.4 | -48.3 | 30.2 | -36.2 | -0.01 | 7 |
| G47 | 0.4 | 0.6 | 0.7 | 0.4 | 0.5 | -54.3 | -87.7 | -12.2 | -51.4 | 0.00 | 6 |
| G48 | 0.4 | 0.4 | 0.4 | 0.4 | 0.4 | 14.6 | 5.6 | 5.5 | 8.6 | 0.00 | 6 |
| G49 | 0.4 | 0.5 | 0.6 | 0.3 | 0.5 | -23.6 | -28.6 | 22.3 | -10.0 | 0.00 | 6 |
| G50 | 0.4 | 0.6 | 0.4 | 0.5 | 0.5 | -69.7 | 2.9 | -30.7 | -32.5 | 0.00 | 6 |
| Mean (T) | 0.4 | 0.6 | 0.6 | 0.6 | | | | | | | |

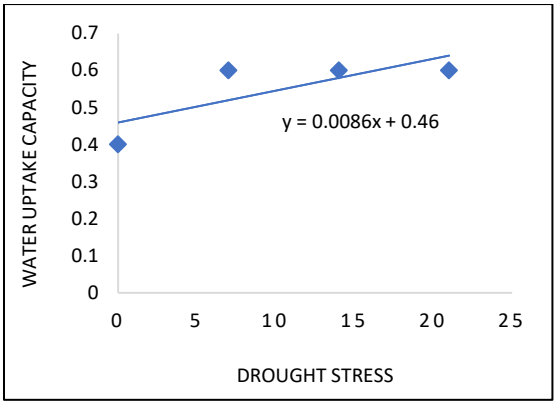



**Figure 38. Relationships between water uptake capacity of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

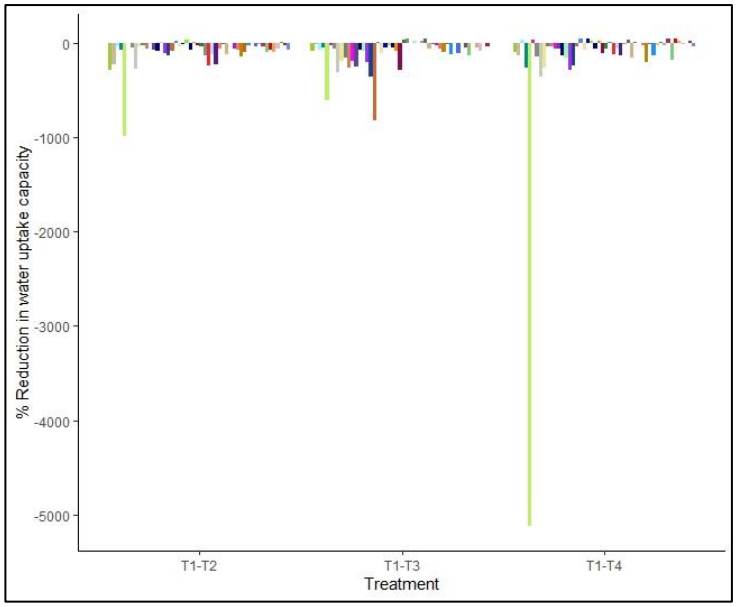
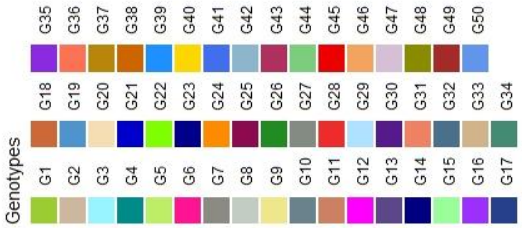



**Figure 39. Reduction percentage of water uptake capacity of fifty cotton genotypes under different drought stresses compared with control**



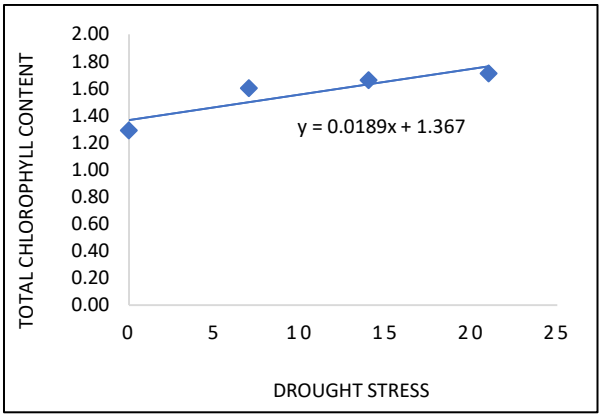




**Figure 40. Relationships between total chlorophyll content of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

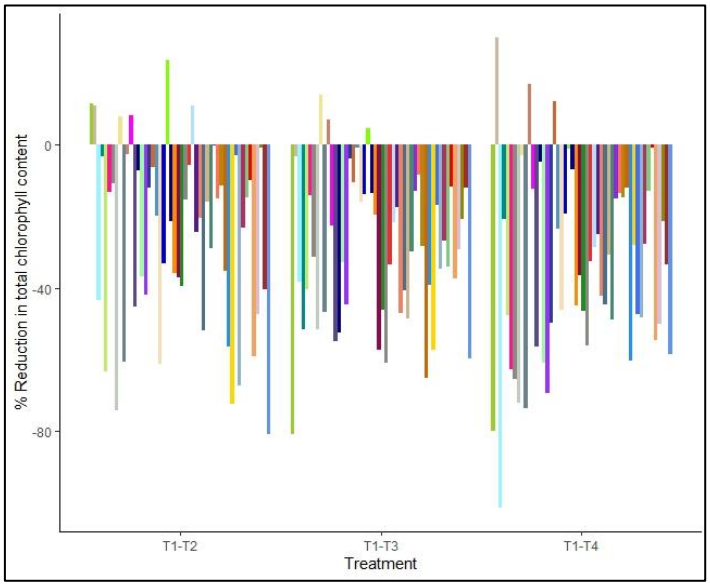



**Figure 41. Reduction percentage of total chlorophyll content of fifty cotton genotypes under different drought stresses compared with control**

#### 4.2.1.6 Total Chlorophyll content (mg/g)

Genotype, treatment and their interaction significantly affected the total chlorophyll content. The highest mean chlorophyll content (1.71 mg/g) was observed in T4 drought stress whereas the lowest total chlorophyll content (1.29 mg/g) was observed in T1 drought stress (Table 31). Among the genotypes, highest total chlorophyll content (1.82 mg/g) was observed in G2 followed by G49 (1.80 mg/g) and lowest (1.28 mg/g) in G4. Based on the genotype stress interaction, highest total chlorophyll content (2.23 mg/g) was observed in G7 under T4 and G14 under T3 whereas lowest (0.98 mg/g) in G1 under T2 stress. On the basis of b values, the best performance (highest b value) was observed in genotype G1 (0.05) followed by G3 and G7 (0.04) whereas lowest in G2 (-0.02). With the increase of drought stress, total chlorophyll content was increased as shown in linear regression in Figure 40. The minimum reduction% (-101.4%) was observed in G3 under T4 drought stress (Figure 41, Table 31). Maximum reduction% (30.18%) was observed in G2 under T4 stress (Figure 41). The result showed the positive effect of drought stress on total chlorophyll content in genotypic dependent manner. Some of the genotypes showed an increase in total chlorophyll content at mild and moderate drought stress. However, all the genotypes showed a decrease of total chlorophyll content under the severe drought stress. Similar result has been observed in (Ullah *et. al*., 2017; Kader *et. al*., 2015). Parida et al. (2007) found significant decrease in chlorophyll content, carotenoids, proteins, and starch after applying drought stress for 7 days. Ahmad *et. al*., (2020) were also evaluated 10 cotton leaf chlorophyll contents and observed that water stress adversely reduced leaf chlorophyll. Hafeez *et al*. (2015) observed chlorophyll content and photosynthesis rate of cotton plant under drought stress were also sharply decreased.

#### 4.2.1.7 Nitrogen Concentration (%)

Genotype, treatment and their interaction significantly affected the nitrogen concentration. The highest mean nitrogen concentration (1.64%) was observed T4 drought stress whereas the lowest nitrogen concentration (1.28%) was observed in T1 drought stress (Table 32). Among the genotypes, highest nitrogen concentration (1.73%) was observed in G2 whereas lowest (1.28%) in G4. Based on the genotype stress interaction, highest nitrogen concentration (2.09%) was observed in G7 under T4 whereas lowest (1.02%) in G1 under T2 stress. On the basis of b values, the best

## Table 31. Total Chlorophyll content (Tchl) of fifty genotypes at different drought treatments

| Genotype | T-chl (mg/g) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 1.11 | 0.98 | 2.01 | 2.00 | 1.52 | 11.49 | -80.71 | -79.88 | -49.70 | 0.05 | 1 |
| G2 | 2.01 | 1.78 | 2.07 | 1.40 | 1.82 | 11.11 | -3.29 | 30.18 | 12.67 | -0.02 | 8 |
| G3 | 1.05 | 1.51 | 1.46 | 2.12 | 1.54 | -43.48 | -38.23 | -101.4 | -61.04 | 0.04 | 2 |
| G4 | 1.08 | 1.11 | 1.64 | 1.30 | 1.28 | -3.13 | -51.61 | -20.62 | -25.12 | 0.02 | 5 |
| G5 | 1.22 | 1.99 | 1.71 | 1.80 | 1.68 | -63.41 | -40.21 | -47.52 | -50.38 | 0.02 | 4 |
| G6 | 1.27 | 1.43 | 1.44 | 2.06 | 1.55 | -13.00 | -14.09 | -62.80 | -29.96 | 0.03 | 3 |
| G7 | 1.35 | 1.49 | 1.77 | 2.23 | 1.71 | -10.83 | -31.23 | -65.43 | -35.83 | 0.04 | 2 |
| G8 | 1.05 | 1.82 | 1.58 | 1.80 | 1.56 | -74.09 | -51.60 | -72.17 | -65.95 | 0.03 | 4 |
| G9 | 1.58 | 1.45 | 1.36 | 1.62 | 1.50 | 8.07 | 14.20 | -2.72 | 6.52 | 0.00 | 6 |
| G10 | 1.04 | 1.67 | 1.53 | 1.81 | 1.51 | -60.68 | -46.66 | -73.68 | -60.34 | 0.03 | 3 |
| G11 | 1.53 | 1.57 | 1.42 | 1.27 | 1.45 | -2.61 | 7.23 | 17.06 | 7.23 | -0.01 | 7 |
| G12 | 1.35 | 1.24 | 1.66 | 1.52 | 1.44 | 8.18 | -22.38 | -12.15 | -8.78 | 0.01 | 5 |
| G13 | 1.06 | 1.54 | 1.64 | 1.66 | 1.47 | -45.12 | -54.98 | -56.29 | -52.13 | 0.03 | 4 |
| G14 | 1.46 | 1.56 | 2.23 | 1.53 | 1.70 | -7.04 | -52.35 | -4.63 | -21.34 | 0.01 | 5 |
| G15 | 1.09 | 1.49 | 1.44 | 1.75 | 1.44 | -36.85 | -32.75 | -60.99 | -43.53 | 0.03 | 4 |
| G16 | 1.12 | 1.59 | 1.62 | 1.90 | 1.56 | -41.82 | -44.70 | -69.24 | -51.92 | 0.03 | 3 |
| G17 | 1.39 | 1.56 | 1.44 | 2.09 | 1.62 | -11.92 | -3.75 | -49.76 | -21.81 | 0.03 | 4 |
| G18 | 1.46 | 1.55 | 1.61 | 1.28 | 1.47 | -6.33 | -10.55 | 12.13 | -1.58 | -0.01 | 7 |
| G19 | 1.28 | 1.54 | 1.29 | 1.58 | 1.42 | -19.87 | -0.72 | -23.34 | -14.65 | 0.01 | 5 |
| G20 | 1.25 | 2.02 | 1.45 | 1.83 | 1.64 | -61.16 | -15.84 | -46.17 | -41.06 | 0.02 | 5 |
| G21 | 1.41 | 1.87 | 1.60 | 1.68 | 1.64 | -33.21 | -13.77 | -19.12 | -22.03 | 0.01 | 5 |
| G22 | 1.59 | 1.21 | 1.52 | 1.61 | 1.48 | 23.66 | 4.73 | -1.06 | 9.11 | 0.01 | 6 |
| G23 | 1.43 | 1.74 | 1.63 | 1.53 | 1.58 | -21.43 | -13.50 | -6.86 | -13.93 | 0.00 | 6 |
| G24 | 1.31 | 1.78 | 1.56 | 1.90 | 1.64 | -35.86 | -19.34 | -44.77 | -33.32 | 0.02 | 4 |
| G25 | 1.23 | 1.68 | 1.93 | 1.68 | 1.63 | -36.99 | -57.23 | -36.36 | -43.53 | 0.02 | 4 |
| G26 | 1.11 | 1.55 | 1.63 | 1.63 | 1.48 | -39.29 | -46.05 | -46.33 | -43.89 | 0.02 | 4 |
| G27 | 1.25 | 1.43 | 2.00 | 1.94 | 1.66 | -15.18 | -60.97 | -56.03 | -44.06 | 0.04 | 3 |
| G28 | 1.40 | 1.48 | 1.87 | 1.86 | 1.66 | -5.47 | -33.36 | -32.37 | -23.73 | 0.03 | 4 |
| G29 | 1.33 | 1.18 | 1.62 | 1.71 | 1.46 | 10.88 | -21.75 | -28.46 | -13.11 | 0.02 | 4 |
| G30 | 1.33 | 1.66 | 1.56 | 1.66 | 1.55 | -24.21 | -17.41 | -24.90 | -22.18 | 0.01 | 5 |
| G31 | 1.30 | 1.56 | 1.91 | 1.84 | 1.65 | -20.51 | -47.08 | -42.10 | -36.56 | 0.03 | 4 |
| G32 | 1.16 | 1.77 | 1.64 | 1.68 | 1.56 | -51.76 | -40.54 | -44.63 | -45.64 | 0.02 | 4 |
| G33 | 1.13 | 1.31 | 1.67 | 1.48 | 1.40 | -15.93 | -48.35 | -30.78 | -31.69 | 0.02 | 4 |
| G34 | 1.15 | 1.49 | 1.50 | 1.72 | 1.46 | -28.75 | -29.68 | -48.72 | -35.72 | 0.02 | 4 |
| G35 | 1.56 | 1.56 | 1.76 | 1.80 | 1.67 | -0.20 | -12.79 | -15.05 | -9.35 | 0.01 | 5 |
| G36 | 1.38 | 1.59 | 1.50 | 1.57 | 1.51 | -14.98 | -8.43 | -13.43 | -12.28 | 0.01 | 5 |
| G37 | 1.40 | 1.56 | 1.80 | 1.61 | 1.59 | -11.37 | -28.11 | -14.55 | -18.01 | 0.01 | 5 |
| G38 | 1.29 | 1.74 | 2.13 | 1.44 | 1.65 | -35.31 | -65.01 | -11.81 | -37.38 | 0.01 | 5 |
| G39 | 1.15 | 1.80 | 1.60 | 1.85 | 1.60 | -56.38 | -39.18 | -60.24 | -51.93 | 0.03 | 4 |
| G40 | 1.02 | 1.76 | 1.60 | 1.31 | 1.42 | -72.37 | -57.29 | -28.04 | -52.57 | 0.01 | 5 |
| G41 | 1.32 | 1.36 | 1.54 | 1.94 | 1.54 | -2.79 | -16.87 | -47.25 | -22.31 | 0.03 | 3 |
| G42 | 1.16 | 1.95 | 1.57 | 1.72 | 1.60 | -67.34 | -34.73 | -48.20 | -50.09 | 0.02 | 4 |
| G43 | 1.36 | 1.67 | 1.72 | 1.73 | 1.62 | -23.12 | -26.64 | -27.66 | -25.80 | 0.02 | 5 |
| G44 | 1.39 | 1.59 | 1.86 | 1.56 | 1.60 | -14.72 | -33.88 | -12.73 | -20.44 | 0.01 | 5 |
| G45 | 1.43 | 1.57 | 1.60 | 1.44 | 1.51 | -9.88 | -11.70 | -0.86 | -7.48 | 0.00 | 6 |
| G46 | 1.23 | 1.95 | 1.69 | 1.90 | 1.69 | -58.93 | -37.41 | -54.42 | -50.25 | 0.02 | 4 |
| G47 | 1.24 | 1.83 | 1.60 | 1.86 | 1.64 | -47.38 | -29.07 | -50.11 | -42.19 | 0.02 | 4 |
| G48 | 1.34 | 1.35 | 1.61 | 1.62 | 1.48 | -0.69 | -20.71 | -21.40 | -14.26 | 0.02 | 5 |
| G49 | 1.49 | 2.09 | 1.66 | 1.98 | 1.80 | -40.42 | -11.99 | -33.29 | -28.57 | 0.02 | 5 |
| G50 | 1.08 | 1.96 | 1.73 | 1.72 | 1.62 | -80.68 | -59.55 | -58.56 | -66.26 | 0.02 | 4 |
| Mean (T) | 1.29 | 1.60 | 1.66 | 1.71 | | | | | | | |

## Table 32. Nitrogen concentration of fifty genotypes at different drought treatments

| Genotype | Nitrogen concentration (%) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 1.13 | 1.02 | 1.89 | 1.89 | 1.48 | 9.74 | -68.39 | -67.69 | -42.12 | 0.05 | 1 |
| G2 | 1.89 | 1.70 | 1.95 | 1.37 | 1.73 | 10.10 | -3.00 | 27.45 | 11.52 | -0.02 | 8 |
| G3 | 1.08 | 1.47 | 1.42 | 1.99 | 1.49 | -36.55 | -32.13 | -85.23 | -51.30 | 0.04 | 2 |
| G4 | 1.10 | 1.13 | 1.58 | 1.29 | 1.28 | -2.64 | -43.56 | -17.40 | -21.20 | 0.01 | 5 |
| G5 | 1.22 | 1.88 | 1.64 | 1.72 | 1.61 | -54.47 | -34.55 | -40.83 | -43.28 | 0.02 | 4 |
| G6 | 1.26 | 1.40 | 1.41 | 1.94 | 1.50 | -11.22 | -12.17 | -54.23 | -25.87 | 0.03 | 3 |
| G7 | 1.33 | 1.46 | 1.69 | 2.09 | 1.64 | -9.43 | -27.20 | -56.98 | -31.20 | 0.04 | 2 |
| G8 | 1.07 | 1.74 | 1.53 | 1.72 | 1.51 | -62.19 | -43.31 | -60.59 | -55.36 | 0.02 | 4 |
| G9 | 1.53 | 1.42 | 1.34 | 1.57 | 1.46 | 7.16 | 12.60 | -2.42 | 5.78 | 0.00 | 6 |
| G10 | 1.07 | 1.61 | 1.48 | 1.72 | 1.47 | -50.90 | -39.14 | -61.80 | -50.61 | 0.03 | 3 |
| G11 | 1.49 | 1.52 | 1.39 | 1.26 | 1.42 | -2.31 | 6.39 | 15.09 | 6.39 | -0.01 | 7 |
| G12 | 1.33 | 1.24 | 1.59 | 1.47 | 1.41 | 7.13 | -19.50 | -10.59 | -7.65 | 0.01 | 5 |
| G13 | 1.08 | 1.49 | 1.58 | 1.59 | 1.44 | -37.95 | -46.25 | -47.35 | -43.85 | 0.02 | 4 |
| G14 | 1.43 | 1.52 | 2.08 | 1.49 | 1.63 | -6.20 | -46.05 | -4.07 | -18.77 | 0.01 | 5 |
| G15 | 1.11 | 1.45 | 1.41 | 1.68 | 1.41 | -31.13 | -27.67 | -51.53 | -36.78 | 0.02 | 4 |
| G16 | 1.13 | 1.54 | 1.56 | 1.80 | 1.51 | -35.49 | -37.93 | -58.76 | -44.06 | 0.03 | 3 |
| G17 | 1.37 | 1.51 | 1.41 | 1.96 | 1.56 | -10.42 | -3.28 | -43.52 | -19.07 | 0.02 | 4 |
| G18 | 1.42 | 1.50 | 1.56 | 1.27 | 1.44 | -5.56 | -9.27 | 10.66 | -1.39 | -0.01 | 7 |
| G19 | 1.27 | 1.49 | 1.28 | 1.53 | 1.40 | -17.19 | -0.62 | -20.20 | -12.67 | 0.01 | 5 |
| G20 | 1.25 | 1.90 | 1.42 | 1.74 | 1.58 | -52.73 | -13.66 | -39.81 | -35.40 | 0.01 | 5 |
| G21 | 1.38 | 1.78 | 1.55 | 1.61 | 1.58 | -29.08 | -12.05 | -16.74 | -19.29 | 0.01 | 5 |
| G22 | 1.54 | 1.21 | 1.47 | 1.55 | 1.44 | 21.02 | 4.20 | -0.94 | 8.09 | 0.00 | 6 |
| G23 | 1.40 | 1.67 | 1.57 | 1.49 | 1.53 | -18.81 | -11.85 | -6.02 | -12.22 | 0.00 | 6 |
| G24 | 1.30 | 1.70 | 1.52 | 1.80 | 1.58 | -31.12 | -16.78 | -38.84 | -28.91 | 0.02 | 4 |
| G25 | 1.23 | 1.62 | 1.83 | 1.61 | 1.57 | -31.81 | -49.23 | -31.28 | -37.44 | 0.02 | 4 |
| G26 | 1.13 | 1.51 | 1.57 | 1.57 | 1.44 | -33.32 | -39.05 | -39.28 | -37.21 | 0.02 | 4 |
| G27 | 1.24 | 1.40 | 1.89 | 1.84 | 1.59 | -13.08 | -52.53 | -48.28 | -37.96 | 0.03 | 3 |
| G28 | 1.38 | 1.44 | 1.78 | 1.77 | 1.59 | -4.79 | -29.20 | -28.34 | -20.78 | 0.02 | 4 |
| G29 | 1.31 | 1.19 | 1.56 | 1.64 | 1.42 | 9.45 | -18.91 | -24.74 | -11.40 | 0.02 | 4 |
| G30 | 1.32 | 1.59 | 1.52 | 1.60 | 1.51 | -21.05 | -15.14 | -21.66 | -19.28 | 0.01 | 5 |
| G31 | 1.28 | 1.51 | 1.81 | 1.75 | 1.59 | -17.77 | -40.78 | -36.47 | -31.68 | 0.02 | 4 |
| G32 | 1.17 | 1.69 | 1.58 | 1.62 | 1.51 | -44.17 | -34.60 | -38.09 | -38.95 | 0.02 | 4 |
| G33 | 1.14 | 1.30 | 1.61 | 1.44 | 1.37 | -13.54 | -41.07 | -26.15 | -26.92 | 0.02 | 4 |
| G34 | 1.16 | 1.45 | 1.46 | 1.65 | 1.43 | -24.51 | -25.30 | -41.52 | -30.44 | 0.02 | 4 |
| G35 | 1.51 | 1.52 | 1.68 | 1.72 | 1.61 | -0.17 | -11.34 | -13.35 | -8.29 | 0.01 | 5 |
| G36 | 1.36 | 1.54 | 1.46 | 1.52 | 1.47 | -13.09 | -7.37 | -11.73 | -10.73 | 0.01 | 5 |
| G37 | 1.38 | 1.52 | 1.72 | 1.55 | 1.54 | -9.96 | -24.61 | -12.73 | -15.77 | 0.01 | 5 |
| G38 | 1.28 | 1.67 | 2.00 | 1.41 | 1.59 | -30.57 | -56.28 | -10.22 | -32.36 | 0.01 | 5 |
| G39 | 1.16 | 1.72 | 1.55 | 1.76 | 1.55 | -48.05 | -33.39 | -51.34 | -44.26 | 0.02 | 4 |
| G40 | 1.05 | 1.68 | 1.55 | 1.29 | 1.39 | -60.50 | -47.89 | -23.44 | -43.95 | 0.01 | 5 |
| G41 | 1.31 | 1.34 | 1.50 | 1.84 | 1.50 | -2.43 | -14.66 | -41.03 | -19.37 | 0.03 | 3 |
| G42 | 1.17 | 1.84 | 1.52 | 1.65 | 1.55 | -57.47 | -29.64 | -41.13 | -42.75 | 0.02 | 4 |
| G43 | 1.34 | 1.61 | 1.65 | 1.66 | 1.56 | -20.15 | -23.21 | -24.10 | -22.49 | 0.01 | 5 |
| G44 | 1.36 | 1.54 | 1.77 | 1.52 | 1.55 | -12.87 | -29.61 | -11.13 | -17.87 | 0.01 | 5 |
| G45 | 1.40 | 1.52 | 1.54 | 1.41 | 1.47 | -8.67 | -10.27 | -0.75 | -6.56 | 0.00 | 6 |
| G46 | 1.23 | 1.85 | 1.62 | 1.80 | 1.62 | -50.68 | -32.17 | -46.80 | -43.22 | 0.02 | 4 |
| G47 | 1.24 | 1.74 | 1.55 | 1.77 | 1.58 | -40.81 | -25.04 | -43.16 | -36.34 | 0.02 | 4 |
| G48 | 1.32 | 1.33 | 1.56 | 1.56 | 1.44 | -0.60 | -18.01 | -18.61 | -12.41 | 0.01 | 5 |
| G49 | 1.45 | 1.96 | 1.60 | 1.87 | 1.72 | -35.63 | -10.57 | -29.34 | -25.18 | 0.01 | 5 |
| G50 | 1.10 | 1.85 | 1.66 | 1.65 | 1.57 | -68.11 | -50.27 | -49.44 | -55.94 | 0.02 | 4 |
| Mean (T) | 1.28 | 1.55 | 1.60 | 1.64 | | | | | | | |

performance (highest b value) was observed in genotype G1 (0.05) followed by G3 and G7 (0.04) whereas lowest (-0.02) in G2. With the increase of drought stress, nitrogen concentration was increased as shown in linear regression in Figure 42. The minimum reduction% (-85.23 %) was observed in G3 under T4 drought stress (Figure 43, Table 32). Maximum reduction% (27.45%) was observed in G2 under T4 stress (Figure 43). The result showed the positive effect of drought stress on nitrogen concentration in genotypic dependent manner. Similar results were found in the study of Iqbal *et al*. (2020). Drought stress disturbs the plant metabolism by affecting the uptake and translocation of N to above ground parts through reduction in transpiration (Xiong *et al*., 2018). Under drought stress conditions, nitrogen concentration showed both an increase and decrease depending on the genetic structure of cotton genotypes (Mahmood *et al*., 2022; Xiao *et al*., 2020). Likewise, exogenous N supply improved the N uptake, photosynthesis, relative water contents of cotton leaves under drought stress conditions.

#### 4.2.1.8 Membrane Stability Index (MSI)

Genotype, treatment and their interaction significantly affected the membrane stability index. The highest mean membrane stability index (50.86) was observed in T1 drought stress whereas the lowest membrane stability index (34.65) was observed in T4 drought stress (Table 33). Among the genotypes, highest membrane stability index (55.99) was observed in G14 followed by G50 (55.79) and lowest (30.08) in G1. Based on the genotype stress interaction, highest membrane stability index (63.35) was observed in G45 under T1 and lowest (12.25) in G37 under T4 stress. On the basis of b values, the best performance (highest b value) was observed in genotype G3 (-0.26) followed by G9 (-0.27) whereas lowest in G37 (-1.83). With the increase of drought stress, membrane stability index was decreased as shown in linear regression in Figure 44. The minimum reduction% (0.25%) was observed in G3 under T2 drought stress (Figure 45, Table 33). Maximum reduction% (77.29%) was observed in G37 under T4 stress (Figure 45). The result showed the negative effect of drought stress on membrane stability index in genotypic dependent manner. Some of the genotypes showed an increase in membrane stability index at mild and moderate drought stress. However, all the genotypes showed a decrease of membrane stability index under the severe drought stress. Similar result has been observed in Hafeez *et al*. (2015). Oxidative injury at the cellular level under water stress has high lipid

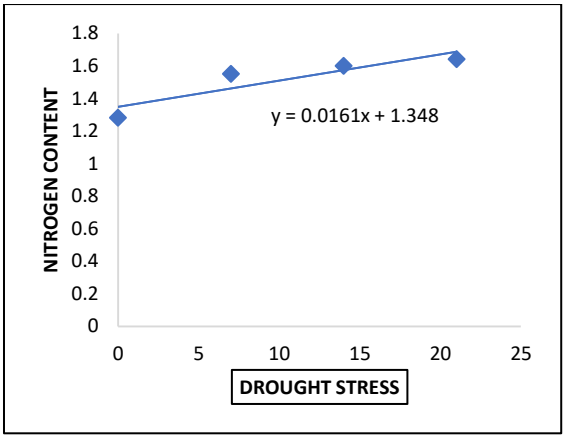



**Figure 42. Relationships between nitrogen concentration of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

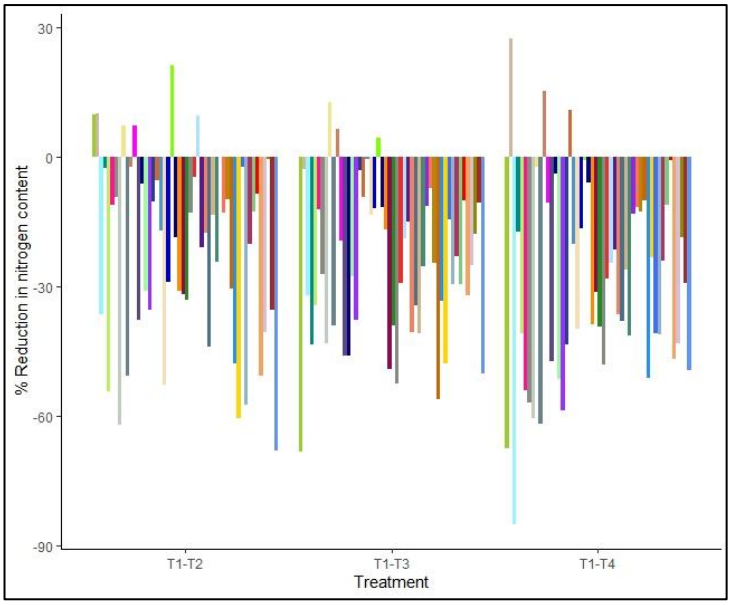
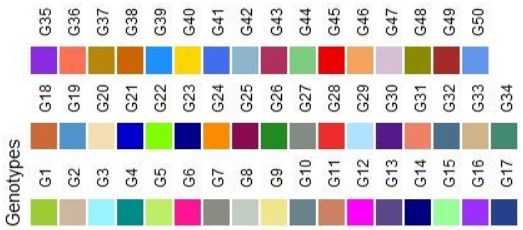



**Figure 43. Reduction percentage of nitrogen content of fifty cotton genotypes under different drought stresses compared with control**



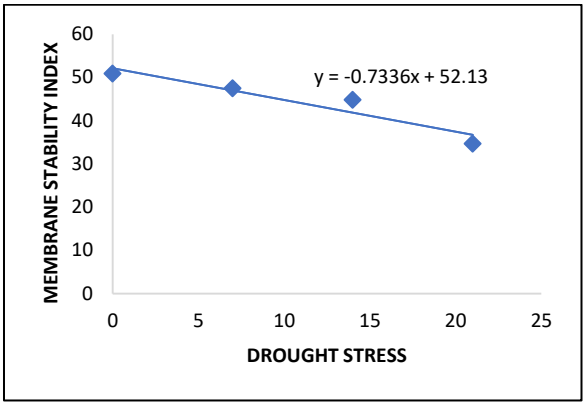




**Figure 44. Relationships between membrane stability index of cotton genotypes and different drought stresses (0, 7, 14, 21 days interval)**

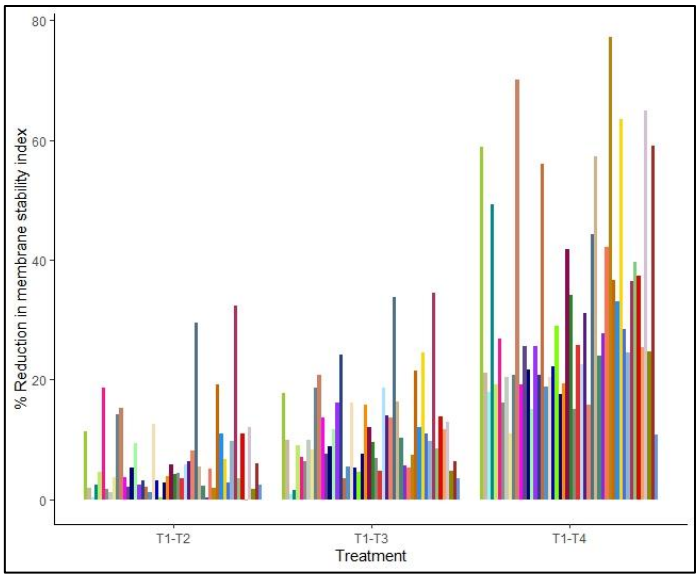



**Figure 45. Reduction percentage of membrane stability index of fifty cotton genotypes under different drought stresses compared with control**

**Table 33. Membrane Stability Index (MSI) of fifty genotypes at different drought treatments**

| Genotype | MSI at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 38.54 | 34.20 | 31.70 | 15.87 | 30.08 | 11.27 | 17.74 | 58.81 | 29.27 | -1.01 | 31 |
| G2 | 54.50 | 53.44 | 49.10 | 43.00 | 50.01 | 1.95 | 9.91 | 21.10 | 10.98 | -0.55 | 15 |
| G3 | 33.88 | 33.79 | 33.59 | 27.82 | 32.27 | 0.25 | 0.85 | 17.89 | 6.33 | -0.26 | 1 |
| G4 | 44.11 | 43.03 | 43.41 | 22.39 | 38.23 | 2.46 | 1.59 | 49.24 | 17.76 | -0.93 | 30 |
| G5 | 40.87 | 39.00 | 37.21 | 33.00 | 37.52 | 4.58 | 8.95 | 19.25 | 10.93 | -0.36 | 6 |
| G6 | 37.32 | 30.37 | 34.69 | 27.28 | 32.41 | 18.62 | 7.04 | 26.90 | 17.52 | -0.37 | 7 |
| G7 | 48.96 | 48.10 | 45.84 | 41.08 | 46.00 | 1.77 | 6.37 | 16.11 | 8.08 | -0.37 | 7 |
| G8 | 35.64 | 35.24 | 32.09 | 28.38 | 32.84 | 1.14 | 9.98 | 20.39 | 10.50 | -0.36 | 6 |
| G9 | 49.30 | 47.50 | 45.17 | 43.88 | 46.46 | 3.65 | 8.36 | 10.99 | 7.67 | -0.27 | 2 |
| G10 | 50.89 | 43.65 | 41.42 | 40.34 | 44.08 | 14.21 | 18.60 | 20.72 | 17.84 | -0.48 | 11 |
| G11 | 44.00 | 37.32 | 34.84 | 13.20 | 32.34 | 15.18 | 20.80 | 70.01 | 35.33 | -1.36 | 38 |
| G12 | 47.67 | 45.91 | 41.12 | 38.53 | 43.31 | 3.68 | 13.74 | 19.17 | 12.20 | -0.46 | 10 |
| G13 | 48.87 | 47.89 | 45.13 | 36.39 | 44.57 | 2.02 | 7.67 | 25.55 | 11.74 | -0.57 | 17 |
| G14 | 61.50 | 58.26 | 56.09 | 48.12 | 55.99 | 5.27 | 8.79 | 21.76 | 11.94 | -0.60 | 20 |
| G15 | 49.67 | 44.98 | 43.84 | 42.21 | 45.17 | 9.44 | 11.74 | 15.02 | 12.07 | -0.34 | 5 |
| G16 | 50.01 | 48.79 | 41.93 | 37.18 | 44.48 | 2.44 | 16.16 | 25.65 | 14.75 | -0.65 | 22 |
| G17 | 61.64 | 59.67 | 46.74 | 48.79 | 54.21 | 3.20 | 24.17 | 20.85 | 16.07 | -0.74 | 25 |
| G18 | 46.86 | 45.88 | 45.24 | 20.63 | 39.65 | 2.09 | 3.47 | 55.97 | 20.51 | -1.13 | 35 |
| G19 | 45.73 | 45.22 | 43.21 | 37.12 | 42.82 | 1.12 | 5.52 | 18.83 | 8.49 | -0.40 | 8 |
| G20 | 53.56 | 46.77 | 44.90 | 42.58 | 46.95 | 12.68 | 16.16 | 20.50 | 16.45 | -0.50 | 13 |
| G21 | 45.15 | 43.71 | 42.77 | 35.15 | 41.69 | 3.19 | 5.28 | 22.16 | 10.21 | -0.44 | 9 |
| G22 | 44.89 | 44.76 | 42.85 | 31.86 | 41.09 | 0.30 | 4.55 | 29.03 | 11.29 | -0.59 | 19 |
| G23 | 53.28 | 51.75 | 49.22 | 43.88 | 49.53 | 2.87 | 7.62 | 17.64 | 9.38 | -0.44 | 9 |
| G24 | 48.67 | 46.77 | 41.00 | 39.26 | 43.93 | 3.90 | 15.76 | 19.34 | 13.00 | -0.49 | 12 |
| G25 | 56.26 | 52.93 | 49.45 | 32.73 | 47.84 | 5.91 | 12.09 | 41.82 | 19.94 | -1.06 | 33 |
| G26 | 53.00 | 50.75 | 47.90 | 34.87 | 46.63 | 4.25 | 9.61 | 34.21 | 16.02 | -0.82 | 27 |
| G27 | 43.80 | 41.86 | 40.80 | 37.20 | 40.91 | 4.42 | 6.85 | 15.07 | 8.78 | -0.30 | 4 |
| G28 | 47.07 | 45.39 | 44.86 | 34.94 | 43.07 | 3.58 | 4.69 | 25.77 | 11.35 | -0.53 | 14 |
| G29 | 60.05 | 56.51 | 48.86 | 46.53 | 52.99 | 5.90 | 18.63 | 22.51 | 15.68 | -0.69 | 24 |
| G30 | 56.93 | 53.35 | 48.95 | 39.26 | 49.62 | 6.29 | 14.01 | 31.04 | 17.11 | -0.82 | 27 |
| G31 | 53.17 | 48.85 | 45.91 | 44.73 | 48.17 | 8.13 | 13.67 | 15.88 | 12.56 | -0.40 | 8 |
| G32 | 57.27 | 40.36 | 37.91 | 31.92 | 41.86 | 29.53 | 33.81 | 44.27 | 35.87 | -1.12 | 34 |
| G33 | 48.66 | 46.02 | 40.69 | 20.77 | 39.03 | 5.43 | 16.37 | 57.31 | 26.37 | -1.27 | 37 |
| G34 | 56.99 | 55.67 | 51.11 | 43.27 | 51.76 | 2.31 | 10.32 | 24.06 | 12.23 | -0.65 | 23 |
| G35 | 54.91 | 54.71 | 51.79 | 39.71 | 50.28 | 0.36 | 5.68 | 27.68 | 11.24 | -0.69 | 24 |
| G36 | 46.14 | 43.82 | 43.70 | 26.67 | 40.08 | 5.03 | 5.28 | 42.19 | 17.50 | -0.84 | 28 |
| G37 | 53.95 | 52.94 | 49.97 | 12.25 | 42.28 | 1.87 | 7.37 | 77.29 | 28.84 | -1.83 | 41 |
| G38 | 57.20 | 46.25 | 44.94 | 36.24 | 46.16 | 19.14 | 21.42 | 36.64 | 25.73 | -0.92 | 29 |
| G39 | 56.14 | 49.93 | 49.39 | 37.61 | 48.27 | 11.06 | 12.02 | 33.00 | 18.70 | -0.80 | 26 |
| G40 | 61.24 | 57.11 | 46.22 | 22.40 | 46.74 | 6.75 | 24.54 | 63.42 | 31.57 | -1.82 | 40 |
| G41 | 41.73 | 40.56 | 37.15 | 29.88 | 37.33 | 2.80 | 10.98 | 28.40 | 14.06 | -0.56 | 16 |
| G42 | 55.13 | 49.79 | 49.73 | 41.57 | 49.05 | 9.68 | 9.78 | 24.60 | 14.69 | -0.58 | 18 |
| G43 | 52.06 | 35.24 | 34.09 | 33.12 | 38.63 | 32.31 | 34.52 | 36.39 | 34.40 | -0.83 | 28 |
| G44 | 56.84 | 54.84 | 51.98 | 34.32 | 49.49 | 3.51 | 8.55 | 39.62 | 17.22 | -1.01 | 31 |
| G45 | 63.35 | 56.43 | 54.61 | 39.73 | 53.53 | 10.92 | 13.79 | 37.28 | 20.66 | -1.04 | 32 |
| G46 | 54.55 | 54.69 | 48.17 | 40.68 | 49.52 | -0.26 | 11.70 | 25.42 | 12.29 | -0.69 | 24 |
| G47 | 58.84 | 51.75 | 51.24 | 20.67 | 45.63 | 12.06 | 12.92 | 64.88 | 29.95 | -1.64 | 39 |
| G48 | 55.62 | 54.69 | 52.93 | 41.86 | 51.27 | 1.67 | 4.82 | 24.74 | 10.41 | -0.61 | 21 |
| G49 | 48.55 | 45.68 | 45.47 | 19.88 | 39.90 | 5.92 | 6.36 | 59.05 | 23.78 | -1.23 | 36 |
| G50 | 58.24 | 56.77 | 56.21 | 51.94 | 55.79 | 2.52 | 3.50 | 10.83 | 5.62 | -0.28 | 3 |
| Mean (T) | 50.86 | 47.46 | 44.74 | 34.65 | | | | | | | |

peroxidation which decreased stability of cell membrane and led to lose more water from cells (Abdalla and Khoshiban, 2007; Sanchez-Blanco *et al*., 2006 and Sairam and Saxena, 2000). The plasma membrane is generally protected from desiccation-induced damage by presence of membrane compatible solutes, such as sugars and amino acid. Therefore, a link may exist between the capacity for osmotic adjustment and degree of membrane protection (Sibet and Birol, 2007).

#### 4.2.1.9 Proline content (µg/g)

Genotype, treatment and their interaction significantly affected the proline content. The highest mean proline content (21.9 µg/g) was observed in T4 drought stress whereas the lowest proline content (7.1 µg/g)) was observed in T1 drought stress (Table 34). Among the genotypes, highest proline content (20.8 µg/g) was observed in G35 followed by G36 and G43 (19.6 µg/g) whereas lowest (5.3 µg/g) in G33. Based on the genotype stress interaction, highest proline content (36.3 µg/g) was observed in G35 under T4 and lowest (1.7 µg/g) in G18 under T1 stress. On the basis of b values, the best performance (highest b value) was observed in genotype G31 (1.20) followed by G27 (1.19) whereas lowest in G24 (-0.22). With the increase of drought stress, proline content was increased as shown in linear regression in Figure 46. The minimum reduction% (-1289%) was observed in G18 under T4 drought stress (Figure 47, Table 34). Maximum reduction% (40.5%) was observed in G24 under T4 stress (Figure 47). The result showed the positive effect of drought stress on proline content in genotypic dependent manner. Some of the genotypes showed an increase in proline content at mild and moderate drought stress. However, all the genotypes showed a decrease of proline content under the severe drought stress. Similar result has been observed in Eid *et al*. (2022). Proline accumulates in the cytosol and the vacuole during drought condition shelters cotton plant cells against shrinkage caused by $1O_2$ or $HO^-$ (McNeil *et al*., 2002; Matysik *et al*., 2002). Proline plays a vital role to protect proteins, DNA and membranes by quenching $^1O_2$ and directly scavenging $HO^-$ (Smirnoff and Cumbes, 1989).

#### 4.2.1.10 Pollen viability (%)

Genotype, treatment, and their interaction significantly affected the pollen viability. The highest mean pollen viability (98.81%) was observed T1 drought stress whereas the lowest pollen viability (80.51%) was observed in T4 drought stress (Table 35). Among the genotypes, highest pollen viability (95.47%) was observed in G14 whereas

## Table 34. Proline content (µg/g) of fifty genotypes at different drought treatments

| Genotype | Proline content at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 4.3 | 8.7 | 16.8 | 20.8 | 12.7 | -104.7 | -295.7 | -390.0 | -263.5 | 0.83 | 18 |
| G2 | 15.2 | 16.2 | 17.9 | 11.8 | 15.3 | -6.6 | -17.9 | 22.1 | -0.8 | -0.12 | 38 |
| G3 | 4.7 | 6.0 | 8.1 | 28.0 | 11.7 | -26.4 | -71.6 | -491.6 | -196.5 | 1.03 | 9 |
| G4 | 7.4 | 8.5 | 14.3 | 8.1 | 9.6 | -14.9 | -91.9 | -8.2 | -38.3 | 0.11 | 35 |
| G5 | 9.2 | 11.1 | 15.4 | 17.0 | 13.2 | -19.8 | -66.8 | -84.4 | -57.0 | 0.40 | 29 |
| G6 | 5.9 | 9.8 | 11.3 | 11.9 | 9.7 | -66.4 | -92.0 | -100.8 | -86.4 | 0.28 | 31 |
| G7 | 16.2 | 17.0 | 19.2 | 20.9 | 18.3 | -5.1 | -18.7 | -28.7 | -17.5 | 0.23 | 33 |
| G8 | 2.8 | 5.8 | 7.2 | 7.0 | 5.7 | -111.9 | -161.8 | -152.7 | -142.1 | 0.20 | 34 |
| G9 | 4.1 | 8.8 | 10.8 | 24.1 | 12.0 | -114.1 | -163.8 | -486.3 | -254.7 | 0.89 | 15 |
| G10 | 5.7 | 9.4 | 16.0 | 26.3 | 14.4 | -64.5 | -179.8 | -359.2 | -201.2 | 0.97 | 12 |
| G11 | 3.0 | 8.0 | 14.3 | 21.2 | 11.6 | -168.9 | -381.1 | -613.5 | -387.8 | 0.87 | 16 |
| G12 | 5.2 | 6.6 | 20.4 | 23.5 | 13.9 | -25.3 | -290.1 | -349.1 | -221.5 | 0.98 | 11 |
| G13 | 6.1 | 8.3 | 9.0 | 12.9 | 9.1 | -36.8 | -47.0 | -111.9 | -65.2 | 0.30 | 30 |
| G14 | 7.3 | 7.8 | 14.4 | 12.2 | 10.4 | -6.8 | -97.7 | -67.0 | -57.1 | 0.30 | 30 |
| G15 | 5.1 | 6.0 | 13.3 | 24.0 | 12.1 | -16.9 | -160.7 | -370.8 | -182.8 | 0.92 | 14 |
| G16 | 5.3 | 11.1 | 20.4 | 29.8 | 16.7 | -108.6 | -281.5 | -458.8 | -283.0 | 1.18 | 3 |
| G17 | 4.3 | 8.2 | 15.3 | 25.0 | 13.2 | -92.2 | -257.1 | -483.6 | -277.6 | 0.99 | 10 |
| G18 | 1.7 | 6.2 | 13.2 | 24.0 | 11.3 | -260.1 | -662.8 | -1289 | -737.4 | 1.06 | 8 |
| G19 | 8.0 | 13.1 | 26.9 | 16.6 | 16.1 | -65.1 | -237.4 | -107.9 | -136.8 | 0.56 | 28 |
| G20 | 6.1 | 8.5 | 13.2 | 19.6 | 11.9 | -39.0 | -115.6 | -220.1 | -124.9 | 0.65 | 24 |
| G21 | 12.3 | 9.5 | 11.7 | 20.9 | 13.6 | 22.8 | 5.5 | -69.8 | -13.8 | 0.40 | 29 |
| G22 | 12.1 | 12.6 | 18.7 | 27.2 | 17.6 | -4.8 | -54.9 | -125.5 | -61.7 | 0.74 | 21 |
| G23 | 3.4 | 12.8 | 20.6 | 23.3 | 15.0 | -280.0 | -512.3 | -593.3 | -461.8 | 0.97 | 12 |
| G24 | 13.3 | 13.5 | 14.3 | 7.9 | 12.2 | -1.5 | -7.6 | 40.5 | 10.4 | -0.22 | 39 |
| G25 | 6.3 | 8.4 | 11.1 | 32.4 | 14.6 | -32.8 | -76.1 | -412.2 | -173.7 | 1.16 | 4 |
| G26 | 5.1 | 9.4 | 14.4 | 29.9 | 14.7 | -85.1 | -183.2 | -486.8 | -251.7 | 1.13 | 6 |
| G27 | 4.2 | 6.8 | 14.4 | 29.5 | 13.7 | -63.4 | -244.1 | -606.6 | -304.7 | 1.19 | 2 |
| G28 | 8.6 | 13.6 | 24.5 | 29.0 | 18.9 | -58.0 | -184.4 | -236.8 | -159.7 | 1.03 | 9 |
| G29 | 2.3 | 8.9 | 21.3 | 25.0 | 14.4 | -278.1 | -809.7 | -967.1 | -685.0 | 1.15 | 5 |
| G30 | 2.5 | 5.5 | 9.3 | 18.0 | 8.8 | -121.3 | -274.3 | -628.3 | -341.3 | 0.72 | 22 |
| G31 | 2.9 | 6.7 | 11.3 | 29.4 | 12.5 | -133.5 | -293.8 | -929.1 | -452.1 | 1.20 | 1 |
| G32 | 11.6 | 13.7 | 15.5 | 30.2 | 17.8 | -17.5 | -33.4 | -160.0 | -70.3 | 0.82 | 19 |
| G33 | 6.0 | 6.3 | 4.9 | 3.8 | 5.3 | -4.9 | 19.1 | 36.5 | 16.9 | -0.11 | 37 |
| G34 | 15.3 | 15.9 | 16.3 | 17.3 | 16.2 | -3.5 | -6.4 | -12.9 | -7.6 | 0.09 | 36 |
| G35 | 10.5 | 15.1 | 21.2 | 36.3 | 20.8 | -44.0 | -102.3 | -245.5 | -130.6 | 1.19 | 2 |
| G36 | 11.7 | 14.5 | 19.2 | 33.1 | 19.6 | -24.1 | -63.8 | -183.0 | -90.3 | 0.98 | 11 |
| G37 | 2.9 | 8.6 | 9.7 | 25.4 | 11.6 | -196.4 | -235.2 | -777.9 | -403.2 | 0.98 | 11 |
| G38 | 10.6 | 18.6 | 21.3 | 27.5 | 19.5 | -76.5 | -101.4 | -160.6 | -112.8 | 0.76 | 20 |
| G39 | 8.9 | 15.4 | 18.6 | 13.5 | 14.1 | -73.6 | -109.7 | -52.1 | -78.5 | 0.24 | 32 |
| G40 | 6.0 | 8.7 | 19.0 | 16.3 | 12.5 | -43.8 | -215.0 | -170.5 | -143.1 | 0.59 | 26 |
| G41 | 7.4 | 12.5 | 21.2 | 20.6 | 15.4 | -68.9 | -187.4 | -179.3 | -145.2 | 0.69 | 23 |
| G42 | 12.9 | 9.7 | 15.5 | 24.2 | 15.5 | 24.8 | -20.5 | -87.9 | -27.9 | 0.57 | 27 |
| G43 | 13.7 | 17.5 | 21.3 | 25.7 | 19.6 | -27.8 | -55.3 | -87.4 | -56.8 | 0.57 | 27 |
| G44 | 3.9 | 8.5 | 13.9 | 19.5 | 11.4 | -115.4 | -254.2 | -396.2 | -255.3 | 0.74 | 21 |
| G45 | 5.8 | 13.3 | 21.5 | 30.2 | 17.7 | -127.3 | -267.3 | -415.7 | -270.1 | 1.16 | 4 |
| G46 | 7.5 | 9.8 | 14.8 | 20.6 | 13.2 | -30.5 | -98.0 | -174.8 | -101.1 | 0.63 | 25 |
| G47 | 3.2 | 7.5 | 15.5 | 18.3 | 11.1 | -133.3 | -385.6 | -472.3 | -330.4 | 0.76 | 20 |
| G48 | 6.5 | 9.2 | 16.2 | 30.1 | 15.5 | -42.0 | -150.4 | -365.5 | -185.9 | 1.11 | 7 |
| G49 | 2.1 | 13.0 | 15.2 | 23.4 | 13.4 | -521.8 | -624.2 | -1017 | -721.3 | 0.95 | 13 |
| G50 | 6.6 | 13.5 | 21.5 | 24.1 | 16.5 | -104.0 | -224.6 | -263.0 | -197.2 | 0.86 | 17 |
| Mean (T) | 7.1 | 10.5 | 15.8 | 21.9 | | | | | | | |

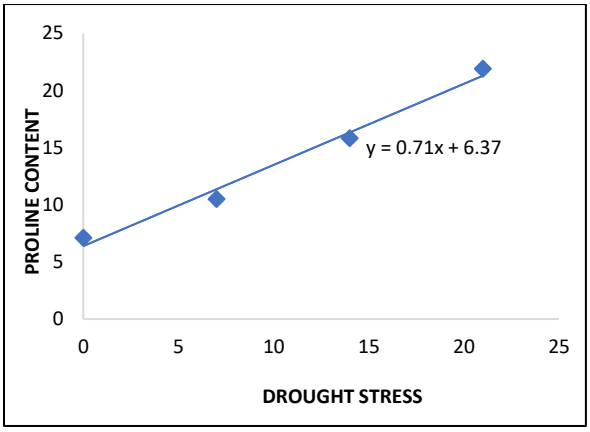



**Figure 46. Relationship between the proline content of different cotton genotypes and four drought stresses (0, 7, 14, 21 days interval)**

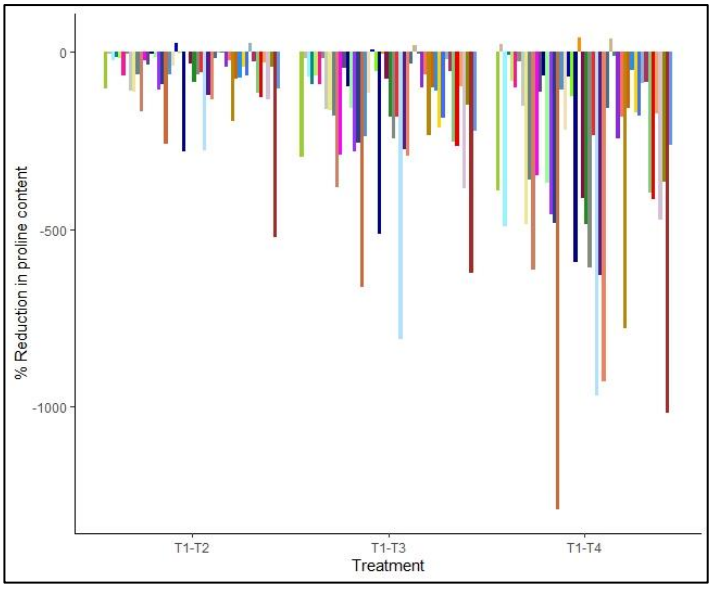
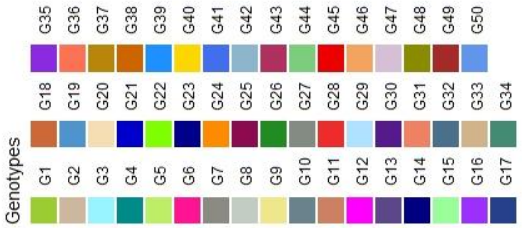



**Figure 47. Reduction percentage of proline content of fifty cotton genotypes under different drought stresses compared with control**



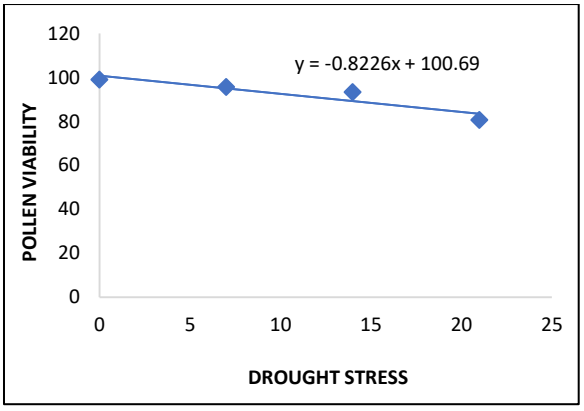




**Figure 48. Relationship between the pollen viability of cotton genotypes and four drought stresses (0, 7, 14, 21 days interval)**

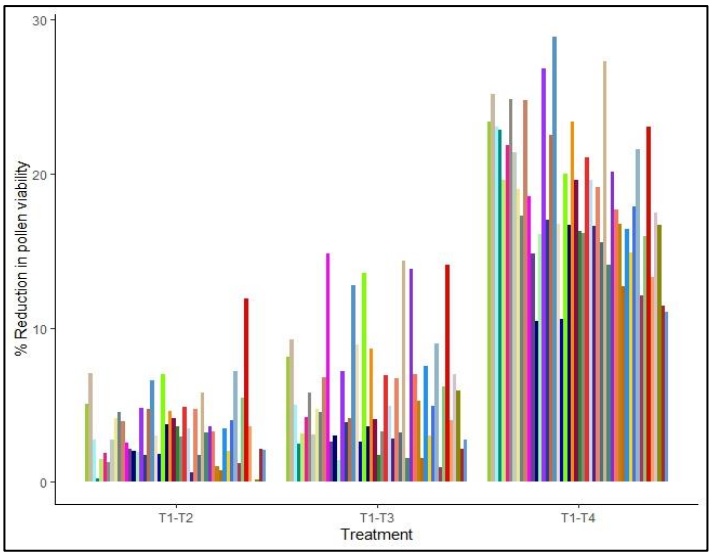



**Figure 49. Reduction percentage of pollen viability of fifty cotton genotypes under different drought stresses compared with control**

## Table 35. Pollen viability (%) of fifty genotypes at different drought treatments

| Genotype | Pollen viability at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 98.87 | 93.87 | 90.86 | 75.76 | 89.84 | 5.05 | 8.10 | 23.38 | 12.18 | -1.03 | 32 |
| G2 | 99.23 | 92.24 | 90.04 | 74.28 | 88.95 | 7.05 | 9.26 | 25.14 | 13.82 | -1.10 | 35 |
| G3 | 99.45 | 96.71 | 94.51 | 76.56 | 91.81 | 2.76 | 4.96 | 23.02 | 10.25 | -1.01 | 31 |
| G4 | 97.47 | 97.29 | 95.08 | 75.17 | 91.25 | 0.19 | 2.46 | 22.88 | 8.51 | -0.99 | 30 |
| G5 | 98.93 | 97.48 | 95.84 | 79.54 | 92.95 | 1.46 | 3.12 | 19.59 | 8.06 | -0.85 | 23 |
| G6 | 98.35 | 96.54 | 94.20 | 76.89 | 91.49 | 1.84 | 4.22 | 21.82 | 9.29 | -0.95 | 28 |
| G7 | 98.31 | 97.06 | 92.60 | 73.90 | 90.47 | 1.27 | 5.80 | 24.83 | 10.63 | -1.11 | 36 |
| G8 | 98.94 | 96.27 | 95.93 | 77.80 | 92.24 | 2.70 | 3.04 | 21.36 | 9.03 | -0.91 | 25 |
| G9 | 99.01 | 94.96 | 94.35 | 80.22 | 92.13 | 4.10 | 4.71 | 18.98 | 9.26 | -0.81 | 20 |
| G10 | 98.57 | 94.11 | 94.14 | 81.52 | 92.09 | 4.52 | 4.49 | 17.30 | 8.77 | -0.73 | 14 |
| G11 | 98.55 | 94.66 | 91.90 | 74.11 | 89.81 | 3.95 | 6.75 | 24.80 | 11.83 | -1.09 | 34 |
| G12 | 99.35 | 96.81 | 84.61 | 80.94 | 90.43 | 2.55 | 14.84 | 18.53 | 11.97 | -0.96 | 29 |
| G13 | 99.34 | 97.22 | 96.73 | 84.61 | 94.47 | 2.13 | 2.62 | 14.82 | 6.53 | -0.64 | 7 |
| G14 | 99.30 | 97.30 | 96.34 | 88.93 | 95.47 | 2.01 | 2.98 | 10.45 | 5.15 | -0.46 | 1 |
| G15 | 97.64 | 95.78 | 96.29 | 81.95 | 92.91 | 1.91 | 1.38 | 16.07 | 6.45 | -0.67 | 10 |
| G16 | 98.51 | 93.79 | 91.44 | 72.06 | 88.95 | 4.79 | 7.18 | 26.85 | 12.94 | -1.17 | 37 |
| G17 | 98.68 | 96.94 | 94.88 | 81.87 | 93.09 | 1.76 | 3.85 | 17.03 | 7.55 | -0.75 | 15 |
| G18 | 98.32 | 93.70 | 94.29 | 76.18 | 90.62 | 4.70 | 4.10 | 22.52 | 10.44 | -0.94 | 27 |
| G19 | 99.38 | 92.82 | 86.73 | 70.64 | 87.39 | 6.60 | 12.73 | 28.92 | 16.08 | -1.32 | 39 |
| G20 | 99.26 | 96.30 | 90.43 | 82.64 | 92.16 | 2.99 | 8.90 | 16.75 | 9.54 | -0.80 | 19 |
| G21 | 98.90 | 97.09 | 96.35 | 88.43 | 95.19 | 1.83 | 2.58 | 10.58 | 5.00 | -0.46 | 1 |
| G22 | 99.38 | 92.46 | 85.90 | 79.53 | 89.32 | 6.97 | 13.57 | 19.98 | 13.50 | -0.94 | 27 |
| G23 | 99.49 | 95.81 | 95.92 | 82.91 | 93.53 | 3.70 | 3.58 | 16.67 | 7.99 | -0.71 | 13 |
| G24 | 99.37 | 94.82 | 90.81 | 76.14 | 90.29 | 4.58 | 8.61 | 23.38 | 12.19 | -1.05 | 33 |
| G25 | 98.57 | 94.47 | 94.58 | 79.28 | 91.73 | 4.16 | 4.04 | 19.57 | 9.26 | -0.83 | 21 |
| G26 | 98.64 | 95.12 | 96.90 | 82.58 | 93.31 | 3.57 | 1.76 | 16.28 | 7.20 | -0.66 | 9 |
| G27 | 99.35 | 96.43 | 96.08 | 83.33 | 93.80 | 2.94 | 3.29 | 16.12 | 7.45 | -0.69 | 12 |
| G28 | 99.27 | 94.44 | 92.39 | 78.40 | 91.12 | 4.87 | 6.93 | 21.02 | 10.94 | -0.92 | 26 |
| G29 | 99.27 | 95.87 | 94.41 | 79.80 | 92.34 | 3.43 | 4.89 | 19.61 | 9.31 | -0.86 | 24 |
| G30 | 98.58 | 98.01 | 95.85 | 82.23 | 93.67 | 0.58 | 2.77 | 16.58 | 6.65 | -0.73 | 14 |
| G31 | 99.31 | 94.59 | 92.61 | 80.31 | 91.71 | 4.75 | 6.74 | 19.14 | 10.21 | -0.84 | 22 |
| G32 | 99.21 | 97.48 | 96.03 | 83.76 | 94.12 | 1.74 | 3.20 | 15.57 | 6.84 | -0.68 | 11 |
| G33 | 99.30 | 93.55 | 85.03 | 72.18 | 87.51 | 5.79 | 14.37 | 27.31 | 15.82 | -1.28 | 38 |
| G34 | 98.39 | 95.22 | 96.90 | 84.52 | 93.76 | 3.23 | 1.52 | 14.10 | 6.28 | -0.57 | 6 |
| G35 | 98.48 | 94.92 | 84.90 | 78.69 | 89.25 | 3.62 | 13.80 | 20.10 | 12.50 | -0.99 | 30 |
| G36 | 99.38 | 96.12 | 92.43 | 81.80 | 92.43 | 3.28 | 7.00 | 17.69 | 9.32 | -0.81 | 20 |
| G37 | 98.91 | 97.92 | 93.72 | 82.38 | 93.23 | 1.00 | 5.25 | 16.71 | 7.65 | -0.77 | 17 |
| G38 | 98.62 | 97.90 | 97.11 | 86.14 | 94.94 | 0.74 | 1.53 | 12.66 | 4.98 | -0.55 | 5 |
| G39 | 99.16 | 95.71 | 91.72 | 82.87 | 92.37 | 3.49 | 7.51 | 16.43 | 9.14 | -0.76 | 16 |
| G40 | 99.19 | 97.19 | 96.20 | 84.43 | 94.25 | 2.02 | 3.01 | 14.89 | 6.64 | -0.65 | 8 |
| G41 | 98.56 | 94.61 | 93.73 | 80.96 | 91.97 | 4.00 | 4.89 | 17.86 | 8.92 | -0.77 | 17 |
| G42 | 99.32 | 92.18 | 90.43 | 77.87 | 89.95 | 7.19 | 8.95 | 21.59 | 12.58 | -0.94 | 27 |
| G43 | 98.30 | 97.14 | 97.36 | 86.40 | 94.80 | 1.17 | 0.95 | 12.10 | 4.74 | -0.51 | 4 |
| G44 | 99.44 | 94.05 | 93.31 | 83.61 | 92.60 | 5.42 | 6.17 | 15.92 | 9.17 | -0.69 | 12 |
| G45 | 99.19 | 87.40 | 85.20 | 76.31 | 87.03 | 11.88 | 14.10 | 23.06 | 16.35 | -1.01 | 31 |
| G46 | 99.39 | 95.85 | 95.45 | 86.16 | 94.21 | 3.56 | 3.97 | 13.32 | 6.95 | -0.57 | 6 |
| G47 | 98.43 | 98.43 | 91.54 | 81.23 | 92.41 | 0.00 | 7.00 | 17.48 | 8.16 | -0.84 | 22 |
| G48 | 97.94 | 97.82 | 92.18 | 81.61 | 92.39 | 0.12 | 5.88 | 16.68 | 7.56 | -0.78 | 18 |
| G49 | 99.21 | 97.09 | 97.08 | 87.87 | 95.31 | 2.13 | 2.15 | 11.43 | 5.24 | -0.49 | 3 |
| G50 | 99.29 | 97.26 | 96.61 | 88.35 | 95.38 | 2.04 | 2.70 | 11.01 | 5.25 | -0.48 | 2 |
| Mean (T) | 98.91 | 95.58 | 93.20 | 80.51 | | | | | | | |

lowest (87.03%) in G45. Based on the genotype stress interaction, highest pollen viability (99.49%) was observed in G23 under T1 whereas lowest (70.64%) in G19 under T4 stress. On the basis of b values, the best performance (highest b value) was observed in genotype G14 and G21 (-0.46) followed by G50 (-0.48) whereas lowest (-1.32) in G19. With the increase of drought stress, pollen viability was decreased as shown in linear regression in Figure 48. The minimum reduction% (0.00 %) was observed in G47 under T2 drought stress (Figure 49, Table 35). Maximum reduction% (28.92%) was observed in G19 under T4 stress (Figure 49). The result showed the negative effect of drought stress on pollen viability in genotypic dependent manner. Similar result has been observed in (SamiUl-Allah *et al.*, 2021; Zhang *et al*., 2020; Hu *et al*., 2020a; Hu *et al*., 2020b; Wang *et al*., 2016a). WeiHu *et al.* (2020) reported that drought reduced the deposition of starch, the hydrolysis of sucrose into hexoses, the generation of adenosine triphosphate (ATP) in anthers, restricting pollen viability, inhibited male fertility and germination of cotton.

### 4.2.2 Drought Response Index (DRI)

Drought Response Index (DRI) was calculated from the observed phenotypic value of each character. DRI value represents the relative change for each of the character caused by drought treatment. The DRI value was considered as the indicator from drought tolerance. Comparing the DRI value, we have received important information about the drought tolerance in different genotypes of cotton. Finding from this study will provide theoretical bases and practical guidance for distinguishing drought tolerant germplasm resources and breeding for drought tolerant cultivar.

Fifty cotton genotypes showed a wider range of drought tolerance index (Table 36). DRI value for soil moisture content showed a wide range having maximum DRI (72.2) and minimum (40.4) in G41 and G50 respectively. The genotypes G5 and G35 showed the minimum (71.2) and maximum (100.3) DRI value for relative water content. G35 and G5 showed the minimum (98.1) and maximum (934.0) DRI value for water saturation deficit. In case of water retention capacity, the minimum (38.0) and maximum (174.4) DRI value was observed in G6 and G5 respectively. The genotypes G19 and G5 showed the minimum (73.0) and maximum (2338.9) DRI value for water uptake capacity. Minimum (87.3) and maximum (166.3) DRI value for

## Table 36. Drought Response Index (DRI) values of fifty cotton genotypes for ten physiological characters

| Genotypes | Soil moisture content | Relative water content | Water saturation deficit | Water retention capacity | Water uptake capacity | Total chlorophyll content | Nitrogen content | Membrane stability index | Proline content | Pollen viability | Grouping |
|---|---|---|---|---|---|---|---|---|---|---|---|
| G1 | 65.0 | 86.7 | 204.0 | 118.2 | 251.1 | 149.7 | 142.1 | 70.7 | 363.5 | 87.8 | T |
| G2 | 69.9 | 77.6 | 333.7 | 84.7 | 221.1 | 87.3 | 88.5 | 89.0 | 100.8 | 86.2 | T |
| G3 | 56.9 | 96.2 | 191.9 | 65.0 | 118.2 | 161.0 | 151.3 | 93.7 | 296.5 | 89.8 | T |
| G4 | 61.6 | 83.9 | 348.8 | 74.4 | 224.5 | 125.1 | 121.2 | 82.2 | 138.3 | 91.5 | T |
| G5 | 64.5 | 71.2 | 934.0 | 174.4 | 2338.9 | 150.4 | 143.3 | 89.1 | 157.0 | 91.9 | T |
| G6 | 57.7 | 85.5 | 318.0 | 38.0 | 98.1 | 130.0 | 125.9 | 82.5 | 186.4 | 90.7 | T |
| G7 | 59.0 | 85.2 | 320.9 | 65.1 | 184.1 | 135.8 | 131.2 | 91.9 | 117.5 | 89.4 | T |
| G8 | 64.3 | 85.0 | 372.7 | 110.3 | 412.4 | 166.0 | 155.4 | 89.5 | 242.1 | 91.0 | T |
| G9 | 58.0 | 82.5 | 318.0 | 89.5 | 259.5 | 93.5 | 94.2 | 92.3 | 354.7 | 90.7 | T |
| G10 | 71.6 | 91.6 | 173.9 | 104.8 | 170.7 | 160.3 | 150.6 | 82.2 | 301.2 | 91.2 | T |
| G11 | 62.8 | 88.3 | 325.1 | 77.5 | 215.7 | 92.8 | 93.6 | 64.7 | 487.8 | 88.2 | T |
| G12 | 69.1 | 92.3 | 197.1 | 97.2 | 180.5 | 108.8 | 107.7 | 87.8 | 321.5 | 88.0 | T |
| G13 | 69.3 | 96.1 | 154.0 | 130.0 | 227.2 | 152.1 | 143.9 | 88.3 | 165.2 | 93.5 | T |
| G14 | 50.9 | 93.7 | 136.9 | 133.4 | 194.3 | 121.3 | 118.8 | 88.1 | 157.1 | 94.9 | T |
| G15 | 59.2 | 84.2 | 257.2 | 85.4 | 176.4 | 143.5 | 136.8 | 87.9 | 282.8 | 93.5 | T |
| G16 | 59.0 | 73.0 | 408.4 | 79.1 | 294.2 | 151.9 | 144.1 | 85.3 | 383.0 | 87.1 | T |
| G17 | 61.9 | 87.1 | 350.3 | 101.2 | 342.3 | 121.8 | 119.1 | 83.9 | 377.6 | 92.4 | T |
| G18 | 56.1 | 90.4 | 228.2 | 136.2 | 413.7 | 101.6 | 101.4 | 79.5 | 837.4 | 89.6 | T |
| G19 | 58.2 | 92.7 | 156.7 | 57.8 | 73.0 | 114.6 | 112.7 | 91.5 | 236.8 | 83.9 | T |
| G20 | 57.2 | 88.7 | 357.4 | 64.7 | 174.0 | 141.1 | 135.4 | 83.6 | 224.9 | 90.5 | T |
| G21 | 59.3 | 96.4 | 141.9 | 73.3 | 101.1 | 122.0 | 119.3 | 89.8 | 113.8 | 95.0 | T |
| G22 | 54.9 | 95.0 | 139.0 | 76.6 | 89.1 | 90.9 | 91.9 | 88.7 | 161.7 | 86.5 | T |
| G23 | 60.6 | 90.1 | 214.2 | 84.1 | 160.1 | 113.9 | 112.2 | 90.6 | 561.8 | 92.0 | T |
| G24 | 61.0 | 98.6 | 110.8 | 111.6 | 112.4 | 133.3 | 128.9 | 87.0 | 89.6 | 87.8 | T |
| G25 | 46.7 | 74.7 | 278.7 | 93.1 | 240.1 | 143.5 | 137.4 | 80.1 | 273.7 | 90.7 | T |
| G26 | 61.0 | 81.0 | 310.8 | 48.7 | 119.0 | 143.9 | 137.2 | 84.0 | 351.7 | 92.8 | T |
| G27 | 53.6 | 94.9 | 116.6 | 109.5 | 122.5 | 144.1 | 138.0 | 91.2 | 404.7 | 92.6 | T |
| G28 | 51.4 | 85.0 | 268.9 | 95.9 | 216.1 | 123.7 | 120.8 | 88.7 | 259.7 | 89.1 | T |
| G29 | 52.1 | 85.2 | 232.7 | 74.2 | 148.0 | 113.1 | 111.4 | 84.3 | 785.0 | 90.7 | T |
| G30 | 52.7 | 88.2 | 198.4 | 107.6 | 218.1 | 122.2 | 119.3 | 82.9 | 441.3 | 93.4 | T |
| G31 | 62.3 | 89.0 | 159.5 | 81.3 | 115.9 | 136.6 | 131.7 | 87.4 | 552.1 | 89.8 | T |
| G32 | 60.6 | 98.3 | 105.4 | 80.2 | 75.1 | 145.6 | 139.0 | 64.1 | 170.3 | 93.2 | T |
| G33 | 55.2 | 83.5 | 216.0 | 110.0 | 207.7 | 131.7 | 126.9 | 73.6 | 83.1 | 84.2 | T |
| G34 | 55.1 | 93.7 | 136.2 | 82.0 | 99.9 | 135.7 | 130.4 | 87.8 | 107.6 | 93.7 | T |
| G35 | 57.1 | 100.3 | 98.1 | 123.0 | 125.5 | 109.3 | 108.3 | 88.8 | 230.6 | 87.5 | T |
| G36 | 65.1 | 87.4 | 164.9 | 95.3 | 149.2 | 112.3 | 110.7 | 82.5 | 190.3 | 90.7 | T |
| G37 | 56.8 | 71.6 | 330.1 | 93.9 | 243.4 | 118.0 | 115.8 | 71.2 | 503.2 | 92.3 | T |
| G38 | 64.6 | 79.3 | 279.7 | 69.5 | 139.8 | 137.4 | 132.4 | 74.3 | 212.8 | 95.0 | T |
| G39 | 64.4 | 87.6 | 193.8 | 98.1 | 189.9 | 151.9 | 144.3 | 81.3 | 178.5 | 90.9 | T |
| G40 | 65.2 | 90.1 | 147.9 | 79.7 | 108.2 | 152.6 | 143.9 | 68.4 | 243.1 | 93.4 | T |
| G41 | 72.2 | 92.6 | 202.5 | 86.1 | 142.7 | 122.3 | 119.4 | 85.9 | 245.2 | 91.1 | T |
| G42 | 54.5 | 86.6 | 197.0 | 66.5 | 111.9 | 150.1 | 142.7 | 85.3 | 127.9 | 87.4 | T |
| G43 | 52.4 | 96.1 | 124.2 | 92.6 | 112.0 | 125.8 | 122.5 | 65.6 | 156.8 | 95.3 | T |
| G44 | 60.2 | 85.8 | 269.4 | 93.3 | 230.4 | 120.4 | 117.9 | 82.8 | 355.3 | 90.8 | T |
| G45 | 59.3 | 92.2 | 183.8 | 66.2 | 107.6 | 107.5 | 106.6 | 79.3 | 370.1 | 83.6 | T |
| G46 | 62.1 | 89.2 | 225.7 | 65.6 | 136.2 | 150.3 | 143.2 | 87.7 | 201.1 | 93.1 | T |
| G47 | 63.3 | 90.5 | 213.3 | 75.5 | 151.4 | 142.2 | 136.3 | 70.0 | 430.4 | 91.8 | T |
| G48 | 69.9 | 97.1 | 119.3 | 86.1 | 91.4 | 114.3 | 112.4 | 89.6 | 285.9 | 92.4 | T |
| G49 | 46.8 | 89.1 | 181.5 | 70.3 | 110.0 | 128.6 | 125.2 | 76.2 | 821.3 | 94.8 | T |
| G50 | 40.4 | 81.9 | 256.4 | 62.3 | 132.5 | 166.3 | 155.9 | 94.4 | 297.2 | 94.8 | T |

**Table 37. Grouping of 50 genotypes based on DRI values under drought stress**

| Sl No. | Scale | % DRI values | Drought tolerant group | Name of genotypes |
|---|---|---|---|---|
| **1** | I | >90 | Tolerant (T) | G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G24, G25, G26, G27, G28, G29, G30, G31, G32, G33, G34, G35, G36, G37, G38, G39, G40, G41, G42, G43, G44, G45, G46, G47, G48, G49, G50. |
| **2** | II | 80-90 | Moderately tolerant (MT) | - |
| **3** | III | 70-80 | Moderately susceptible (MS) | - |
| **4** | IV | <70 | Susceptible (S) | - |

total chlorophyll content were observed in G2 and G50 respectively. In case of nitrogen concentration, minimum (88.5) and maximum (155.9) DRI value in G2 and G50, respectively. DRI value for membrane stability index showed wider range having minimum DRI (64.1) and maximum (94.4) in G32 and G50 respectively. In case of proline content, minimum (83.1) and maximum (837.4) DRI were observed in G33 and G18, respectively. The genotypes G45 and G43 showed the minimum (83.6) and maximum (95.3) DRI value for pollen viability.

Based on the average DRI value of each genotype for ten physiological traits, genotypes were grouped into four groups such as drought tolerant, moderately tolerant, moderately susceptible and susceptible genotypes (Table 37). All of the 50 genotypes showed drought tolerant based on the average DRI values.

### 4.2.3 Genetic variability analysis

The extent of variation among the genotypes in respect of ten characters was studied and mean sum of square, phenotypic variance ($\sigma^2p$), genotypic variance ($\sigma^2g$), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ($h^2b$), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) presented in Table 38.

#### 4.2.3.1 Soil moisture content

Minimum and Maximum value of soil moisture content were 18.55% and 25.73%, respectively which showed the presence of variation in soil moisture content among the genotypes (Table 38). The genotypic and phenotypic variance for this trait was 2.15 and 2.23, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (6.49 and 6.36 respectively). PCV was higher than the GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this

trait were very high (96%) with low genetic advance (2.96) and genetic advance in mean (12.85%). The high heritability coupled with lower genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding.

#### 4.2.3.2 Relative water content

Minimum and Maximum value of relative water content were 67.51% and 93.92%, respectively which showed the presence of variation in relative water content among the genotypes (Table 38). The genotypic and phenotypic variance for this trait was 25.56 and 27.85, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (6.46 and 6.19, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (92%) with low genetic advance (9.98) and genetic advance in mean (12.21%). The high heritability coupled with lower genetic advance indicated the non-additive gene action. The high heritability is due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low genetic advance for relative water content in cotton was also observed in Riaz *et al*. (2012) where they carried out the drought stress experiment.

#### 4.2.3.3 Water saturation deficit

Minimum and Maximum value of water saturation deficit were 6.08% and 32.49%, respectively which showed the presence of variation in water saturation deficit among the genotypes (Table 38). The genotypic and phenotypic variance for this trait was 25.56 and 27.85, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the

**Table 38. Estimation of genetic parameters of ten characters of fifty genotypes in cotton**

| Genetic parameters | Soil Moisture content | Relative water content | Water saturation deficit | Water retention capacity | Water uptake capacity | Total chlorophyll content | Nitrogen content | Membrane stability index | Proline content | Pollen viability |
|---|---|---|---|---|---|---|---|---|---|---|
| **Minimum** | 18.55 | 67.51 | 6.08 | 2.87 | 0.24 | 1.25 | 1.24 | 29.70 | 5.22 | 86.90 |
| **Maximum** | 25.73 | 93.92 | 32.49 | 6.04 | 1.19 | 1.84 | 1.75 | 56.28 | 20.87 | 95.56 |
| **GM** | 23.02 | 81.72 | 18.28 | 4.15 | 0.52 | 1.57 | 1.52 | 44.43 | 13.83 | 92.05 |
| **σ2e** | 0.09 | 2.28 | 2.28 | 0.02 | 0.00 | 0.00 | 0.00 | 0.09 | 0.13 | 0.07 |
| **σ2g** | 2.15 | 25.56 | 25.56 | 0.41 | 0.02 | 0.01 | 0.01 | 40.04 | 11.48 | 4.57 |
| **σ2p** | 2.23 | 27.85 | 27.85 | 0.44 | 0.03 | 0.01 | 0.01 | 40.13 | 11.61 | 4.64 |
| **ECV** | 1.28 | 1.85 | 8.27 | 3.65 | 11.38 | 3.03 | 2.69 | 0.68 | 2.60 | 0.29 |
| **GCV** | 6.36 | 6.19 | 27.66 | 15.51 | 28.64 | 6.45 | 5.71 | 14.24 | 24.50 | 2.32 |
| **PCV** | 6.49 | 6.46 | 28.87 | 15.94 | 30.85 | 7.14 | 6.32 | 14.26 | 24.64 | 2.34 |
| **Heritability** | 0.96 | 0.92 | 0.92 | 0.95 | 0.86 | 0.82 | 0.82 | 1.00 | 0.99 | 0.98 |
| **GA (5%)** | 2.96 | 9.98 | 9.98 | 1.29 | 0.29 | 0.19 | 0.16 | 13.02 | 6.94 | 4.37 |
| **GA (% mean)** | 12.85 | 12.21 | 54.60 | 31.11 | 54.78 | 12.00 | 10.62 | 29.31 | 50.19 | 4.75 |
| **SEM** | 0.17 | 0.87 | 0.87 | 0.09 | 0.03 | 0.03 | 0.02 | 0.17 | 0.21 | 0.16 |
| **CD 5%** | 0.48 | 2.45 | 2.45 | 0.25 | 0.10 | 0.08 | 0.07 | 0.49 | 0.58 | 0.44 |
| **CD1%** | 0.63 | 3.24 | 3.24 | 0.32 | 0.13 | 0.10 | 0.09 | 0.64 | 0.77 | 0.58 |

Here, GM= Grand mean; $\sigma^2$g= Genotypic variance; σ2e= environmental variance; σ2p= phenotypic variance; GCV= genotypic coefficient of variation; ECV=Environmental coefficient of variation, PCV= Phenotypic coefficient of variation, GA= genetic advance; SEM=Standard error of mean, CD= Critical differences.

expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high (28.87 and 27.66, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (92%) with low genetic advance (9.98) and genetic advance in mean (54.60%). The high heritability coupled with lower genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low genetic advance for water saturation deficit in cotton was also observed in Riaz *et al*. (2012) where they carried out the drought stress experiment.

#### 4.2.3.4 Water retention capacity

Minimum and Maximum value of water retention capacity were 2.87 and 6.04, respectively which showed the presence of variation in water retention capacity among the genotypes (Table 38). The genotypic and phenotypic variance for this trait was 0.41 and 0.44, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were medium (15.94 and 15.51, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimated for this trait were very high (95%) with low genetic advance (1.29) and genetic advance in mean (31.11%). The high heritability coupled with lower genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and

selection based on this trait will not be rewarding. High heritability for water retention capacity in cotton was also observed in Riaz *et al*. (2012) where they carried out the drought stress experiment. The high heritability does not necessarily, means that the character would show high genetic gain but such associations accrued, the additive gene effects were most important (Sardana *et al*., 2007).

#### 4.2.3.5 Water uptake capacity

Minimum and Maximum value of water uptake capacity were 0.24 and 1.19, respectively which showed the presence of variation in water uptake capacity among the genotypes (Table 38). The genotypic and phenotypic variance for this trait was 0.02 and 0.03, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high (30.85 and 28.64, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (86%) with low genetic advance (0.29) and genetic advance in mean (54.78%). The high heritability coupled with lower genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low genetic advance for water uptake capacity in cotton was also observed in Riaz *et al*. (2012). The high heritability does not necessarily, means that the character would show high genetic gain but such associations accrued, the additive gene effects were most important (Sardana *et al*., 2007).

#### 4.2.3.6 Total chlorophyll content

Minimum and Maximum value of total chlorophyll content were 1.25 mg/g and 1.84 mg/g, respectively which showed the presence of variation in total chlorophyll content among the genotypes (Table 38). The genotypic and phenotypic variance for this trait

was 0.01 and 0.01, respectively. The phenotypic variance appeared to be equaled compared to the genotypic variance suggested not the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (7.14 and 6.45 respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (82%) with low genetic advance (0.19) and genetic advance in mean (12.0%). The high heritability coupled with lower genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability for total chlorophyll content in cotton was also observed in Baloch *et al*. (2015) and Rathinavel *et al*. (2017). High estimates of heritability revealed that successful and effective selection can be helpful in the improvement of this trait.

#### 4.2.3.7 Nitrogen concentration

Minimum and Maximum value of nitrogen concentration were 1.24% and 1.75%, respectively which showed the presence of variation in nitrogen concentration among the genotypes (Table 38). The genotypic and phenotypic variance for this trait was 0.01 and 0.01, respectively. The phenotypic variance appeared to be equaled compared to the genotypic variance suggested not the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (6.32 and 5.71, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (82%) with low genetic advance (0.16) and genetic advance

in mean (10.62%). The high heritability coupled with lower genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability for nitrogen content in cotton was also observed in Baloch *et al*. (2015) and Rathinavel *et al*. (2017). High estimates of heritability revealed that successful and effective selection can be helpful in the improvement of this trait.

### .4.2.3.8 Membrane stability index

Minimum and Maximum value of membrane stability index were 29.70 and 56.28, respectively which showed the presence of variation in membrane stability index among the genotypes (Table 38). The genotypic and phenotypic variance for this trait was 40.04 and 40.13, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were medium (14.26 and 14.24, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (100%) with medium genetic advance (13.02) and genetic advance in mean (29.31%). The high heritability coupled with medium genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability for membrane stability index in cotton was also observed in Baloch *et al*. (2015). High estimates of heritability revealed that successful and effective selection can be helpful in the improvement of this trait.

### 4.2.3.9 Proline content

Minimum and Maximum value of proline content were 5.22 µg/g and 20.87 µg/g, respectively which showed the presence of variation in proline content among the

genotypes (Table 38). The genotypic and phenotypic variance for this trait was 11.48 and 11.61, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high (24.64 and 24.50, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (99%) with low genetic advance (6.94) and genetic advance in mean (50.19%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability for membrane stability index in cotton was also observed in Eid *et al*. (2022). High estimates of heritability revealed that successful and effective selection can be helpful in the improvement of this trait.

#### 4.2.3.10 Pollen viability

Minimum and Maximum value of pollen viability were 86.90% and 95.56%, respectively which showed the presence of variation in pollen viability among the genotypes (Table 38). The genotypic and phenotypic variance for this trait was 4.57 and 4.64, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (2.34 and 2.32, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (98%) with low genetic advance (4.37) and genetic advance in

mean (4.75%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability for pollen viability in cotton was also observed in Razzaq *et al*. (2019) and Burke and Ulloa (2017). High estimates of heritability revealed that successful and effective selection can be helpful in the improvement of this trait.

### 4.2.4 Correlation coefficient

Correlation studies along with path analysis provide a better understanding of the association of different characters with yield related traits. Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components as suggested by Sing and Chaudhary 1985. Genotypic and phenotypic correlation coefficients among the different pairs for different genotypes of cotton are given in Table 39 and Table 40 respectively. In case of genotypic correlation coefficient, soil moisture content showed non-significant correlation with relative water content (0.13), water saturation deficit (-0.13), water retention capacity (0.09), water uptake capacity (0.03), total chlorophyll content (-0.19), nitrogen concentration (-0.19), membrane stability index (-0.17), proline content (-0.05) and pollen viability (-0.07) (Table 39). Relative water content showed statistical positive significant correlation with water retention capacity (0.29), negative significant correlation with water saturation deficit (-1.0), water uptake capacity (-0.74) and non-significant correlation with total chlorophyll content (-0.16), nitrogen concentration (-0.16), membrane stability index (-0.13), proline content (-0.15) and pollen viability (-0.09). Water saturation deficit showed significant positive correlation with water uptake capacity (0.74), significant negative correlation with water retention capacity (-0.29) and non-significant relation with total chlorophyll content (0.16), nitrogen concentration (0.16), membrane stability index (0.13), proline content (0.15) and pollen viability (0.09). Water retention capacity showed significant positive correlation with water uptake capacity (0.30) and non-significant correlation with total chlorophyll content (-0.18), nitrogen concentration (-0.18), membrane stability index (-0.26), proline content (-0.05) and pollen viability (-0.27). Water uptake capacity showed non-significant correlation with total chlorophyll content (0.05), nitrogen concentration (0.05), membrane stability index (-0.08), proline

**Table 39. Genotypic correlation coefficient among different pairs of physiological characters of fifty genotypes of cotton**

| Characters | Soil Moisture content | Relative water content | Water saturation deficit | Water retention capacity | Water uptake capacity | Total chlorophyll content | Nitrogen content | Membrane stability index | Proline content | Pollen viability |
|---|---|---|---|---|---|---|---|---|---|---|
| **Soil moisture content** | | 0.13$^{NS}$ | -0.13$^{NS}$ | 0.09$^{NS}$ | 0.03$^{NS}$ | -0.19$^{NS}$ | -0.19$^{NS}$ | -0.17$^{NS}$ | -0.05$^{NS}$ | -0.07$^{NS}$ |
| **Relative water content** | | | -1$^{**}$ | 0.29$^{*}$ | -0.74$^{**}$ | -0.16$^{NS}$ | -0.16$^{NS}$ | -0.13$^{NS}$ | -0.15$^{NS}$ | -0.09$^{NS}$ |
| **Water saturation deficit** | | | | -0.29$^{*}$ | 0.74$^{**}$ | 0.16$^{NS}$ | 0.16$^{NS}$ | 0.13$^{NS}$ | 0.15$^{NS}$ | 0.09$^{NS}$ |
| **Water retention capacity** | | | | | 0.30$^{*}$ | -0.18$^{NS}$ | -0.18$^{NS}$ | -0.26$^{NS}$ | -0.05$^{NS}$ | -0.27$^{NS}$ |
| **Water uptake capacity** | | | | | | 0.05$^{NS}$ | 0.05$^{NS}$ | -0.08$^{NS}$ | 0.04$^{NS}$ | -0.06$^{NS}$ |
| **Total chlorophyll content** | | | | | | | 1$^{**}$ | 0.24$^{NS}$ | 0.26 $^{NS}$ | 0.28$^{*}$ |
| **Nitrogen content** | | | | | | | | 0.24$^{NS}$ | 0.26$^{NS}$ | 0.28$^{*}$ |
| **Membrane stability index** | | | | | | | | | 0.27$^{NS}$ | 0.18$^{NS}$ |
| **Proline content** | | | | | | | | | | -0.05$^{NS}$ |
| **Pollen viability** | | | | | | | | | | |

$^{*}$Significant at 5% level
$^{**}$Significant at 1% level
$^{NS}$ Non-significant

**Table 40. Phenotypic correlation coefficient among different pairs of physiological characters of fifty genotypes of cotton**

| Characters | Soil Moisture content | Relative water content | Water saturation deficit | Water retention capacity | Water uptake capacity | Total chlorophyll content | Nitrogen content | Membrane stability index | Proline content | Pollen viability |
|---|---|---|---|---|---|---|---|---|---|---|
| **Soil moisture content** | | $0.12^{NS}$ | $-0.12^{NS}$ | $0.09^{NS}$ | $0.03^{NS}$ | $-0.18^{*}$ | $-0.18^{*}$ | $-0.17^{*}$ | $-0.04^{NS}$ | $-0.06^{NS}$ |
| **Relative water content** | | | $-1^{**}$ | $0.29^{**}$ | $-0.73^{**}$ | $-0.14^{NS}$ | $-0.14^{NS}$ | $-0.13^{NS}$ | $-0.14^{NS}$ | $-0.08^{NS}$ |
| **Water saturation deficit** | | | | $-0.29^{**}$ | $0.73^{**}$ | $0.14^{NS}$ | $0.14^{NS}$ | $0.13^{NS}$ | $0.14^{NS}$ | $0.08^{NS}$ |
| **Water retention capacity** | | | | | $0.31^{**}$ | $-0.17^{*}$ | $-0.17^{*}$ | $-0.25^{**}$ | $-0.05^{NS}$ | $-0.26^{**}$ |
| **Water uptake capacity** | | | | | | $0.03^{NS}$ | $0.03^{NS}$ | $-0.06^{NS}$ | $0.04^{NS}$ | $-0.06^{NS}$ |
| **Total chlorophyll content** | | | | | | | $1^{**}$ | $0.22^{**}$ | $0.23^{**}$ | $0.25^{**}$ |
| **Nitrogen content** | | | | | | | | $0.22^{**}$ | $0.23^{**}$ | $0.25^{**}$ |
| **Membrane stability index** | | | | | | | | | $0.27^{**}$ | $0.18^{*}$ |
| **Proline content** | | | | | | | | | | $-0.05^{NS}$ |
| **Pollen viability** | | | | | | | | | | |

$^{*}$Significant at 5% level
$^{**}$Significant at 1% level
$^{NS}$ Non-significant

content (0.04) and pollen viability (-0.06). Total chlorophyll content showed significant positive correlation with nitrogen concentration (1.0), pollen viability (0.28) and non-significant correlation with membrane stability index (0.24), proline content (0.26). Nitrogen concentration showed significant positive correlation with pollen viability (0.28) and non-significant correlation with membrane stability index (0.24), proline content (0.26). Membrane stability index showed non-significant correlation with proline content (0.27) and pollen viability (0.18). Proline content showed non-significant correlation with pollen viability (-0.05). Kader *et. al*., (2015) found that yield was positively and significantly correlated with total chlorophyll, chlorophyll 'b', chlorophyll 'a', membrane stability index and relative water content and negatively and significantly correlated with electrolyte leakage. He also showed that vegetative branches per plant showed non-significant positive correlation with number of reproductive branches which have been observed in our experiment as well. Farooq *et al*. (2018) and Karademir *et al*. (2009) were mentioned significant positive association of leaf chlorophyll and yield with yield contributing traits.

In case of phenotypic correlation coefficient, soil moisture content showed negative significant correlation with total chlorophyll content (-0.18), nitrogen concentration (-0.18), membrane stability index (-0.17) and non-significant correlation with relative water content (0.12), water saturation deficit (-0.12), water retention capacity (0.09), water uptake capacity (0.03), proline content (-0.04) and pollen viability (-0.06) (Table 40). You may add discussion for root length here. Relative water content showed statistical positive significant correlation with water retention capacity (0.29), negative significant correlation with water saturation deficit (-1.0), water uptake capacity (-0.73) and non-significant correlation with total chlorophyll content (-0.14), Nitrogen concentration (-0.14), membrane stability index (-0.13), proline content (-0.14) and pollen viability (-0.08). Water saturation deficit showed significant positive correlation with water uptake capacity (0.73), significant negative correlation with water retention capacity (-0.29) and non-significant relation with total chlorophyll content (0.14), nitrogen concentration (0.14), membrane stability index (0.13), proline content (0.14) and pollen viability (0.08). Water retention capacity showed significant positive correlation with water uptake capacity (0.31), significant negative correlation with total chlorophyll content (-0.17), nitrogen concentration (-0.17), membrane stability index (-0.25), pollen viability (-0.26) and non-significant correlation with

proline content (-0.05). Water uptake capacity showed non-significant correlation with total chlorophyll content (0.03), nitrogen concentration (0.03), membrane stability index (-0.06), proline content (0.04) and pollen viability (-0.06). Total chlorophyll content showed significant positive correlation with nitrogen concentration (1.0), membrane stability index (0.22), proline content (0.23) and pollen viability (0.25). Nitrogen concentration showed significant positive correlation with membrane stability index (0.22), proline content (0.23) and pollen viability (0.25). Membrane stability index showed significant positive correlation with proline content (0.27) and pollen viability (0.18). Proline content showed non-significant correlation with pollen viability (-0.05). At the phenotypic level, similar result has been observed in Adeela *et al*. (2021) and Reddy *et al*. (2019) and Kumbhar *et al*. (2020). They reported a significantly positive association of plant height with sympodial branches. Salahuddin *et al*. (2010) found that at the phenotypic level, yield was positively associated with sympodial and bolls. Pujer *et al*. (2014), Joshi *et al*. (2006), Anandan (2009) indicated that sympodial branches/plant positively correlated with plant height and number of vegetative branches.

### 4.2.5 Path coefficient analysis

Path coefficient is a means of measuring the direct and indirect effects of one variable through the other variables on the end-product. Here pollen viability was considered as effect (dependent variable) and soil moisture content, relative water content, water saturation deficit, water retention capacity, water uptake capacity, total chlorophyll content, nitrogen concentration, membrane stability index and proline content were considered as independent variables. Wright (1921) developed the path coefficient analysis technique and later demonstrated by Deway and Lu (1959) facilitates the partitioning of correlation coefficients into direct and indirect contribution of various characters on pollen viability. It is standardized partial regression coefficient analysis. As such, it measures the direct influence if one variable upon other. Estimation of direct and indirect effect of path coefficient analysis is presented in Table 41 and Table 42.

In case of genotypic path coefficient analysis, soil moisture content had positive direct effect on pollen viability (0.31) which was contributed to result non-significant negative genotypic correlation (-0.07) (Table 41). Soil moisture content had positive

indirect effect on relative water content (21.26), water uptake capacity (0.03), total chlorophyll content (0.46), membrane stability index (0.01) and negative indirect effect on water saturation deficit (-21.56), water retention capacity (-0.06), nitrogen concentration (-0.50) and proline content (-0.01) (Table 41). Relative water content showed positive direct effect (163.75) on pollen viability with non-significant negative genotypic correlation (-0.09). Relative water content had positive indirect effect on soil moisture content (0.04), total chlorophyll content (0.40), membrane stability index (0.01) and negative indirect effect on water saturation deficit (-163.01), water retention capacity (-0.18), water uptake capacity (-0.62), nitrogen content (-0.43), proline content (-0.04). Water saturation deficit had positive direct effect on pollen viability (163.01) which was contributed to result on non-significant positive genotypic correlation (0.09). Water saturation deficit had negative indirect effect on soil moisture content (-0.04), relative water content (-163.75), total chlorophyll content (-0.40), membrane stability index (-0.01) and positive indirect effect on water retention capacity (0.18), water uptake capacity (0.62), nitrogen content (0.43), proline content (0.04). Water retention capacity had negative direct effect on pollen viability (-0.62) which was contributed to result in non-significant negative genotypic correlation (-0.27). Water retention capacity had positive indirect effect on soil moisture content (0.03), relative water content (48.13), water uptake capacity (0.25), total chlorophyll content (0.44), membrane stability index (0.02) and negative indirect effect on water saturation deficit (-48.03), nitrogen content (-0.48), proline content (-0.02). Water uptake capacity had direct positive effect on pollen viability (0.84) which was contributed non-significant negative genotypic correlation (-0.06). Water uptake capacity had positive indirect effect on soil moisture content (0.01), water saturation deficit (120.61), nitrogen content (0.12), membrane stability index (0.00), proline content (0.01) and indirect negative effect on relative water content (-121.35), water retention capacity (-0.19) and total chlorophyll content (-0.12). Total chlorophyll content had negative direct effect on pollen viability (-2.43) which is contributed significant positive genotypic correlation (0.28). Total chlorophyll content had positive indirect effect on water saturation deficit (26.81), water retention capacity (0.11), water uptake capacity (0.04), nitrogen content (2.63), proline content (0.07) and negative indirect effect on soil moisture content (-0.06), relative water content (-26.88) and membrane stability index (-0.02). Nitrogen content had positive direct effect on pollen viability (2.63) which was contributed significant positive genotypic

**Table 41. Genotypic path coefficient analysis showing the direct (bold) and indirect effect of different characters on pollen viability of cotton**

| Characters | Soil Moisture content | Relative water content | Water saturation deficit | Water retention capacity | Water uptake capacity | Total chlorophyll content | Nitrogen content | Membrane stability index | Proline content | Genotypic correlation coefficient with pollen viability |
|---|---|---|---|---|---|---|---|---|---|---|
| **Soil moisture content** | **0.31** | 21.26 | -21.56 | -0.06 | 0.03 | 0.46 | -0.50 | 0.01 | -0.01 | -0.07$^{NS}$ |
| **Relative water content** | 0.04 | **163.75** | -163.01 | -0.18 | -0.62 | 0.40 | -0.43 | 0.01 | -0.04 | -0.09$^{NS}$ |
| **Water saturation deficit** | -0.04 | -163.75 | **163.01** | 0.18 | 0.62 | -0.40 | 0.43 | -0.01 | 0.04 | 0.09$^{NS}$ |
| **Water retention capacity** | 0.03 | 48.13 | -48.03 | **-0.62** | 0.25 | 0.44 | -0.48 | 0.02 | -0.02 | -0.27$^{NS}$ |
| **Water uptake capacity** | 0.01 | -121.35 | 120.61 | -0.19 | **0.84** | -0.12 | 0.12 | 0.00 | 0.01 | -0.06$^{NS}$ |
| **Total chlorophyll content** | -0.06 | -26.88 | 26.81 | 0.11 | 0.04 | **-2.43** | 2.63 | -0.02 | 0.07 | 0.28$^{*}$ |
| **Nitrogen content** | -0.06 | -26.88 | 26.80 | 0.11 | 0.04 | -2.43 | **2.63** | -0.02 | 0.07 | 0.28$^{*}$ |
| **Membrane stability index** | -0.05 | -22.06 | 22.13 | 0.16 | -0.06 | -0.57 | 0.62 | **-0.07** | 0.08 | 0.18$^{NS}$ |
| **Proline content** | -0.02 | -24.69 | 24.26 | 0.03 | 0.04 | -0.63 | 0.69 | -0.02 | **0.28** | -0.05$^{NS}$ |

**Table 42. Phenotypic path coefficient analysis showing the direct (bold) and indirect effect of different characters on pollen viability of cotton**

| Characters | Soil Moisture content | Relative water content | Water saturation deficit | Water retention capacity | Water uptake capacity | Total chlorophyll content | Nitrogen content | Membrane stability index | Proline content | Phenotypic correlation coefficient with pollen viability |
|---|---|---|---|---|---|---|---|---|---|---|
| **Soil moisture content** | **-0.005** | -0.439 | 0.453 | -0.020 | 0.001 | -0.021 | -0.018 | -0.021 | 0.006 | $-0.06^{NS}$ |
| **Relative water content** | -0.001 | **-3.685** | 3.727 | -0.065 | -0.029 | -0.017 | -0.014 | -0.016 | 0.021 | $-0.08^{NS}$ |
| **Water saturation deficit** | 0.001 | 3.684 | **-3.728** | 0.065 | 0.029 | 0.017 | 0.014 | 0.016 | -0.021 | $0.08^{NS}$ |
| **Water retention capacity** | 0.000 | -1.053 | 1.068 | **-0.228** | 0.012 | -0.021 | -0.018 | -0.031 | 0.008 | $-0.26^{**}$ |
| **Water uptake capacity** | 0.000 | 2.693 | -2.720 | -0.068 | **0.039** | 0.007 | 0.007 | -0.008 | -0.006 | $-0.06^{NS}$ |
| **Total chlorophyll content** | 0.001 | 0.506 | -0.513 | 0.040 | 0.002 | **0.116** | 0.104 | 0.027 | -0.034 | $0.25^{**}$ |
| **Nitrogen content** | 0.001 | 0.510 | -0.517 | 0.039 | 0.003 | 0.124 | **0.100** | 0.026 | -0.035 | $0.25^{**}$ |
| **Membrane stability index** | 0.001 | 0.478 | -0.488 | 0.057 | -0.002 | 0.026 | 0.022 | **0.124** | -0.040 | $0.18^{*}$ |
| **Proline content** | 0.000 | 0.527 | -0.527 | 0.012 | 0.002 | 0.028 | 0.024 | 0.033 | **-0.149** | $-0.05^{NS}$ |

correlation (0.28). Nitrogen content had positive indirect effect on water saturation deficit (26.28), water retention capacity (0.11), water uptake capacity (0.04), proline content (0.07) and negative indirect effect soil moisture content (-0.06), relative water content (-26.88), total chlorophyll content (-2.43), membrane stability index (-0.02). Membrane stability index had negative direct effect on pollen viability (-0.07) which was contributed non-significant positive genotypic correlation (0.18). Membrane stability index had positive indirect effect on water saturation deficit (22.13), water retention capacity (0.16), nitrogen content (0.62), proline content (0.08) and negative indirect effect on soil moisture content (-0.05), relative water content (-22.06), water uptake capacity (0.06), total chlorophyll content (-0.57). Proline content had positive direct effect on pollen viability (0.28) which was contributed non-significant negative genotypic correlation (-0.05). Proline content had positive indirect effect on water saturation deficit (24.26), water retention capacity (0.03), water uptake capacity (0.04), nitrogen content (0.69) and negative indirect effect soil moisture content (-0.02), relative water content (-24.69), total chlorophyll content (-0.63), membrane stability index (-0.02). Genotypic path coefficient analysis carried out by Manonmani *et al*. (2019) and Ali *et al*. (2020) reported a direct positive effect of seed per boll on yield. Some scientists also reported indirect significant effect of leaf chlorophyll on seed cotton yield (Reddy and Kumari, 2004).

In case of phenotypic path coefficient analysis, soil moisture content had negative direct effect on pollen viability (-0.005) which was contributed to result non-significant negative genotypic correlation (-0.06) (Table 42). Soil moisture content had positive indirect effect on water saturation deficit (0.453), water uptake capacity (0.001), proline content (0.006) and negative indirect effect on relative water content (-0.439), water retention capacity (-0.020), total chlorophyll content (-0.021), nitrogen concentration (-0.018) and membrane stability index (-0.021) (Table 42). Relative water content showed negative direct effect (-3.685) on pollen viability with non-significant negative genotypic correlation (-0.08). Relative water content had positive indirect effect on water saturation deficit (3.727), proline content (0.021) and negative indirect effect on soil moisture content (-0.001), water retention capacity (-0.065), water uptake capacity (-0.029), total chlorophyll content (-0.017), membrane stability index (-0.014) nitrogen content (-0.016). Water saturation deficit had negative direct effect on pollen viability (-3.728) which was contributed to result on non-significant

positive genotypic correlation (0.08). Water saturation deficit had positive indirect effect on soil moisture content (0.001), relative water content (3.684), water retention capacity (0.065), water uptake capacity (0.029), total chlorophyll content (0.017), nitrogen content (0.014), membrane stability index (0.016) and negative indirect effect on proline content (-0.021). Water retention capacity had negative direct effect on pollen viability (-0.228) which was contributed to result in significant negative genotypic correlation (-0.26). Water retention capacity had positive indirect effect on soil moisture content (0.000), water saturation deficit (1.068), water uptake capacity (0.012), proline content (0.008) and negative indirect effect on relative water content (-1.053), total chlorophyll content (-0.021), nitrogen content (-0.018), membrane stability index (-0.031). Water uptake capacity had direct positive effect on pollen viability (0.039) which was contributed non-significant negative genotypic correlation (-0.06). Water uptake capacity had positive indirect effect on soil moisture content (0.000), relative water content (2.693), total chlorophyll content (0.007), nitrogen content (0.007) and indirect negative effect on water saturation deficit (-2.720), water retention capacity (-0.068), membrane stability index (-0.008), proline content (-0.006). Total chlorophyll content had positive direct effect on pollen viability (0.116) which was contributed significant positive genotypic correlation (0.25). Total chlorophyll content had positive indirect effect on soil moisture content (0.001), relative water content (0.506), water retention capacity (0.040), water uptake capacity (0.002), nitrogen content (0.104), membrane stability index (0.027) and negative indirect effect on water saturation deficit (-0.513), proline content (-0.034). Nitrogen content had positive direct effect on pollen viability (0.100) which was contributed significant positive genotypic correlation (0.25). Nitrogen content had positive indirect effect on soil moisture content (0.001), relative water content (0.510), water retention capacity (0.039), water uptake capacity (0.003), total chlorophyll content (0.124), membrane stability index (0.026) and negative indirect effect on water saturation deficit (-0.517), proline content (-0.035). Membrane stability index had positive direct effect on pollen viability (0.124) which was contributed non-significant positive genotypic correlation (0.18). Membrane stability index had positive indirect effect on soil moisture content (0.001), relative water content (0.478), water retention capacity (0.057), total chlorophyll content (0.026), nitrogen content (0.022), and negative indirect effect on water saturation deficit (-0.488), water uptake capacity (-0.002), proline content (-0.040). Proline content had negative direct effect on pollen viability

(-0.149) which was contributed non-significant negative genotypic correlation (-0.05). Proline content had positive indirect effect on soil moisture content (0.000), relative water content (0.527), water retention capacity (0.012), water uptake capacity (0.002), total chlorophyll content (0.028), nitrogen content (0.024), membrane stability index (0.033) and negative indirect effect on water saturation deficit (-0.527). Genotypic path coefficient analysis carried out by Reddy and Kumari (2004) reported indirect significant effect of leaf chlorophyll on seed cotton yield.

### 4.2.6 Selection of genotypes based on selection index

Screening of cotton genotypes for tolerance to drought stress was undertaken at flowering stage at net house of Sher-e-Bangla Agricultural University, Shere Bangla Nagar, Dhaka. After 32 days of seed sowing, drought builds up to 7, 14, 21 days interval by irrigation. After 74 days of seed sowing, the plant characters were count the final plant survival and growth rate was noted. So selection based on agromorphological characters may not be as effective for population improvement as it would be effective on the basis of selection indices for which some more physiological characters are given relative weightage. Discriminant functions is a biometrical technique which provides information about the relative contribution of the various component traits to physiology and aids in the isolation from populations of superior genotypes by providing information for indirect selection for yield and fibre quality. On the basis of fitted discriminate functions, selection scores were computed for all the 50 genotypes and ranked (Table 43). These 50 genotypes having good plant morphology as well as plant physiology at flowering stage which may generate primary information regarding suitability of deferent genotypes for drought tolerance. The 25 genotypes were selected acceding to top ranking, 4 cultivars and 2 descending genotypes as negative controls based on selection scores (Experiment-1 and Experiment-2). These 25 genotypes were used as a plant material for the next experiments for yield contributing and fibre quality characters (Experiment 3) and selection suitable genotypes for Barind tract.

**Table 43. Relative selection index scores and ranking of fifty cotton genotypes based on physiological characters**

| Sl. No. | Genotypes | Variety / line | Selection Index score | Rank |
|---|---|---|---|---|
| 1 | G1 | CB-1 | 253.44 | 46 |
| 2 | G2 | CB-2 | 274.95 | 15 |
| 3 | G3 | CB-3 | 254.17 | 45 |
| 4 | G4 | CB-4 | 260.29 | 43 |
| 5 | G5 | CB-5 | 265.03 | 41 |
| 6 | G6 | CB-6 | 253.21 | 47 |
| 7 | G7 | CB-7 | 273.74 | 17 |
| 8 | G8 | CB-8 | 250.74 | 49 |
| 9 | G9 | CB-9 | 268.94 | 31 |
| 10 | G10 | CB-10 | 269.49 | 30 |
| 11 | G11 | CB-11 | 252.74 | 48 |
| 12 | G12 | CB-12 | 267.02 | 35 |
| 13 | G13 | CB-13 | 267.26 | 33 |
| 14 | G14 | CB-14 | 279.18 | 4 |
| 15 | G15 | CB-15 | 269.49 | 29 |
| 16 | G16 | Ra-2 | 268.90 | 32 |
| 17 | G17 | Ra-3 | 280.05 | 2 |
| 18 | G18 | Ra-4 | 259.64 | 44 |
| 19 | G19 | Ra-5 | 267.21 | 34 |
| 20 | G20 | Ra-9 | 270.53 | 25 |
| 21 | G21 | Ra-15 | 270.59 | 24 |
| 22 | G22 | Ra-16 | 266.55 | 36 |
| 23 | G23 | JA-08/9 | 277.30 | 11 |
| 24 | G24 | JA-11/M | 266.41 | 38 |
| 25 | G25 | JA-10/55 | 269.85 | 28 |
| 26 | G26 | JA-08/B | 275.36 | 13 |
| 27 | G27 | JA-11/L | 266.49 | 37 |
| 28 | G28 | JA-09/H | 271.12 | 22 |
| 29 | G29 | JA-13/R | 277.50 | 9 |
| 30 | G30 | SR-15 | 270.42 | 27 |
| 31 | G31 | SR-16 | 273.30 | 18 |
| 32 | G32 | SR-17 | 274.07 | 16 |
| 33 | G33 | BC-272 | 248.72 | 50 |
| 34 | G34 | BC-385 | 278.80 | 5 |
| 35 | G35 | BC-394 | 278.75 | 6 |
| 36 | G36 | BC-397 | 272.53 | 20 |
| 37 | G37 | BC-410 | 265.83 | 40 |
| 38 | G38 | BC-413 | 279.93 | 3 |
| 39 | G39 | BC-415 | 275.79 | 12 |
| 40 | G40 | BC-419 | 274.99 | 14 |
| 41 | G41 | BC-423 | 266.40 | 39 |
| 42 | G42 | BC-430 | 272.53 | 21 |
| 43 | G43 | BC-433 | 271.06 | 23 |
| 44 | G44 | BC-435 | 272.56 | 19 |
| 45 | G45 | BC-442 | 278.00 | 7 |
| 46 | G46 | BC-462 | 277.49 | 10 |
| 47 | G47 | BC-509 | 270.49 | 26 |
| 48 | G48 | BC-510 | 277.96 | 8 |
| 49 | G49 | BC-511 | 264.27 | 42 |
| 50 | G50 | BC-512 | 281.68 | 1 |

## 4.3 Experiment 3. Selection of drought tolerant cotton genotypes in AEZ of Barind tract

This investigation was conducted to evaluate the twenty-five cotton genotypes under drought stresses based on thirteen yield contributing and ten fibre quality characters and to assess the genetic variation among the genotypes for drought tolerance. Thirteen yield contributing and ten fibre quality traits of twenty five cotton genotypes were observed under four drought stress conditions. The yield contributing traits included shoot length, days to first square initiation, days to first flower initiation, days to first boll split, number of vegetative branches, number of reproductive branches, number of bolls per plant, days to first boll bursting, single boll weight, ginning out turn, seed index, lint index, seed cotton yield per hectare and ten fibre quality traits were fibre length, uniformity index, short fibre index, fibre strength, micronaire value, elongation, maturity ratio, moisture content/regain, reflectance degree (Rd) and yellowness value (+b). Data are presented in Table, Figures for better understanding.

### 4.3.1 Yield contributing characters of cotton genotypes under drought stress

Yield contributing characters of twenty-five genotypes were observed under four different drought stress conditions. ANOVA showed the significant effect of genotypes, treatment, and interaction on all thirteen yield contributing characters (Appendix VI).

#### 4.3.1.1 Plant height

Genotype, treatment and their interaction significantly affected the plant height. The highest mean plant height (147.69 cm) was observed in T1 drought stress whereas the lowest plant height (136.04 cm) was observed in T3 drought stress (Table 44). Among the genotypes, highest plant height (159.75 cm) was observed in G43 and lowest (132.92 cm) in G11. Based on the genotype stress interaction, highest plant height (176.33 cm) and lowest (118.67 cm) was observed in G43 under T1 and G29 under T3 stress respectively. On the basis of b values, the best performance (highest b value) was observed in genotype G43 (7.70) followed by G29 (7.28) and lowest in G50 (-0.76). With the increase of drought stress, plant height was increased as shown in linear regression in Figure 50. The minimum reduction% (-9.86%) was observed in

## Table 44. Plant height of twenty-five genotypes at different drought treatments

| Genotype | Plant height (cm) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 140.00 | 139.67 | 126.33 | 131.33 | 134.33 | 0.24 | 9.76 | 6.19 | 5.40 | 2.51 | 12 |
| G2 | 147.67 | 133.33 | 129.33 | 131.33 | 135.42 | 9.71 | 12.42 | 11.06 | 11.06 | 4.43 | 5 |
| G8 | 150.67 | 145.33 | 145.67 | 157.33 | 149.75 | 3.54 | 3.32 | -4.42 | 0.81 | 1.65 | 16 |
| G10 | 136.33 | 130.33 | 133.33 | 133.00 | 133.25 | 4.40 | 2.20 | 2.44 | 3.02 | 1.02 | 17 |
| G11 | 138.33 | 132.00 | 128.67 | 132.67 | 132.92 | 4.58 | 6.99 | 4.10 | 5.22 | 2.31 | 13 |
| G12 | 138.67 | 141.67 | 140.33 | 142.67 | 140.83 | -2.16 | -1.20 | -2.88 | -2.08 | -0.48 | 24 |
| G13 | 143.00 | 136.33 | 137.33 | 150.67 | 141.83 | 4.66 | 3.96 | -5.36 | 1.09 | 1.92 | 14 |
| G14 | 158.33 | 157.00 | 157.33 | 161.00 | 158.42 | 0.84 | 0.63 | -1.68 | -0.07 | 0.39 | 19 |
| G15 | 145.33 | 141.33 | 151.33 | 159.67 | 149.42 | 2.75 | -4.13 | -9.86 | -3.75 | -0.45 | 22 |
| G17 | 141.00 | 138.33 | 127.00 | 126.33 | 133.17 | 1.89 | 9.93 | 10.40 | 7.41 | 2.61 | 11 |
| G18 | 139.33 | 138.00 | 143.67 | 149.33 | 142.58 | 0.96 | -3.11 | -7.18 | -3.11 | -0.47 | 23 |
| G22 | 147.33 | 149.00 | 129.67 | 141.33 | 141.83 | -1.13 | 11.99 | 4.07 | 4.98 | 3.22 | 9 |
| G23 | 156.33 | 151.67 | 121.33 | 126.33 | 138.92 | 2.99 | 22.39 | 19.19 | 14.85 | 6.54 | 3 |
| G29 | 159.00 | 156.33 | 118.67 | 123.33 | 139.33 | 1.68 | 25.37 | 22.43 | 16.49 | 7.28 | 2 |
| G30 | 150.67 | 143.00 | 129.67 | 134.33 | 139.42 | 5.09 | 13.94 | 10.84 | 9.96 | 4.39 | 6 |
| G33 | 140.67 | 139.00 | 131.33 | 135.67 | 136.67 | 1.18 | 6.64 | 3.55 | 3.79 | 1.87 | 15 |
| G34 | 134.33 | 134.33 | 130.67 | 136.67 | 134.00 | 0.00 | 2.73 | -1.74 | 0.33 | 0.80 | 18 |
| G35 | 153.67 | 155.00 | 134.00 | 142.33 | 146.25 | -0.87 | 12.80 | 7.38 | 6.44 | 3.50 | 8 |
| G38 | 146.00 | 139.67 | 123.33 | 128.33 | 134.33 | 4.34 | 15.53 | 12.10 | 10.65 | 4.57 | 4 |
| G39 | 148.33 | 151.67 | 150.33 | 157.00 | 151.83 | -2.25 | -1.35 | -5.84 | -3.15 | -0.44 | 21 |
| G43 | 176.33 | 173.67 | 135.67 | 153.33 | 159.75 | 1.51 | 23.06 | 13.04 | 12.54 | 7.70 | 1 |
| G45 | 151.33 | 138.67 | 140.67 | 149.67 | 145.08 | 8.37 | 7.05 | 1.10 | 5.51 | 3.17 | 10 |
| G46 | 138.67 | 136.67 | 142.33 | 145.67 | 140.83 | 1.44 | -2.64 | -5.05 | -2.08 | -0.36 | 20 |
| G48 | 157.67 | 158.33 | 136.67 | 141.67 | 148.58 | -0.42 | 13.32 | 10.15 | 7.68 | 3.69 | 7 |
| G50 | 153.33 | 156.67 | 156.33 | 157.67 | 156.00 | -2.17 | -1.96 | -2.83 | -2.32 | -0.76 | 25 |
| Mean (T) | 147.69 | 144.68 | 136.04 | 141.95 | | | | | | | |

G15 under T4 drought stress (Figure 50, Table 44). Maximum reduction% (25.37%) was observed in G29 under T3 stress (Figure 51). The result showed the positive effect of drought stress on plant height in genotypic dependent manner. Some of the genotypes showed an increase in plant height at mild and moderate drought stress. However, the maximum genotypes showed a decrease of plant height under the severe drought stress. Guinn *et al*. (1981) concluded that a moderated drought stress early in the season could be beneficial to the plants since it would mildly retard growth, however either delaying or limiting water supply could lead to stunted growth.

#### 4.3.1.2 Days to first square initiation

Genotype, treatment and their interaction significantly affected the days to first square initiation. Maximum mean days to first square initiation (48.23) was observed in T4 drought stress whereas the minimum days to first square initiation (43.29) was observed in T1 drought stress (Table 45). Among the genotypes, maximum days to first square initiation (50.92) were observed in G43 and lowest (41.67) in G29. Based on the genotype stress interaction, maximum days to first square initiation (60.0) and lowest (39.67) was observed in G43 under T4 and G29 under T4 stress, respectively. On the basis of b values, the best performance (lowest b value) was observed in genotype G46 (-1.44) followed by G18 (-1.40) and highest in G43 (0.68). With the increase of drought stress, days to first square initiation was decreased as shown in linear regression in Figure 52. The minimum reduction% (-28.91%) was observed in G22 under T4 drought stress (Figure 52, Table 45). Maximum reduction% (5.30%) was observed in G13 under T2 stress (Figure 53). The result showed the negative effect of drought stress on days to first square initiation in genotypic dependent manner. Some of the genotypes showed an increase in days to first square initiation at mild and moderate drought stress. However, the maximum genotypes showed an increase of days to first square initiation under the drought stress. Similar result has been observed in Veesar *et al*. (2020). Water availability was the most critical part for cotton on the plants from the first square stage until the first flower because early fruit setting were capable of maturing under a short growing period ( Marani and Amirav, 1971; Boyer, 1970).

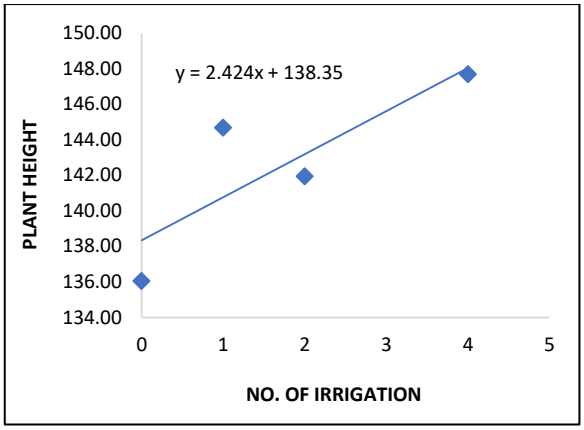



**Figure 50. Relationships between plant height of cotton genotypes and different drought stresses**

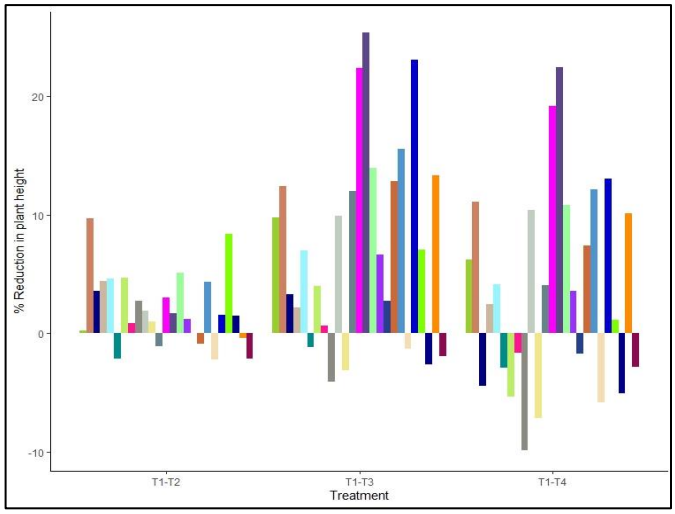
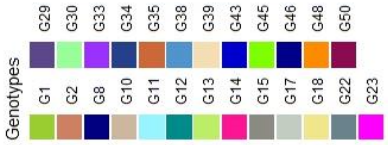



**Figure 51. Reduction percentage of plant height of twenty-five cotton genotypes under different drought stresses compared with control**



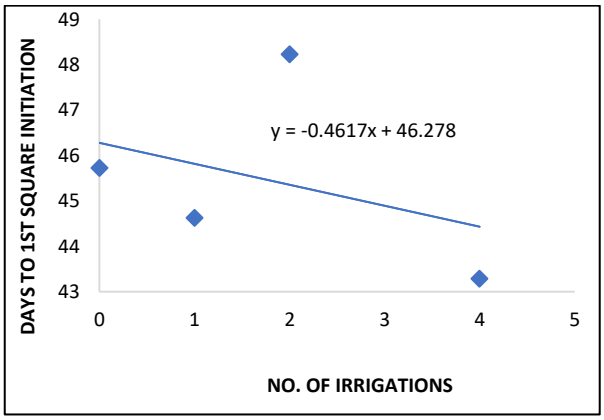




**Figure 52. Relationships between days to 1st square initiation of cotton genotypes and different drought stresses**

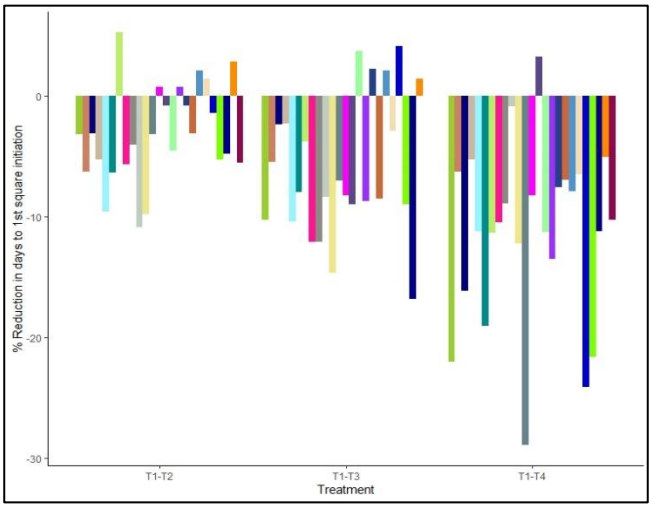



**Figure 53. Reduction percentage of days to 1st square initiation of twenty-five cotton genotypes under different drought stresses compared with control**

**Table 45. Days to first square initiation of twenty-five genotypes at different drought treatments**

| Genotype | Days to 1st square initiation at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 42.33 | 43.67 | 46.67 | 51.67 | 46.08 | -3.15 | -10.24 | -22.05 | -11.81 | -0.71 | 9 |
| G2 | 42.67 | 45.33 | 45.00 | 45.33 | 44.58 | -6.25 | -5.47 | -6.25 | -5.99 | -0.62 | 11 |
| G8 | 43.33 | 44.67 | 44.33 | 50.33 | 45.67 | -3.08 | -2.31 | -16.15 | -7.18 | -0.11 | 17 |
| G10 | 44.33 | 46.67 | 45.33 | 46.67 | 45.75 | -5.26 | -2.26 | -5.26 | -4.26 | -0.33 | 15 |
| G11 | 41.67 | 45.67 | 46.00 | 46.33 | 44.92 | -9.60 | -10.40 | -11.20 | -10.40 | -1.08 | 3 |
| G12 | 42.00 | 44.67 | 45.33 | 50.00 | 45.50 | -6.35 | -7.94 | -19.05 | -11.11 | -0.67 | 10 |
| G13 | 44.00 | 41.67 | 45.67 | 49.00 | 45.08 | 5.30 | -3.79 | -11.36 | -3.28 | 0.01 | 19 |
| G14 | 41.33 | 43.67 | 46.33 | 45.67 | 44.25 | -5.65 | -12.10 | -10.48 | -9.41 | -1.08 | 3 |
| G15 | 41.33 | 43.00 | 46.33 | 45.00 | 43.92 | -4.03 | -12.10 | -8.87 | -8.33 | -1.04 | 4 |
| G17 | 40.00 | 44.33 | 43.33 | 40.33 | 42.00 | -10.83 | -8.33 | -0.83 | -6.67 | -1.03 | 5 |
| G18 | 41.00 | 45.00 | 47.00 | 46.00 | 44.75 | -9.76 | -14.63 | -12.20 | -12.20 | -1.40 | 2 |
| G22 | 42.67 | 44.00 | 45.67 | 55.00 | 46.83 | -3.13 | -7.03 | -28.91 | -13.02 | -0.36 | 14 |
| G23 | 44.67 | 44.33 | 48.33 | 48.33 | 46.42 | 0.75 | -8.21 | -8.21 | -5.22 | -0.60 | 12 |
| G29 | 41.00 | 41.33 | 44.67 | 39.67 | 41.67 | -0.81 | -8.94 | 3.25 | -2.17 | -0.80 | 6 |
| G30 | 44.33 | 46.33 | 42.67 | 49.33 | 45.67 | -4.51 | 3.76 | -11.28 | -4.01 | 0.30 | 21 |
| G33 | 42.00 | 41.67 | 45.67 | 47.67 | 44.25 | 0.79 | -8.73 | -13.49 | -7.14 | -0.54 | 13 |
| G34 | 44.33 | 44.67 | 43.33 | 47.67 | 45.00 | -0.75 | 2.26 | -7.52 | -2.01 | 0.27 | 20 |
| G35 | 43.33 | 44.67 | 47.00 | 46.33 | 45.33 | -3.08 | -8.46 | -6.92 | -6.15 | -0.76 | 7 |
| G38 | 46.33 | 45.33 | 45.33 | 50.00 | 46.75 | 2.16 | 2.16 | -7.91 | -1.20 | 0.39 | 23 |
| G39 | 46.33 | 45.67 | 47.67 | 49.33 | 47.25 | 1.44 | -2.88 | -6.47 | -2.64 | -0.12 | 16 |
| G43 | 48.33 | 49.00 | 46.33 | 60.00 | 50.92 | -1.38 | 4.14 | -24.14 | -7.13 | 0.68 | 24 |
| G45 | 44.67 | 47.00 | 48.67 | 54.33 | 48.67 | -5.22 | -8.96 | -21.64 | -11.94 | -0.72 | 8 |
| G46 | 41.67 | 43.67 | 48.67 | 46.33 | 45.08 | -4.80 | -16.80 | -11.20 | -10.93 | -1.44 | 1 |
| G48 | 46.33 | 45.00 | 45.67 | 48.67 | 46.42 | 2.88 | 1.44 | -5.04 | -0.24 | 0.31 | 22 |
| G50 | 42.33 | 44.67 | 42.33 | 46.67 | 44.00 | -5.51 | 0.00 | -10.24 | -5.25 | -0.08 | 18 |
| Mean (T) | 43.29 | 44.63 | 45.73 | 48.23 | | | | | | | |

#### 4.3.1.3 Days to first flower initiation

Genotype, treatment and their interaction significantly affected the days to first flower initiation. Maximum mean days to first flower initiation (55.07) was observed in T4 drought stress whereas the minimum days to first flower initiation (50.51) was observed in T1 drought stress (Table 46). Among the genotypes, maximum days to first flower initiation (57.58) were observed in G43 and lowest (48.67) in G29. Based on the genotype stress interaction, maximum days to first flower initiation (66.33) and lowest (46.67) were observed in G43 under T4 and G29 under T4 stress, respectively. On the basis of b values, the best performance (lowest b value) was observed in genotype G46 (-1.33) followed by G18 (-1.17) and highest in G43 (0.90). With the increase of drought stress, days to first flower initiation was decreased as shown in linear regression in Figure 60. The minimum reduction% (-25.17%) was observed in G22 under T4 drought stress (Figure 54, Table 46). Maximum reduction% (5.39%) was observed in G43 under T3 stress (Figure 55). The result showed the negative effect of drought stress on days to first flower initiation in genotypic dependent manner. Some of the genotypes showed an increase in days to first flower initiation at moderate drought stress. However, the maximum genotypes showed a increase of days to first flower initiation under the drought stress. Bakhsh *et al*. (2019) noted that water stress caused a reduction of 14% in days to first flower formation, 27% in number of bolls/ plants, 14% in boll weight and 37% in seed cotton yield**.**

#### 4.3.1.4 Days to first boll split

Genotype, treatment and their interaction significantly affected the days to first boll split. Maximum mean days to first boll split (60.91) was observed in T4 drought stress whereas the minimum mean days to first boll split (56.60) was observed in T1 drought stress (Table 47). Among the genotypes, maximum days to first boll split (63.42) were observed in G43 and lowest (54.75) in G29. Based on the genotype stress interaction, maximum days to first boll split (72.00) and lowest (52.67) was observed in G43 under T4 and G29 under T4 stress, respectively. On the basis of b values, the best performance (lowest b value) was observed in genotype G46 (-1.24) followed by G15 (-1.16) and highest in G43 (0.92). With the increase of drought stress, days to first boll split was decreased as shown in linear regression in Figure 56. The minimum reduction% (-20.61%) was observed in G22 under T4 drought stress (Figure 56, Table 47). Maximum reduction% (4.86%) was observed in G43 under T3 stress (Figure 57).

**Table 46. Days to first flower initiation of twenty-five genotypes at different drought treatments**

| Genotype | Days to first flower initiation at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 48.67 | 50.33 | 53.33 | 58.67 | 52.75 | -3.42 | -9.59 | -20.55 | -11.19 | -0.79 | 6 |
| G2 | 49.33 | 51.33 | 52.00 | 52.67 | 51.33 | -4.05 | -5.41 | -6.76 | -5.41 | -0.61 | 10 |
| G8 | 51.33 | 51.33 | 50.67 | 57.00 | 52.58 | 0.00 | 1.30 | -11.04 | -3.25 | 0.30 | 20 |
| G10 | 51.33 | 53.33 | 52.33 | 53.67 | 52.67 | -3.90 | -1.95 | -4.55 | -3.46 | -0.30 | 16 |
| G11 | 49.67 | 52.00 | 53.33 | 53.67 | 52.17 | -4.70 | -7.38 | -8.05 | -6.71 | -0.82 | 5 |
| G12 | 49.33 | 51.33 | 52.00 | 56.00 | 52.17 | -4.05 | -5.41 | -13.51 | -7.66 | -0.51 | 13 |
| G13 | 51.33 | 49.00 | 52.33 | 57.33 | 52.50 | 4.55 | -1.95 | -11.69 | -3.03 | 0.17 | 19 |
| G14 | 48.33 | 50.67 | 53.00 | 52.33 | 51.08 | -4.83 | -9.66 | -8.28 | -7.59 | -1.02 | 3 |
| G15 | 48.33 | 50.00 | 53.00 | 51.33 | 50.67 | -3.45 | -9.66 | -6.21 | -6.44 | -0.99 | 4 |
| G17 | 47.67 | 51.33 | 50.00 | 47.67 | 49.17 | -7.69 | -4.90 | 0.00 | -4.20 | -0.78 | 7 |
| G18 | 48.33 | 51.67 | 53.33 | 52.33 | 51.42 | -6.90 | -10.34 | -8.28 | -8.51 | -1.17 | 2 |
| G22 | 49.00 | 51.00 | 52.00 | 61.33 | 53.33 | -4.08 | -6.12 | -25.17 | -11.79 | -0.42 | 14 |
| G23 | 51.67 | 51.33 | 55.00 | 54.67 | 53.17 | 0.65 | -6.45 | -5.81 | -3.87 | -0.55 | 11 |
| G29 | 48.33 | 48.33 | 51.33 | 46.67 | 48.67 | 0.00 | -6.21 | 3.45 | -0.92 | -0.65 | 8 |
| G30 | 51.67 | 53.00 | 50.00 | 56.33 | 52.75 | -2.58 | 3.23 | -9.03 | -2.80 | 0.35 | 22 |
| G33 | 49.33 | 48.67 | 52.00 | 55.00 | 51.25 | 1.35 | -5.41 | -11.49 | -5.18 | -0.31 | 15 |
| G34 | 51.33 | 51.00 | 50.67 | 56.67 | 52.42 | 0.65 | 1.30 | -10.39 | -2.81 | 0.31 | 21 |
| G35 | 50.33 | 51.00 | 53.67 | 53.33 | 52.08 | -1.32 | -6.62 | -5.96 | -4.64 | -0.64 | 9 |
| G38 | 53.67 | 52.33 | 52.00 | 56.67 | 53.67 | 2.48 | 3.11 | -5.59 | 0.00 | 0.53 | 23 |
| G39 | 54.00 | 52.33 | 54.33 | 55.67 | 54.08 | 3.09 | -0.62 | -3.09 | -0.21 | 0.12 | 18 |
| G43 | 55.67 | 55.67 | 52.67 | 66.33 | 57.58 | 0.00 | 5.39 | -19.16 | -4.59 | 0.90 | 24 |
| G45 | 52.00 | 53.33 | 55.33 | 61.00 | 55.42 | -2.56 | -6.41 | -17.31 | -8.76 | -0.52 | 12 |
| G46 | 49.33 | 50.33 | 56.00 | 52.33 | 52.00 | -2.03 | -13.51 | -6.08 | -7.21 | -1.33 | 1 |
| G48 | 53.33 | 52.00 | 52.67 | 55.33 | 53.33 | 2.50 | 1.25 | -3.75 | 0.00 | 0.30 | 20 |
| G50 | 49.33 | 52.00 | 49.67 | 52.67 | 50.92 | -5.41 | -0.68 | -6.76 | -4.28 | -0.20 | 17 |
| Mean (T) | 50.51 | 51.39 | 52.51 | 55.07 | | | | | | | |

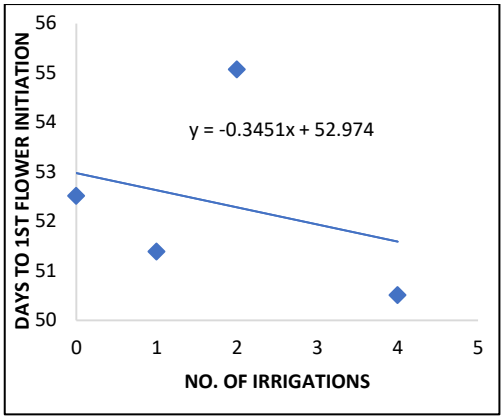



**Figure 54. Relationships between days to 1st flower initiation of cotton genotypes and different drought stresses**

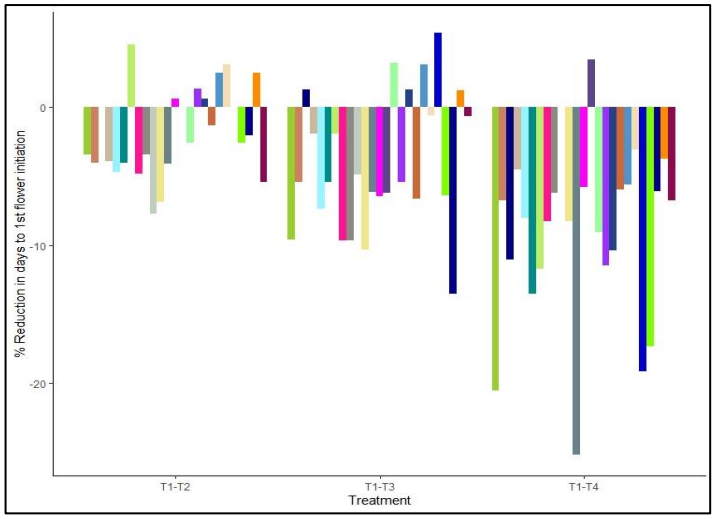
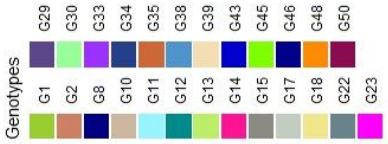



**Figure 55. Reduction percentage of days to 1st flower initiation of twenty-five cotton genotypes under different drought stresses compared with control**



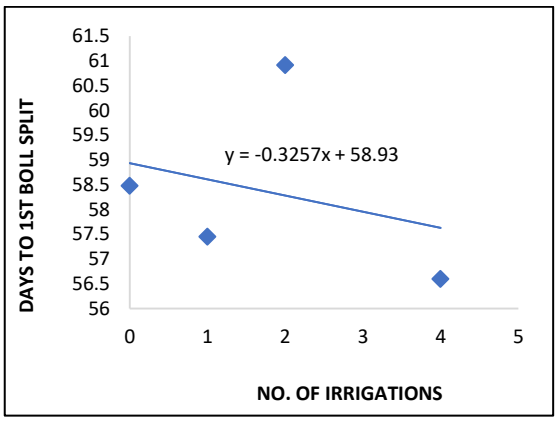




**Figure 56. Relationships between days to 1st boll split of cotton genotypes and different drought stresses**

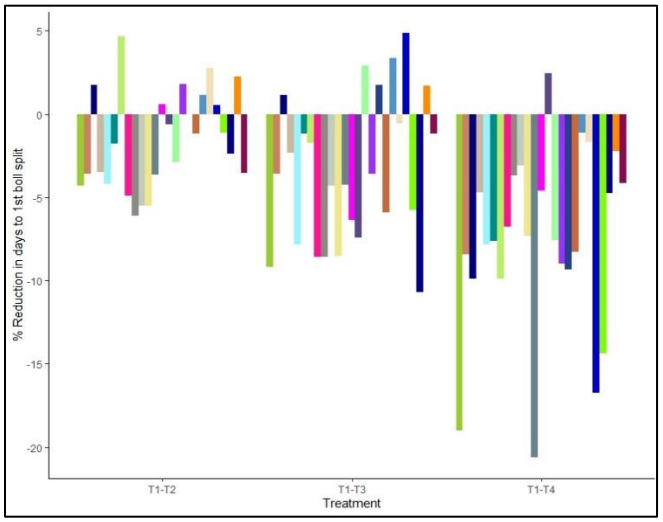



**Figure 57. Reduction percentage of days to 1st boll split of twenty-five cotton genotypes under different drought stresses compared with control**

**Table 47. Days to first boll split of twenty-five genotypes at different drought treatments**

| Genotype | Days to first boll split at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 54.33 | 56.67 | 59.33 | 64.67 | 58.75 | -4.29 | -9.20 | -19.02 | -10.84 | -0.90 | 6 |
| G2 | 55.33 | 57.33 | 57.33 | 60.00 | 57.50 | -3.61 | -3.61 | -8.43 | -5.22 | -0.44 | 12 |
| G8 | 57.33 | 56.33 | 56.67 | 63.00 | 58.33 | 1.74 | 1.16 | -9.88 | -2.33 | 0.38 | 22 |
| G10 | 57.00 | 59.00 | 58.33 | 59.67 | 58.50 | -3.51 | -2.34 | -4.68 | -3.51 | -0.36 | 13 |
| G11 | 55.33 | 57.67 | 59.67 | 59.67 | 58.08 | -4.22 | -7.83 | -7.83 | -6.63 | -0.94 | 5 |
| G12 | 56.67 | 57.67 | 57.33 | 61.00 | 58.17 | -1.76 | -1.18 | -7.65 | -3.53 | -0.10 | 17 |
| G13 | 57.33 | 54.67 | 58.33 | 63.00 | 58.33 | 4.65 | -1.74 | -9.88 | -2.33 | 0.19 | 19 |
| G14 | 54.33 | 57.00 | 59.00 | 58.00 | 57.08 | -4.91 | -8.59 | -6.75 | -6.75 | -1.06 | 4 |
| G15 | 54.33 | 57.67 | 59.00 | 56.33 | 56.83 | -6.13 | -8.59 | -3.68 | -6.13 | -1.16 | 2 |
| G17 | 54.33 | 57.33 | 56.67 | 56.00 | 56.08 | -5.52 | -4.29 | -3.07 | -4.29 | -0.68 | 8 |
| G18 | 54.67 | 57.67 | 59.33 | 58.67 | 57.58 | -5.49 | -8.54 | -7.32 | -7.11 | -1.08 | 3 |
| G22 | 55.00 | 57.00 | 57.33 | 66.33 | 58.92 | -3.64 | -4.24 | -20.61 | -9.49 | -0.31 | 14 |
| G23 | 57.67 | 57.33 | 61.33 | 60.33 | 59.17 | 0.58 | -6.36 | -4.62 | -3.47 | -0.63 | 9 |
| G29 | 54.00 | 54.33 | 58.00 | 52.67 | 54.75 | -0.62 | -7.41 | 2.47 | -1.85 | -0.87 | 7 |
| G30 | 57.33 | 59.00 | 55.67 | 61.67 | 58.42 | -2.91 | 2.91 | -7.56 | -2.52 | 0.31 | 20 |
| G33 | 55.67 | 54.67 | 57.67 | 60.67 | 57.17 | 1.80 | -3.59 | -8.98 | -3.59 | -0.17 | 16 |
| G34 | 57.00 | 57.00 | 56.00 | 62.33 | 58.08 | 0.00 | 1.75 | -9.36 | -2.53 | 0.35 | 21 |
| G35 | 56.33 | 57.00 | 59.67 | 61.00 | 58.50 | -1.18 | -5.92 | -8.28 | -5.13 | -0.59 | 10 |
| G38 | 59.33 | 58.67 | 57.33 | 60.00 | 58.83 | 1.12 | 3.37 | -1.12 | 1.12 | 0.48 | 23 |
| G39 | 60.00 | 58.33 | 60.33 | 61.00 | 59.92 | 2.78 | -0.56 | -1.67 | 0.19 | 0.10 | 18 |
| G43 | 61.67 | 61.33 | 58.67 | 72.00 | 63.42 | 0.54 | 4.86 | -16.76 | -3.78 | 0.92 | 24 |
| G45 | 58.00 | 58.67 | 61.33 | 66.33 | 61.08 | -1.15 | -5.75 | -14.37 | -7.09 | -0.49 | 11 |
| G46 | 56.00 | 57.33 | 62.00 | 58.67 | 58.50 | -2.38 | -10.71 | -4.76 | -5.95 | -1.24 | 1 |
| G48 | 59.67 | 58.33 | 58.67 | 61.00 | 59.42 | 2.23 | 1.68 | -2.23 | 0.56 | 0.35 | 21 |
| G50 | 56.33 | 58.33 | 57.00 | 58.67 | 57.58 | -3.55 | -1.18 | -4.14 | -2.96 | -0.24 | 15 |
| Mean (T) | 56.60 | 57.45 | 58.48 | 60.91 | | | | | | | |

The result showed the negative effect of drought stress on days to first boll split in genotypic dependent manner. Some of the genotypes showed an increase in days to first boll split at moderate drought stress. However, the maximum genotypes showed an increase of days to first boll split under the drought stress. Similar result has been observed in Veesar *et al*. (2020). Pettigrew (2004) observed that the exposed of the bolls, both vertically and horizontally was detrimentally by water stress, with the moisture stressed plants retaining higher number of bolls at bursting and forming lower bolls above node n=11 compared to the control.

#### 4.3.1.5 No. of vegetative branches

Genotype and treatment significantly and their interaction non-significantly affected the no. of vegetative branches. Highest mean no. of vegetative branch (1.92) was observed in T1 drought stress whereas the minimum mean no. of vegetative branches (1.36) was observed in T3 drought stress (Table 48). Among the genotypes, maximum no. of vegetative branches (2.50) was observed in G22, G33, G43 and lowest (0.83) in G46. Based on the genotype stress interaction, maximum no. of vegetative branches (3.00) was observed in G22, G43 under T4 and lowest (0.33) was observed in G46 under T2 and G23 under T3 stress respectively. On the basis of b values, the best performance (lowest b value) was observed in genotype G34 (-0.01) followed by G39 (0.00) and highest in G23 (0.30). With the increase of drought stress, no. of vegetative branch was decreased as shown in linear regression in Figure 58. The minimum reduction% (-33.33%) was observed in G46 under T4 drought stress (Figure 58, Table 48). Maximum reduction% (80.00%) was observed in G23 under T3 stress (Figure 59). The result showed the positive effect of drought stress on no. of vegetative branch in genotypic dependent manner. Some of the genotypes showed a decrease in no. of vegetative branch at moderate drought stress. However, the maximum genotypes showed a decrease of no. of vegetative branch under the drought stress. Similar result has been observed in Veesar *et al*. (2020). Decrease in no. of vegetative branch under drought stress might be due to suppression of cell expansion and cell growth, or due to low turgor pressure (Jaleel *et al*., 2008).

**Table 48. No. of vegetative branches of twenty-five genotypes at different drought treatments**

| Genotype | No. of vegetative branches at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 2.67 | 2.33 | 2.00 | 2.00 | 2.25 | 12.50 | 25.00 | 25.00 | 20.83 | 0.14 | 9 |
| G2 | 2.33 | 1.33 | 1.33 | 1.67 | 1.67 | 42.86 | 42.86 | 28.57 | 38.10 | 0.27 | 16 |
| G8 | 2.33 | 2.67 | 2.00 | 2.33 | 2.33 | -14.29 | 14.29 | 0.00 | 0.00 | 0.04 | 4 |
| G10 | 1.00 | 1.00 | 0.67 | 1.00 | 0.92 | 0.00 | 33.33 | 0.00 | 11.11 | 0.07 | 6 |
| G11 | 2.33 | 1.67 | 1.33 | 2.00 | 1.83 | 28.57 | 42.86 | 14.29 | 28.57 | 0.25 | 15 |
| G12 | 1.33 | 1.67 | 1.00 | 1.00 | 1.25 | -25.00 | 25.00 | 25.00 | 8.33 | 0.03 | 3 |
| G13 | 2.00 | 1.67 | 1.33 | 2.00 | 1.75 | 16.67 | 33.33 | 0.00 | 16.67 | 0.16 | 11 |
| G14 | 1.33 | 1.33 | 1.00 | 1.00 | 1.17 | 0.00 | 25.00 | 25.00 | 16.67 | 0.06 | 5 |
| G15 | 2.00 | 2.00 | 1.00 | 1.67 | 1.67 | 0.00 | 50.00 | 16.67 | 22.22 | 0.19 | 13 |
| G17 | 2.67 | 2.33 | 1.67 | 2.00 | 2.17 | 12.50 | 37.50 | 25.00 | 25.00 | 0.21 | 14 |
| G18 | 2.00 | 2.00 | 1.00 | 1.67 | 1.67 | 0.00 | 50.00 | 16.67 | 22.22 | 0.19 | 13 |
| G22 | 2.33 | 2.67 | 2.00 | 3.00 | 2.50 | -14.29 | 14.29 | -28.57 | -9.52 | 0.06 | 5 |
| G23 | 1.67 | 1.33 | 0.33 | 1.67 | 1.25 | 20.00 | 80.00 | 0.00 | 33.33 | 0.30 | 17 |
| G29 | 2.33 | 2.33 | 2.00 | 2.33 | 2.25 | 0.00 | 14.29 | 0.00 | 4.76 | 0.07 | 6 |
| G30 | 2.33 | 2.67 | 2.00 | 2.00 | 2.25 | -14.29 | 14.29 | 14.29 | 4.76 | 0.03 | 3 |
| G33 | 2.67 | 2.33 | 2.33 | 2.67 | 2.50 | 12.50 | 12.50 | 0.00 | 8.33 | 0.10 | 7 |
| G34 | 1.33 | 1.33 | 1.33 | 1.00 | 1.25 | 0.00 | 0.00 | 25.00 | 8.33 | -0.01 | 1 |
| G35 | 1.67 | 1.33 | 1.33 | 1.67 | 1.50 | 20.00 | 20.00 | 0.00 | 13.33 | 0.10 | 7 |
| G38 | 2.33 | 2.33 | 1.33 | 2.00 | 2.00 | 0.00 | 42.86 | 14.29 | 19.05 | 0.19 | 13 |
| G39 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 2 |
| G43 | 2.67 | 2.33 | 2.00 | 3.00 | 2.50 | 12.50 | 25.00 | -12.50 | 8.33 | 0.17 | 12 |
| G45 | 1.67 | 1.00 | 1.33 | 1.00 | 1.25 | 40.00 | 20.00 | 40.00 | 33.33 | 0.10 | 7 |
| G46 | 1.00 | 0.33 | 0.67 | 1.33 | 0.83 | 66.67 | 33.33 | -33.33 | 22.22 | 0.13 | 8 |
| G48 | 1.33 | 1.67 | 1.00 | 1.33 | 1.33 | -25.00 | 25.00 | 0.00 | 0.00 | 0.04 | 4 |
| G50 | 1.67 | 1.33 | 1.00 | 1.33 | 1.33 | 20.00 | 40.00 | 20.00 | 26.67 | 0.15 | 10 |
| Mean (T) | 1.92 | 1.76 | 1.36 | 1.75 | | | | | | | |

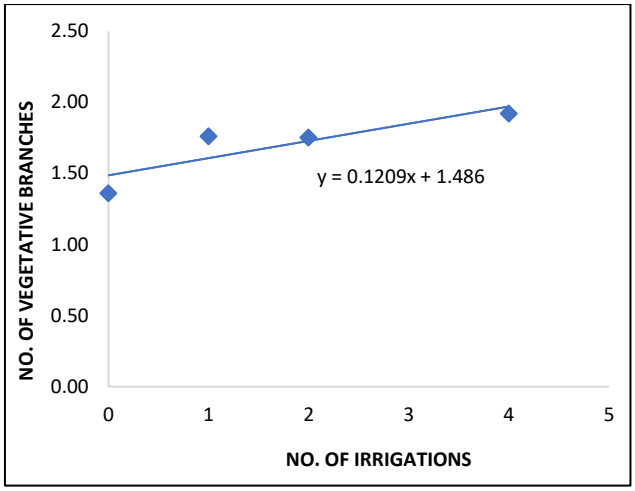



**Figure 58. Relationships between no. of vegetative branches of cotton genotypes and different drought stresses**

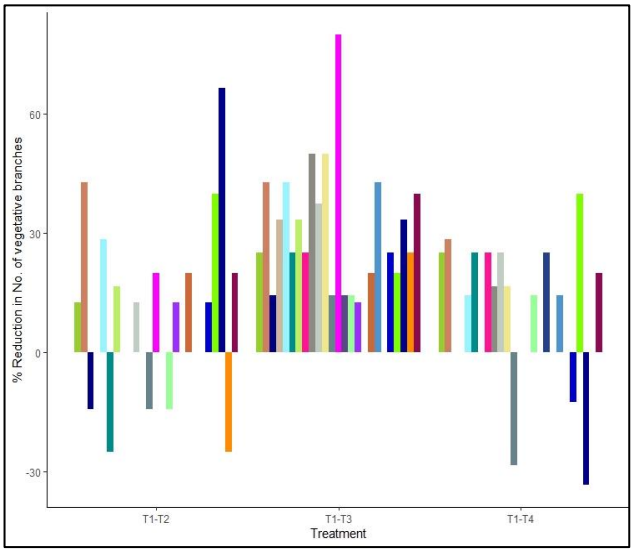
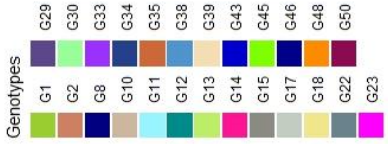



**Figure 59. Reduction percentage of no. of vegetative branches of twenty-five cotton genotypes under different drought stresses compared with control**



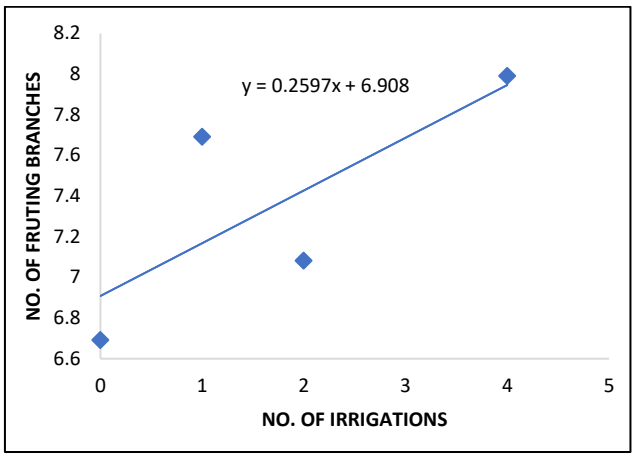




**Figure 60. Relationships between no. of fruiting branches of cotton genotypes and different drought stresses**

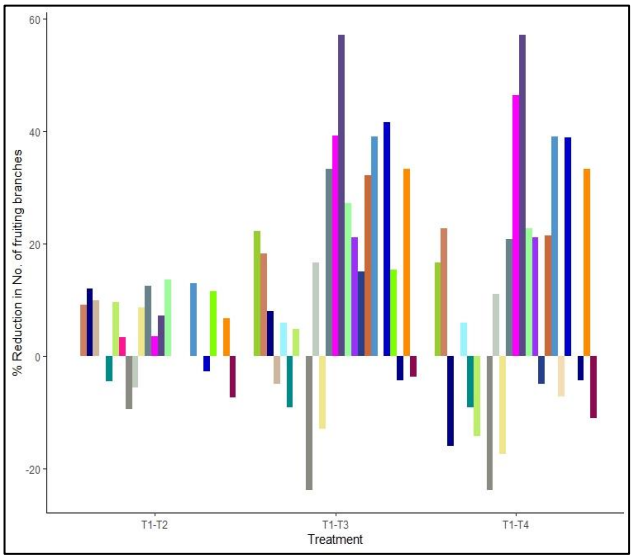



**Figure 61. Reduction percentage of no. of fruiting branches of twenty-five cotton genotypes under different drought stresses compared with control**

#### 4.3.1.6 No. of fruiting branches

Genotype, treatment and their interaction significantly affected the no. of fruiting branches. The highest mean no. of fruiting branches (7.99) was observed in T1 drought stress whereas the lowest no. of fruiting branches (6.69) was observed in T3 drought stress (Table 49). Among the genotypes, highest no. of fruiting branches (9.92) was observed in G14 and lowest (5.42) in G1. Based on the genotype stress interaction, highest no. of fruiting branches (12.33) and lowest (4.00) was observed in G43 under T2 and G29 under T3 and T4 stress respectively. On the basis of b values, the best performance (highest b value) was observed in genotype G29 (0.97) followed by G43 (0.84) and lowest in G15 (-0.34). With the increase of drought stress, no. of fruiting branches was decreased as shown in linear regression in Figure 60. The minimum reduction% (-23.81%) was observed in G15 under T3 and T4 drought stress (Figure 61, Table 49). Maximum reduction% (57.14%) was observed in G29 under T3 and T4 stress (Figure 61). The result showed the negative effect of drought stress on no. of fruiting branches in genotypic dependent manner. Some of the genotypes showed a decrease in no. of fruiting branches at moderate drought stress. However, the maximum genotypes showed a decrease of no. of fruiting branches under the severe drought stress. Similar result has been observed in Veesar *et al*. (2020). Decrease in no. of fruiting branches under drought stress might be due to suppression of cell expansion and cell growth, or due to low turgor pressure (Liu *et al*., 2004).

#### 4.3.1.7 No. of bolls per plant

Genotype, treatment and their interaction significantly affected the no. of bolls per plant. The highest mean no. of bolls per plant (35.16) was observed in T1 drought stress whereas the lowest mean no. of bolls per plant (28.80) was observed in T3 drought stress (Table 50). Among the genotypes, highest no. of bolls per plant (41.08) was observed in G43 and lowest (24.00) in G1. Based on the genotype stress interaction, highest no. of bolls per plant (51.00) and lowest (19.67) was observed in G43 under T1 and G1, G29 under T3 stress respectively. On the basis of b values, the best performance (highest b value) was observed in genotype G43 (3.67) followed by G29 (3.66) and lowest in G18 (-0.53). With the increase of drought stress, no. of bolls per plant was decreased as shown in linear regression in Figure 62. The minimum reduction% (-15.46%) was observed in G15 under T4 drought stress (Figure 63, Table

**Table 49. No. of fruiting branches of twenty-five genotypes at different drought treatments**

| Genotype | No. of fruiting branches at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 6.00 | 6.00 | 4.67 | 5.00 | 5.42 | 0.00 | 22.22 | 16.67 | 12.96 | 0.24 | 12 |
| G2 | 7.33 | 6.67 | 6.00 | 5.67 | 6.42 | 9.09 | 18.18 | 22.73 | 16.67 | 0.28 | 10 |
| G8 | 8.33 | 7.33 | 7.67 | 9.67 | 8.25 | 12.00 | 8.00 | -16.00 | 1.33 | 0.26 | 11 |
| G10 | 6.67 | 6.00 | 7.00 | 6.67 | 6.58 | 10.00 | -5.00 | 0.00 | 1.67 | -0.01 | 19 |
| G11 | 5.67 | 5.67 | 5.33 | 5.33 | 5.50 | 0.00 | 5.88 | 5.88 | 3.92 | 0.06 | 16 |
| G12 | 7.33 | 7.67 | 8.00 | 8.00 | 7.75 | -4.55 | -9.09 | -9.09 | -7.58 | -0.14 | 22 |
| G13 | 7.00 | 6.33 | 6.67 | 8.00 | 7.00 | 9.52 | 4.76 | -14.29 | 0.00 | 0.15 | 15 |
| G14 | 10.00 | 9.67 | 10.00 | 10.00 | 9.92 | 3.33 | 0.00 | 0.00 | 1.11 | 0.03 | 17 |
| G15 | 7.00 | 7.67 | 8.67 | 8.67 | 8.00 | -9.52 | -23.81 | -23.81 | -19.05 | -0.34 | 23 |
| G17 | 6.00 | 6.33 | 5.00 | 5.33 | 5.67 | -5.56 | 16.67 | 11.11 | 7.41 | 0.15 | 15 |
| G18 | 7.67 | 7.00 | 8.67 | 9.00 | 8.08 | 8.70 | -13.04 | -17.39 | -7.25 | -0.10 | 21 |
| G22 | 8.00 | 7.00 | 5.33 | 6.33 | 6.67 | 12.50 | 33.33 | 20.83 | 22.22 | 0.57 | 6 |
| G23 | 9.33 | 9.00 | 5.67 | 5.00 | 7.25 | 3.57 | 39.29 | 46.43 | 29.76 | 0.64 | 3 |
| G29 | 9.33 | 8.67 | 4.00 | 4.00 | 6.50 | 7.14 | 57.14 | 57.14 | 40.48 | 0.97 | 1 |
| G30 | 7.33 | 6.33 | 5.33 | 5.67 | 6.17 | 13.64 | 27.27 | 22.73 | 21.21 | 0.44 | 8 |
| G33 | 6.33 | 6.33 | 5.00 | 5.00 | 5.67 | 0.00 | 21.05 | 21.05 | 14.04 | 0.23 | 13 |
| G34 | 6.67 | 6.67 | 5.67 | 7.00 | 6.50 | 0.00 | 15.00 | -5.00 | 3.33 | 0.21 | 14 |
| G35 | 9.33 | 9.33 | 6.33 | 7.33 | 8.08 | 0.00 | 32.14 | 21.43 | 17.86 | 0.54 | 7 |
| G38 | 7.67 | 6.67 | 4.67 | 4.67 | 5.92 | 13.04 | 39.13 | 39.13 | 30.43 | 0.60 | 5 |
| G39 | 9.33 | 9.33 | 9.33 | 10.00 | 9.50 | 0.00 | 0.00 | -7.14 | -2.38 | 0.02 | 18 |
| G43 | 12.00 | 12.33 | 7.00 | 7.33 | 9.67 | -2.78 | 41.67 | 38.89 | 25.93 | 0.84 | 2 |
| G45 | 8.67 | 7.67 | 7.33 | 8.67 | 8.08 | 11.54 | 15.38 | 0.00 | 8.97 | 0.35 | 9 |
| G46 | 7.67 | 7.67 | 8.00 | 8.00 | 7.83 | 0.00 | -4.35 | -4.35 | -2.90 | -0.06 | 20 |
| G48 | 10.00 | 9.33 | 6.67 | 6.67 | 8.17 | 6.67 | 33.33 | 33.33 | 24.44 | 0.63 | 4 |
| G50 | 9.00 | 9.67 | 9.33 | 10.00 | 9.50 | -7.41 | -3.70 | -11.11 | -7.41 | -0.10 | 21 |
| Mean (T) | 7.99 | 7.69 | 6.69 | 7.08 | | | | | | | |

**Table 50. No. of bolls per plant of twenty-five genotypes at different drought treatments**

| Genotype | No. of bolls per plant at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 27.67 | 26.33 | 19.67 | 22.33 | 24.00 | 4.82 | 28.92 | 19.28 | 17.67 | 1.56 | 9.00 |
| G2 | 30.33 | 28.67 | 25.67 | 25.33 | 27.50 | 5.49 | 15.38 | 16.48 | 12.45 | 0.93 | 13.00 |
| G8 | 37.33 | 34.00 | 35.33 | 41.33 | 37.00 | 8.93 | 5.36 | -10.71 | 1.19 | 0.80 | 16.00 |
| G10 | 29.67 | 27.33 | 28.33 | 29.67 | 28.75 | 7.87 | 4.49 | 0.00 | 4.12 | 0.47 | 20.00 |
| G11 | 27.67 | 26.67 | 23.33 | 26.33 | 26.00 | 3.61 | 15.66 | 4.82 | 8.03 | 0.91 | 14.00 |
| G12 | 33.67 | 33.33 | 33.33 | 33.67 | 33.50 | 0.99 | 0.99 | 0.00 | 0.66 | 0.10 | 23.00 |
| G13 | 30.00 | 28.33 | 28.67 | 33.67 | 30.17 | 5.56 | 4.44 | -12.22 | -0.74 | 0.51 | 19.00 |
| G14 | 42.67 | 39.67 | 40.00 | 40.33 | 40.67 | 7.03 | 6.25 | 5.47 | 6.25 | 0.72 | 17.00 |
| G15 | 32.33 | 31.67 | 35.67 | 37.33 | 34.25 | 2.06 | -10.31 | -15.46 | -7.90 | -0.47 | 24.00 |
| G17 | 28.67 | 27.67 | 22.33 | 25.33 | 26.00 | 3.49 | 22.09 | 11.63 | 12.40 | 1.26 | 11.00 |
| G18 | 34.33 | 32.00 | 38.67 | 39.00 | 36.00 | 6.80 | -12.62 | -13.59 | -6.47 | -0.53 | 25.00 |
| G22 | 36.00 | 32.00 | 25.33 | 30.33 | 30.92 | 11.11 | 29.63 | 15.74 | 18.83 | 2.31 | 6.00 |
| G23 | 39.67 | 38.67 | 20.33 | 21.67 | 30.08 | 2.52 | 48.74 | 45.38 | 32.21 | 3.44 | 3.00 |
| G29 | 39.67 | 37.67 | 19.67 | 21.67 | 29.67 | 5.04 | 50.42 | 45.38 | 33.61 | 3.66 | 2.00 |
| G30 | 33.67 | 29.33 | 25.33 | 26.33 | 28.67 | 12.87 | 24.75 | 21.78 | 19.80 | 1.83 | 8.00 |
| G33 | 29.33 | 28.33 | 23.67 | 25.33 | 26.67 | 3.41 | 19.32 | 13.64 | 12.12 | 1.10 | 12.00 |
| G34 | 28.33 | 28.33 | 25.67 | 29.00 | 27.83 | 0.00 | 9.41 | -2.35 | 2.35 | 0.55 | 18.00 |
| G35 | 39.67 | 38.67 | 26.33 | 30.67 | 33.83 | 2.52 | 33.61 | 22.69 | 19.61 | 2.50 | 5.00 |
| G38 | 35.33 | 31.33 | 20.33 | 22.33 | 27.33 | 11.32 | 42.45 | 36.79 | 30.19 | 2.97 | 4.00 |
| G39 | 39.33 | 38.67 | 38.33 | 40.33 | 39.17 | 1.69 | 2.54 | -2.54 | 0.56 | 0.29 | 21.00 |
| G43 | 51.00 | 48.33 | 31.33 | 33.67 | 41.08 | 5.23 | 38.56 | 33.99 | 25.93 | 3.67 | 1.00 |
| G45 | 38.33 | 33.67 | 32.67 | 37.67 | 35.58 | 12.17 | 14.78 | 1.74 | 9.57 | 1.51 | 10.00 |
| G46 | 33.33 | 29.67 | 31.00 | 35.33 | 32.33 | 11.00 | 7.00 | -6.00 | 4.00 | 0.84 | 15.00 |
| G48 | 41.67 | 39.67 | 30.33 | 29.67 | 35.33 | 4.80 | 27.20 | 28.80 | 20.27 | 2.10 | 7.00 |
| G50 | 39.33 | 40.00 | 38.67 | 42.33 | 40.08 | -1.69 | 1.69 | -7.63 | -2.54 | 0.16 | 22.00 |
| Mean (T) | 35.16 | 33.20 | 28.80 | 31.23 | | | | | | | |

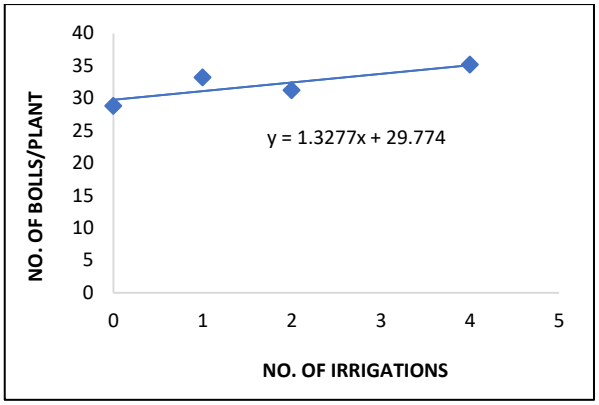



**Figure 62. Relationships between no. of bolls/plant of cotton genotypes and different drought stresses**

.

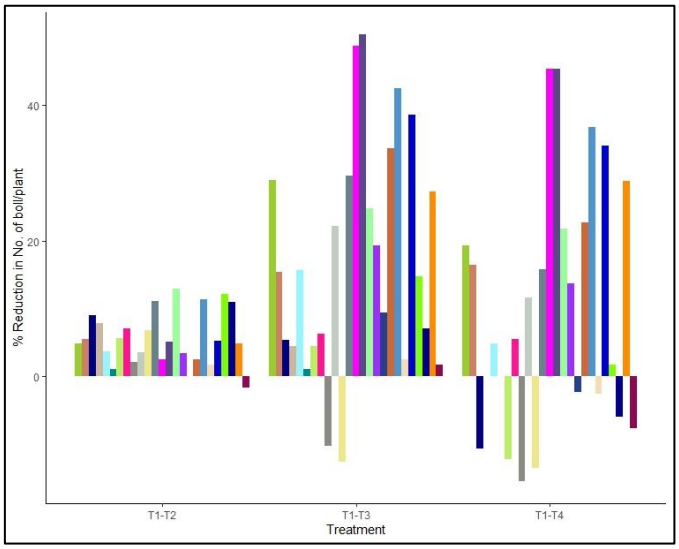
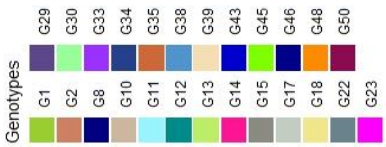



**Figure 63. Reduction percentage of no. of bolls/plant of twenty-five cotton genotypes under different drought stresses compared with control**



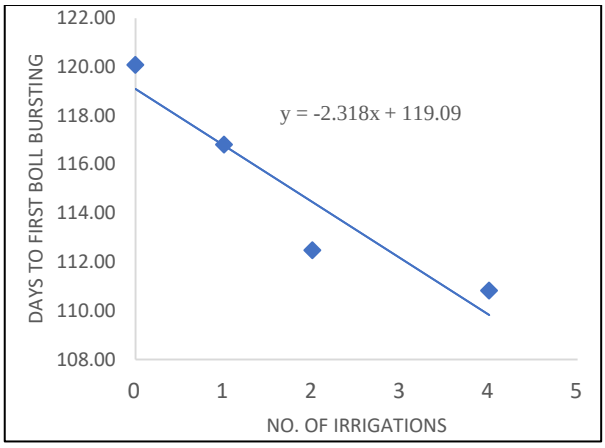




**Figure 64. Relationships between days to1st boll bursting of cotton genotypes and different drought stresses**

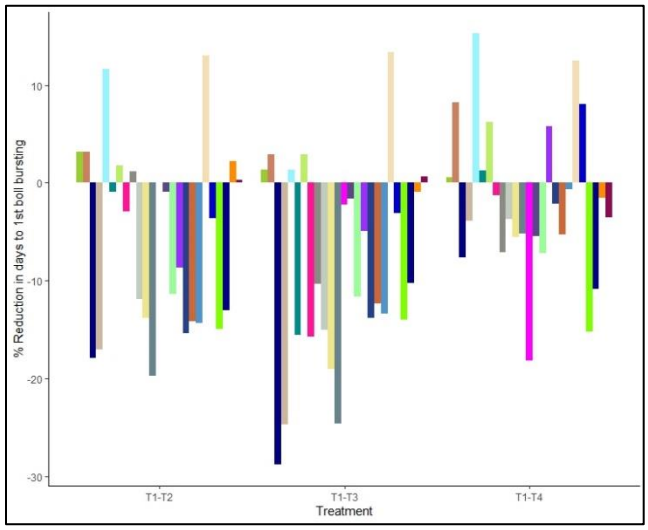



**Figure 65. Reduction percentage of days to 1st boll bursting of twenty-five cotton genotypes under different drought stresses compared with control**

50). Maximum reduction% (50.42%) was observed in G29 under T3 stress (Figure 63). The result showed the negative effect of drought stress on no. of bolls per plant in genotypic dependent manner. Some of the genotypes showed a decrease in no. of bolls per plant at moderate drought stress. However, the maximum genotypes showed a decrease of no. of bolls per plant under the severe drought stress. Similar result has been observed in Bakhsh *et al*. (2019). The reduction in yields could be mainly due to the decrease in lint index, boll weight and seed index rather than a decrease in bolls/plant.

#### 4.3.1.8 Days to first boll bursting

Genotype, treatment and their interaction significantly affected the days to first boll bursting. Maximum mean days to first boll bursting (120.07) was observed in T3 drought stress whereas the minimum mean days to first boll bursting (110.81) was observed in T1 drought stress (Table 51). Among the genotypes, maximum days to first boll bursting (123.42) were observed in G1 and lowest (103.33) in G50. Based on the genotype stress interaction, maximum days to first boll bursting (134.33) and lowest (102.00) was observed in G8 under T3 and G50 under T3 stress respectively. On the basis of b values, the best performance was observed in genotype G8 (-7.37) followed by G22 (-6.66) and highest in G39 (4.20). With the increase of drought stress, days to first boll bursting was increased as shown in linear regression in Figure 64. The minimum reduction% (-28.75%) was observed in G8 under T3 drought stress (Figure 64, Table 51). Maximum reduction% (15.26%) was observed in G11 under T4 stress (Figure 65). The result showed the negative effect of drought stress on days to first boll bursting in genotypic dependent manner. Some of the genotypes showed an increase in days to first boll bursting at moderate drought stress. However, the maximum genotypes showed an increase of days to first boll bursting under the drought stress. Similar result has been observed in Veesar *et al*. (2020).

#### 4.3.1.9 Single boll weight

Genotype, treatment and their interaction significantly affected the single boll weight. The maximum mean single boll weight (5.38 g) was observed in T4 drought stress whereas the minimum mean single boll weight (5.11 g) was observed in T1 drought stress (Table 52). Among the genotypes, maximum single boll weight (5.90 gm) was observed in G12 and minimum (4.57 gm) in G50. Based on the genotype stress

**Table 51. Days to first boll bursting of twenty-five genotypes at different drought treatments**

| Genotype | Days to first boll bursting at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 125.00 | 121.00 | 123.33 | 124.33 | 123.42 | 3.20 | 1.33 | 0.53 | 1.69 | 0.66 | 22 |
| G2 | 126.33 | 122.33 | 122.67 | 116.00 | 121.83 | 3.17 | 2.90 | 8.18 | 4.75 | 0.78 | 23 |
| G8 | 104.33 | 123.00 | 134.33 | 112.33 | 118.50 | -17.89 | -28.75 | -7.67 | -18.10 | -7.37 | 1 |
| G10 | 104.00 | 121.67 | 129.67 | 108.00 | 115.83 | -16.99 | -24.68 | -3.85 | -15.17 | -6.53 | 3 |
| G11 | 126.67 | 112.00 | 125.00 | 107.33 | 117.75 | 11.58 | 1.32 | 15.26 | 9.39 | 1.04 | 24 |
| G12 | 105.00 | 106.00 | 121.33 | 103.67 | 109.00 | -0.95 | -15.56 | 1.27 | -5.08 | -3.39 | 12 |
| G13 | 113.00 | 111.00 | 109.67 | 106.00 | 109.92 | 1.77 | 2.95 | 6.19 | 3.64 | 0.64 | 21 |
| G14 | 104.00 | 107.00 | 120.33 | 105.33 | 109.17 | -2.88 | -15.71 | -1.28 | -6.62 | -3.49 | 10 |
| G15 | 113.00 | 111.67 | 124.67 | 121.00 | 117.58 | 1.18 | -10.32 | -7.08 | -5.41 | -1.99 | 15 |
| G17 | 109.00 | 122.00 | 125.33 | 113.00 | 117.33 | -11.93 | -14.98 | -3.67 | -10.19 | -4.27 | 6 |
| G18 | 108.67 | 123.67 | 129.33 | 114.67 | 119.08 | -13.80 | -19.02 | -5.52 | -12.78 | -5.25 | 4 |
| G22 | 103.00 | 123.33 | 128.33 | 108.33 | 115.75 | -19.74 | -24.60 | -5.18 | -16.50 | -6.66 | 2 |
| G23 | 104.67 | 104.67 | 107.00 | 123.67 | 110.00 | 0.00 | -2.23 | -18.15 | -6.79 | 0.08 | 19 |
| G29 | 104.67 | 105.67 | 106.33 | 110.33 | 106.75 | -0.96 | -1.59 | -5.41 | -2.65 | -0.26 | 17 |
| G30 | 111.67 | 124.33 | 124.67 | 119.67 | 120.08 | -11.34 | -11.64 | -7.16 | -10.05 | -3.46 | 11 |
| G33 | 115.00 | 125.00 | 120.67 | 108.33 | 117.25 | -8.70 | -4.93 | 5.80 | -2.61 | -2.18 | 14 |
| G34 | 108.33 | 125.00 | 123.33 | 110.67 | 116.83 | -15.38 | -13.85 | -2.15 | -10.46 | -4.36 | 5 |
| G35 | 108.00 | 123.33 | 121.33 | 113.67 | 116.58 | -14.20 | -12.35 | -5.25 | -10.60 | -3.82 | 9 |
| G38 | 107.00 | 122.33 | 121.33 | 107.67 | 114.58 | -14.33 | -13.40 | -0.62 | -9.45 | -4.16 | 7 |
| G39 | 122.67 | 106.67 | 106.33 | 107.33 | 110.75 | 13.04 | 13.32 | 12.50 | 12.95 | 4.20 | 25 |
| G43 | 120.00 | 124.33 | 123.67 | 110.33 | 119.58 | -3.61 | -3.06 | 8.06 | 0.46 | -1.38 | 16 |
| G45 | 107.33 | 123.33 | 122.33 | 123.67 | 119.17 | -14.91 | -13.98 | -15.22 | -14.70 | -3.90 | 8 |
| G46 | 110.33 | 124.67 | 121.67 | 122.33 | 119.75 | -12.99 | -10.27 | -10.88 | -11.38 | -3.15 | 13 |
| G48 | 106.00 | 103.67 | 107.00 | 107.67 | 106.08 | 2.20 | -0.94 | -1.57 | -0.10 | 0.05 | 18 |
| G50 | 102.67 | 102.33 | 102.00 | 106.33 | 103.33 | 0.32 | 0.65 | -3.57 | -0.87 | 0.27 | 20 |
| Mean (T) | 110.81 | 116.80 | 120.07 | 112.47 | | | | | | | |

**Table 52. Single boll weight of twenty-five genotypes at different drought treatments**

| Genotype | Single boll weight (gm) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 4.85 | 4.71 | 5.74 | 4.78 | 5.02 | 2.82 | -18.43 | 1.38 | -4.75 | -0.17 | 18 |
| G2 | 5.20 | 5.74 | 5.72 | 5.41 | 5.52 | -10.25 | -9.99 | -4.04 | -8.09 | -0.14 | 17 |
| G8 | 5.16 | 5.02 | 5.27 | 5.87 | 5.33 | 2.84 | -2.00 | -13.69 | -4.28 | 0.01 | 9 |
| G10 | 5.34 | 5.17 | 5.44 | 6.21 | 5.54 | 3.24 | -1.87 | -16.28 | -4.97 | 0.02 | 8 |
| G11 | 4.95 | 4.82 | 5.88 | 6.23 | 5.47 | 2.56 | -18.80 | -25.88 | -14.04 | -0.14 | 17 |
| G12 | 5.86 | 5.66 | 6.23 | 5.85 | 5.90 | 3.47 | -6.26 | 0.23 | -0.85 | -0.06 | 13 |
| G13 | 5.66 | 4.70 | 4.91 | 4.86 | 5.03 | 16.85 | 13.20 | 14.14 | 14.73 | 0.21 | 2 |
| G14 | 4.69 | 5.37 | 5.21 | 6.27 | 5.39 | -14.65 | -11.10 | -33.85 | -19.87 | -0.12 | 15 |
| G15 | 4.77 | 5.40 | 5.38 | 6.41 | 5.49 | -13.20 | -12.64 | -34.29 | -20.04 | -0.13 | 16 |
| G17 | 5.42 | 5.33 | 5.19 | 5.59 | 5.38 | 1.66 | 4.18 | -3.14 | 0.90 | 0.06 | 7 |
| G18 | 4.87 | 5.27 | 5.23 | 5.36 | 5.18 | -8.15 | -7.32 | -9.99 | -8.49 | -0.09 | 14 |
| G22 | 5.22 | 4.96 | 5.58 | 5.71 | 5.37 | 4.86 | -6.90 | -9.39 | -3.81 | -0.04 | 12 |
| G23 | 4.28 | 4.40 | 5.80 | 4.46 | 4.73 | -2.65 | -35.33 | -4.12 | -14.03 | -0.31 | 21 |
| G29 | 5.15 | 4.83 | 5.19 | 4.66 | 4.96 | 6.09 | -0.91 | 9.46 | 4.88 | 0.00 | 10 |
| G30 | 4.77 | 5.83 | 5.29 | 5.36 | 5.31 | -22.29 | -10.83 | -12.44 | -15.19 | -0.18 | 19 |
| G33 | 6.02 | 4.84 | 4.35 | 4.19 | 4.85 | 19.65 | 27.84 | 30.49 | 25.99 | 0.38 | 1 |
| G34 | 5.23 | 5.34 | 4.21 | 4.77 | 4.89 | -2.04 | 19.62 | 8.92 | 8.83 | 0.18 | 3 |
| G35 | 5.34 | 4.42 | 6.47 | 6.11 | 5.59 | 17.34 | -21.15 | -14.35 | -6.05 | -0.12 | 15 |
| G38 | 4.15 | 4.72 | 6.08 | 4.23 | 4.79 | -13.65 | -46.43 | -2.01 | -20.70 | -0.43 | 22 |
| G39 | 4.96 | 5.87 | 5.29 | 6.68 | 5.70 | -18.20 | -6.51 | -34.59 | -19.77 | -0.09 | 14 |
| G43 | 5.59 | 5.77 | 4.71 | 5.97 | 5.51 | -3.22 | 15.85 | -6.79 | 1.95 | 0.17 | 4 |
| G45 | 5.07 | 6.54 | 6.06 | 5.81 | 5.87 | -28.91 | -19.45 | -14.45 | -20.94 | -0.30 | 20 |
| G46 | 5.17 | 5.35 | 5.21 | 5.30 | 5.26 | -3.42 | -0.77 | -2.45 | -2.21 | -0.02 | 11 |
| G48 | 5.14 | 5.37 | 4.45 | 4.20 | 4.79 | -4.54 | 13.49 | 18.22 | 9.06 | 0.09 | 6 |
| G50 | 4.96 | 4.95 | 4.25 | 4.10 | 4.57 | 0.34 | 14.30 | 17.33 | 10.66 | 0.12 | 5 |
| Mean (T) | 5.11 | 5.21 | 5.32 | 5.38 | | | | | | | |

interaction, maximum single boll weight (6.68 gm) and minimum (4.10 gm) was observed in G39 under T4 and G50 under T4 stress, respectively. Based on b values, the best performance was observed in genotype G33 (0.38) followed by G13 (0.21) and lowest in G38 (-0.43). With the increase of drought stress, single boll weight was increased as shown in linear regression in Figure 66. The minimum reduction% (-46.43%) was observed in G38 under T3 drought stress (Figure 66, Table 52). Maximum reduction% (30.49%) was observed in G33 under T4 stress (Figure 67). The result showed the positive effect of drought stress on single boll weight in genotypic dependent manner. Some of the genotypes showed an increase in single boll weight at moderate drought stress. However, the maximum genotypes showed an increase of single boll weight under the moderate drought stress. Similar result has been observed in Yagmur *et al*. (2014). They observed that a drought stress increased, values of traits including plant height, boll number, seed cotton yield, and 100-seed weight decreased in spite of increasing boll weight, first harvest ratio, and ginning percentage.

#### 4.3.1.10 Ginning out turn

Genotype, treatment and their interaction significantly affected the ginning out turn. The maximum mean ginning out turn (40.36%) was observed in T3 drought stress whereas the minimum mean ginning out turn (38.35%) was observed in T4 drought stress (Table 53). Among the genotypes, maximum ginning out turn (43.32%) was observed in G30 and minimum (34.31%) in G35. Based on the genotype stress interaction, maximum ginning out turn (45.81%) and minimum (32.23%) was observed in G29 under T3 and G2 under T4 stress respectively. Based on b values, the best performance was observed in genotype G33 (1.85) followed by G11 (1.54) and lowest in G23 (-1.52). With the increase of drought stress, ginning out turn was increased at severe condition and at moderate condition ginning out turn was decreased as shown in linear regression in Figure 68. The minimum reduction% (-15.30%) was observed in G23 under T3 drought stress (Figure 68, Table 53). Maximum reduction% (22.90%) was observed in G2 under T4 stress (Figure 69). The result showed the positive effect of drought stress on ginning out turn in genotypic dependent manner. Some of the genotypes showed a decrease in ginning out turn at moderate drought stress. However, the maximum genotypes showed an increase of ginning out turn under the severe drought stress. Similar result has been observed in

**Table 53. Ginning out turn (GOT) of twenty-five genotypes at different drought treatments**

| Genotype | GOT (%) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 37.40 | 36.51 | 39.21 | 38.15 | 37.82 | 2.36 | -4.85 | -2.01 | -1.50 | -0.27 | 13 |
| G2 | 41.81 | 42.41 | 39.14 | 32.23 | 38.90 | -1.44 | 6.38 | 22.90 | 9.28 | 0.21 | 7 |
| G8 | 39.55 | 40.72 | 39.61 | 41.42 | 40.33 | -2.96 | -0.14 | -4.71 | -2.60 | -0.06 | 10 |
| G10 | 37.95 | 39.92 | 40.55 | 34.81 | 38.31 | -5.19 | -6.83 | 8.28 | -1.25 | -0.78 | 18 |
| G11 | 42.25 | 38.41 | 35.14 | 34.82 | 37.66 | 9.09 | 16.83 | 17.59 | 14.50 | 1.54 | 2 |
| G12 | 37.61 | 42.39 | 40.43 | 37.75 | 39.55 | -12.72 | -7.49 | -0.38 | -6.86 | -0.97 | 21 |
| G13 | 39.45 | 38.07 | 44.61 | 38.52 | 40.16 | 3.51 | -13.08 | 2.37 | -2.40 | -0.94 | 20 |
| G14 | 40.32 | 38.26 | 40.24 | 36.54 | 38.84 | 5.11 | 0.19 | 9.38 | 4.89 | 0.08 | 9 |
| G15 | 37.57 | 39.31 | 37.74 | 40.71 | 38.83 | -4.61 | -0.43 | -8.36 | -4.47 | -0.09 | 11 |
| G17 | 38.94 | 39.73 | 42.94 | 40.37 | 40.50 | -2.03 | -10.27 | -3.67 | -5.32 | -0.83 | 19 |
| G18 | 41.03 | 38.07 | 39.87 | 35.79 | 38.69 | 7.20 | 2.81 | 12.76 | 7.59 | 0.33 | 6 |
| G22 | 42.54 | 42.78 | 41.21 | 40.78 | 41.83 | -0.57 | 3.12 | 4.14 | 2.23 | 0.19 | 8 |
| G23 | 39.49 | 42.29 | 45.53 | 37.04 | 41.09 | -7.08 | -15.30 | 6.20 | -5.39 | -1.52 | 23 |
| G29 | 43.89 | 43.20 | 45.81 | 40.05 | 43.24 | 1.59 | -4.37 | 8.75 | 1.99 | -0.43 | 17 |
| G30 | 45.70 | 42.27 | 42.94 | 42.38 | 43.32 | 7.51 | 6.03 | 7.25 | 6.93 | 0.75 | 4 |
| G33 | 45.56 | 39.94 | 37.90 | 39.93 | 40.83 | 12.33 | 16.83 | 12.36 | 13.84 | 1.85 | 1 |
| G34 | 37.93 | 36.21 | 40.43 | 37.39 | 37.99 | 4.54 | -6.59 | 1.42 | -0.21 | -0.37 | 16 |
| G35 | 33.90 | 36.78 | 33.79 | 32.79 | 34.31 | -8.51 | 0.32 | 3.25 | -1.64 | -0.26 | 12 |
| G38 | 37.84 | 40.50 | 38.62 | 38.98 | 38.99 | -7.02 | -2.04 | -3.00 | -4.02 | -0.35 | 15 |
| G39 | 38.35 | 38.64 | 38.62 | 37.90 | 38.38 | -0.76 | -0.70 | 1.16 | -0.10 | -0.09 | 11 |
| G43 | 39.45 | 35.43 | 38.72 | 37.58 | 37.80 | 10.20 | 1.85 | 4.73 | 5.59 | 0.44 | 5 |
| G45 | 41.52 | 37.26 | 37.98 | 41.80 | 39.64 | 10.26 | 8.52 | -0.67 | 6.03 | 1.08 | 3 |
| G46 | 39.13 | 41.82 | 44.39 | 41.73 | 41.77 | -6.87 | -13.44 | -6.63 | -8.98 | -1.21 | 22 |
| G48 | 42.38 | 44.98 | 41.97 | 35.68 | 41.25 | -6.15 | 0.95 | 15.79 | 3.53 | -0.33 | 14 |
| G50 | 40.38 | 42.80 | 41.53 | 43.47 | 42.05 | -5.99 | -2.85 | -7.65 | -5.50 | -0.35 | 15 |
| Mean (T) | 40.08 | 39.95 | 40.36 | 38.35 | | | | | | | |

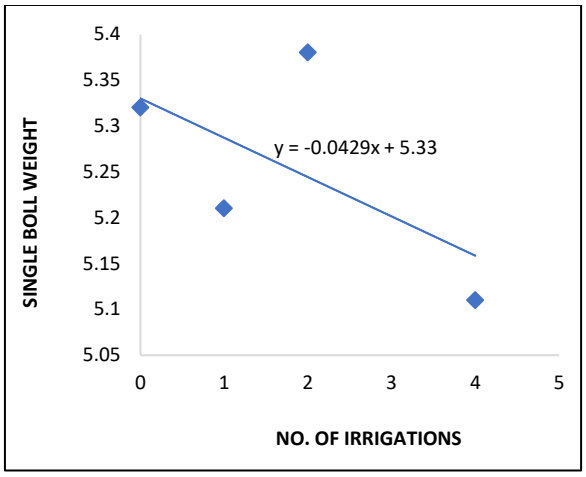



**Figure 66. Relationships between single boll weight of cotton genotypes and different drought stresses**

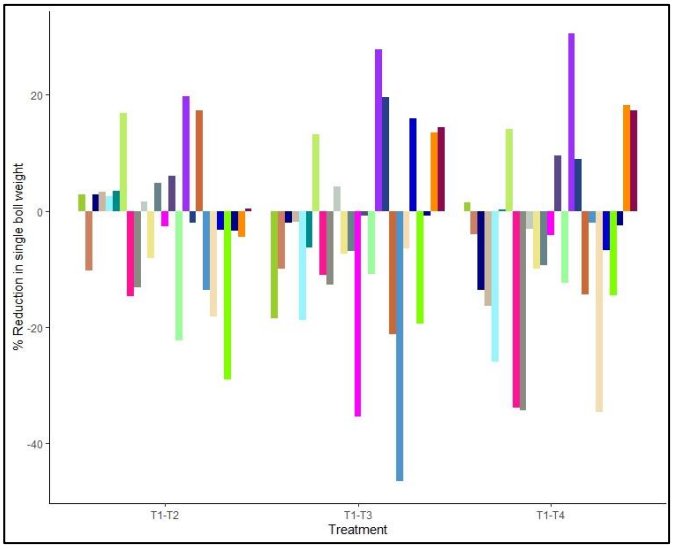



**Figure 67. Reduction percentage of singe boll weight of twenty-five cotton genotypes under different drought stresses compared with control**

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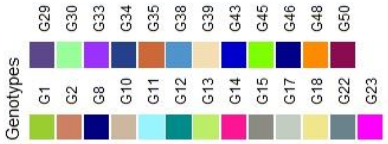


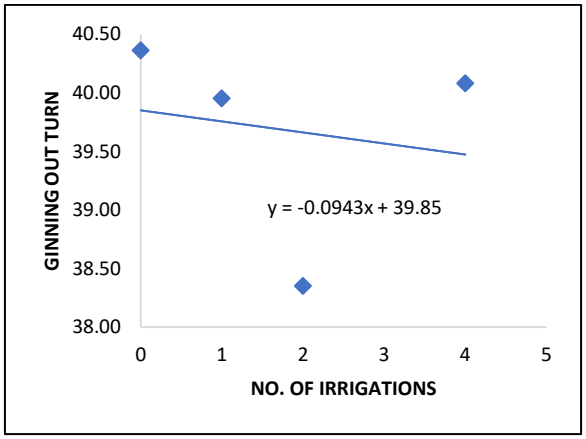




**Figure 68. Relationships between Ginning Out Turn of cotton genotypes and different drought stresses**

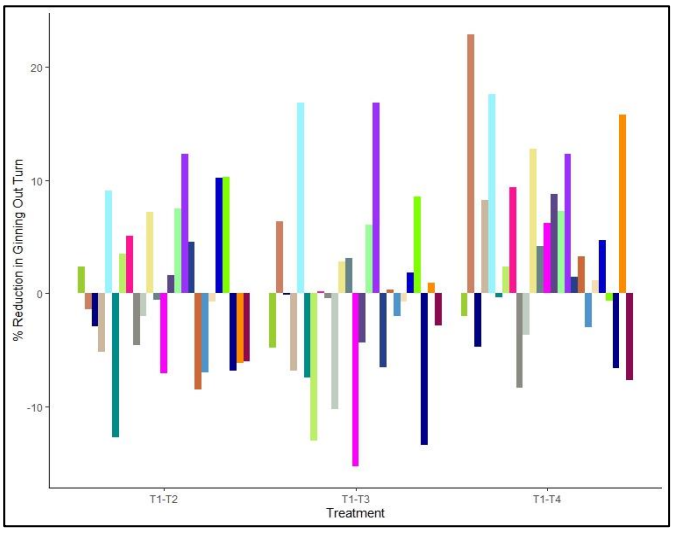



**Figure 69. Reduction percentage of Ginning Out Turn of twenty-five cotton genotypes under different drought stresses compared with control**

Yagmur *et al*. (2014). Ahmad *et al*. (2009) indicated that all three kinds of gene effects (additive, dominance & interactions) were involved in the inheritance of the studied traits.

#### 4.3.1.11 Seed index

Genotype, treatment and their interaction significantly affected the seed index. The maximum mean seed index (8.59) was observed in T4 drought stress whereas the minimum seed index (8.02) was observed in T1 drought stress (Table 54). Among the genotypes, maximum seed index (10.03) was observed in G39 and minimum (7.09) in G50. Based on the genotype stress interaction, maximum seed index (13.77) and minimum (5.47) was observed in G39 under T4 and G50 under T4 stress, respectively. Based on b values, the best performance was observed in genotype G33 and G13 (0.61) followed by G43 (0.34) and lowest in G38 (-0.83). With the increase of drought stress, seed index was highest at moderate condition and at severe condition seed index was increased as shown in linear regression in Figure 70. The minimum reduction% (-79.75%) was observed in G14 under T4 drought stress (Figure 70, Table 54). Maximum reduction% (37.11%) was observed in G13 under T2 stress (Figure 71). The result showed the positive effect of drought stress on seed index in genotypic dependent manner. Some of the genotypes showed an increase in seed index at moderate drought stress. However, the maximum genotypes showed an increase of seed index under the severe drought stress. Kamaran *et al*. (2016) observed that seed yield was showed harmful effects of drought stress as compared with those assessed in non-stressed condition.

#### 4.3.1.12 Lint index

Genotype, treatment and their interaction significantly affected the lint index. The maximum mean lint index (5.77) was observed in T3 drought stress whereas the minimum mean lint index (5.35) was observed in T4 drought stress (Table 55). Among the genotypes, maximum lint index (6.36) was observed in G30 and minimum (4.63) in G35. Based on the genotype stress interaction, maximum lint index (8.41) and minimum (3.57) was observed in G39 under T4 and G48 under T4 stress respectively. Based on b values, the best performance was observed in genotype G33 (0.90) followed by G43 (0.33) and lowest in G23 (-0.66). With the increase of drought stress, lint index was increased as shown in linear regression in Figure 72.

**Table 54. Seed index (SI) of twenty-five genotypes at different drought treatments**

| Genotype | SI at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 8.50 | 10.70 | 9.20 | 7.73 | 9.03 | -25.88 | -8.24 | 9.02 | -8.37 | -0.35 | 17 |
| G2 | 8.10 | 8.47 | 9.03 | 8.40 | 8.50 | -4.53 | -11.52 | -3.70 | -6.58 | -0.21 | 15 |
| G8 | 9.30 | 8.87 | 8.70 | 9.20 | 9.02 | 4.66 | 6.45 | 1.08 | 4.06 | 0.15 | 6 |
| G10 | 8.03 | 7.53 | 8.63 | 9.83 | 8.51 | 6.22 | -7.47 | -22.41 | -7.88 | -0.03 | 11 |
| G11 | 9.07 | 9.90 | 9.27 | 10.00 | 9.56 | -9.19 | -2.21 | -10.29 | -7.23 | -0.08 | 12 |
| G12 | 7.23 | 8.67 | 9.83 | 8.67 | 8.60 | -19.82 | -35.94 | -19.82 | -25.19 | -0.60 | 21 |
| G13 | 9.70 | 6.10 | 7.93 | 7.80 | 7.88 | 37.11 | 18.21 | 19.59 | 24.97 | 0.61 | 1 |
| G14 | 5.43 | 6.87 | 8.50 | 9.77 | 7.64 | -26.38 | -56.44 | -79.75 | -54.19 | -0.61 | 22 |
| G15 | 6.63 | 9.83 | 8.83 | 10.20 | 8.88 | -48.24 | -33.17 | -53.77 | -45.06 | -0.61 | 23 |
| G17 | 8.43 | 8.37 | 8.40 | 8.70 | 8.48 | 0.79 | 0.40 | -3.16 | -0.66 | 0.02 | 9 |
| G18 | 7.23 | 8.50 | 8.40 | 8.50 | 8.16 | -17.51 | -16.13 | -17.51 | -17.05 | -0.31 | 16 |
| G22 | 8.83 | 7.53 | 9.00 | 9.30 | 8.67 | 14.72 | -1.89 | -5.28 | 2.52 | 0.09 | 7 |
| G23 | 6.50 | 6.43 | 8.73 | 7.00 | 7.17 | 1.03 | -34.36 | -7.69 | -13.68 | -0.43 | 19 |
| G29 | 8.13 | 7.43 | 8.10 | 7.27 | 7.73 | 8.61 | 0.41 | 10.66 | 6.56 | 0.04 | 8 |
| G30 | 7.23 | 9.03 | 8.57 | 8.53 | 8.34 | -24.88 | -18.43 | -17.97 | -20.43 | -0.38 | 18 |
| G33 | 9.47 | 7.43 | 6.90 | 6.67 | 7.62 | 21.48 | 27.11 | 29.58 | 26.06 | 0.61 | 1 |
| G34 | 8.23 | 8.57 | 6.83 | 7.43 | 7.77 | -4.05 | 17.00 | 9.72 | 7.56 | 0.23 | 3 |
| G35 | 8.53 | 6.63 | 10.53 | 10.07 | 8.94 | 22.27 | -23.44 | -17.97 | -6.38 | -0.19 | 14 |
| G38 | 5.93 | 7.23 | 9.63 | 6.83 | 7.41 | -21.91 | -62.36 | -15.17 | -33.15 | -0.83 | 24 |
| G39 | 8.03 | 9.53 | 8.80 | 13.77 | 10.03 | -18.67 | -9.54 | -71.37 | -33.20 | -0.12 | 13 |
| G43 | 9.20 | 9.63 | 7.37 | 9.73 | 8.98 | -4.71 | 19.93 | -5.80 | 3.14 | 0.34 | 2 |
| G45 | 8.13 | 11.57 | 9.63 | 8.80 | 9.53 | -42.21 | -18.44 | -8.20 | -22.95 | -0.58 | 20 |
| G46 | 8.20 | 8.43 | 8.17 | 8.57 | 8.34 | -2.85 | 0.41 | -4.47 | -2.30 | 0.00 | 10 |
| G48 | 8.40 | 8.57 | 6.97 | 6.43 | 7.59 | -1.98 | 17.06 | 23.41 | 12.83 | 0.22 | 4 |
| G50 | 8.03 | 7.97 | 6.90 | 5.47 | 7.09 | 0.83 | 14.11 | 31.95 | 15.63 | 0.16 | 5 |
| Mean (T) | 8.02 | 8.39 | 8.51 | 8.59 | | | | | | | |

**Table 55. Lint index of twenty-five genotypes at different drought treatments**

| Genotype | LI at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 5.08 | 6.16 | 5.94 | 4.77 | 5.48 | -21.20 | -16.86 | 6.09 | -10.66 | -0.27 | 16 |
| G2 | 5.82 | 6.24 | 5.81 | 4.00 | 5.46 | -7.17 | 0.15 | 31.33 | 8.10 | -0.09 | 10 |
| G8 | 6.09 | 6.09 | 5.71 | 6.51 | 6.10 | -0.12 | 6.24 | -7.02 | -0.30 | 0.09 | 6 |
| G10 | 4.92 | 5.01 | 5.89 | 5.25 | 5.27 | -1.97 | -19.80 | -6.87 | -9.54 | -0.19 | 15 |
| G11 | 6.63 | 6.18 | 5.02 | 5.34 | 5.79 | 6.89 | 24.27 | 19.46 | 16.88 | 0.32 | 3 |
| G12 | 4.37 | 6.38 | 6.67 | 5.26 | 5.67 | -46.16 | -52.88 | -20.47 | -39.83 | -0.61 | 21 |
| G13 | 6.33 | 3.75 | 6.39 | 4.89 | 5.34 | 40.68 | -1.06 | 22.76 | 20.79 | 0.17 | 4 |
| G14 | 3.67 | 4.23 | 5.72 | 5.63 | 4.81 | -15.36 | -55.93 | -53.32 | -41.54 | -0.40 | 19 |
| G15 | 4.00 | 6.37 | 5.36 | 7.01 | 5.68 | -59.42 | -34.10 | -75.48 | -56.33 | -0.39 | 18 |
| G17 | 5.38 | 5.52 | 6.32 | 5.89 | 5.78 | -2.63 | -17.53 | -9.49 | -9.88 | -0.19 | 15 |
| G18 | 5.03 | 5.23 | 5.57 | 4.74 | 5.14 | -3.88 | -10.76 | 5.84 | -2.93 | -0.13 | 13 |
| G22 | 6.54 | 5.64 | 6.31 | 6.41 | 6.22 | 13.85 | 3.53 | 2.07 | 6.48 | 0.12 | 5 |
| G23 | 4.24 | 4.72 | 7.30 | 4.12 | 5.09 | -11.18 | -72.21 | 2.90 | -26.83 | -0.66 | 22 |
| G29 | 6.36 | 5.65 | 6.85 | 4.90 | 5.94 | 11.16 | -7.64 | 23.05 | 8.86 | -0.08 | 9 |
| G30 | 6.09 | 6.62 | 6.45 | 6.28 | 6.36 | -8.72 | -5.97 | -3.18 | -5.96 | -0.11 | 12 |
| G33 | 7.92 | 4.94 | 4.21 | 4.43 | 5.38 | 37.61 | 46.87 | 44.08 | 42.85 | 0.90 | 1 |
| G34 | 5.03 | 4.86 | 4.64 | 4.44 | 4.74 | 3.31 | 7.83 | 11.75 | 7.63 | 0.08 | 7 |
| G35 | 4.38 | 3.86 | 5.38 | 4.91 | 4.63 | 11.78 | -22.89 | -12.28 | -7.79 | -0.14 | 14 |
| G38 | 3.61 | 4.92 | 6.06 | 4.37 | 4.74 | -36.28 | -67.72 | -20.93 | -41.65 | -0.58 | 20 |
| G39 | 5.00 | 6.00 | 5.54 | 8.41 | 6.24 | -20.13 | -10.86 | -68.18 | -33.06 | -0.10 | 11 |
| G43 | 6.00 | 5.28 | 4.65 | 5.86 | 5.45 | 11.85 | 22.36 | 2.25 | 12.15 | 0.33 | 2 |
| G45 | 5.78 | 6.87 | 5.91 | 6.32 | 6.22 | -18.95 | -2.22 | -9.44 | -10.20 | -0.10 | 11 |
| G46 | 5.28 | 6.06 | 6.52 | 6.14 | 6.00 | -14.92 | -23.58 | -16.39 | -18.30 | -0.29 | 17 |
| G48 | 6.18 | 7.00 | 5.05 | 3.57 | 5.45 | -13.39 | 18.31 | 42.20 | 15.70 | 0.08 | 7 |
| G50 | 5.45 | 5.96 | 4.90 | 4.21 | 5.13 | -9.50 | 10.02 | 22.77 | 7.77 | 0.03 | 8 |
| Mean (T) | 5.41 | 5.58 | 5.77 | 5.35 | | | | | | | |

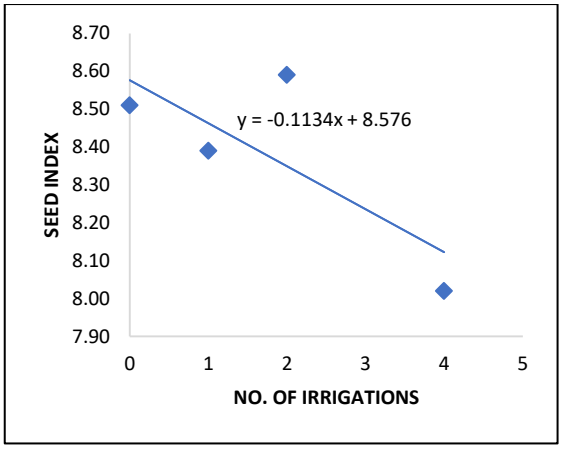



**Figure 70. Relationships between seed index of cotton genotypes and different drought stresses**

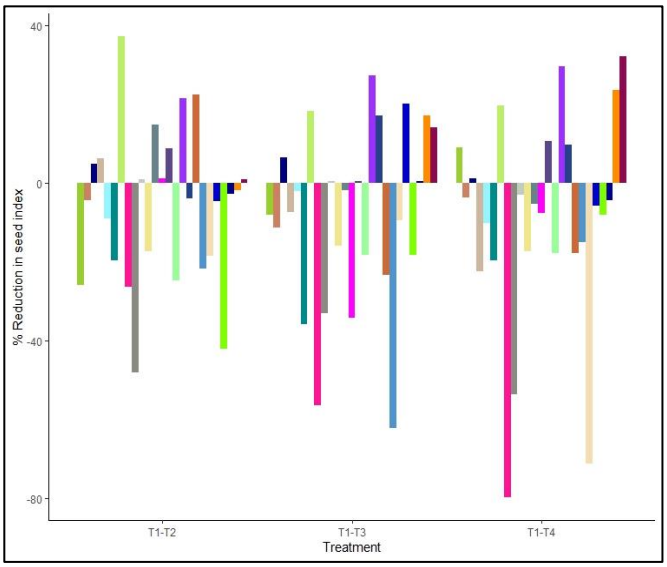
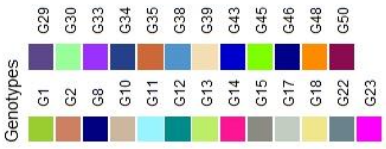



**Figure 71. Reduction percentage of seed index of twenty-five cotton genotypes under different drought stresses compared with control**



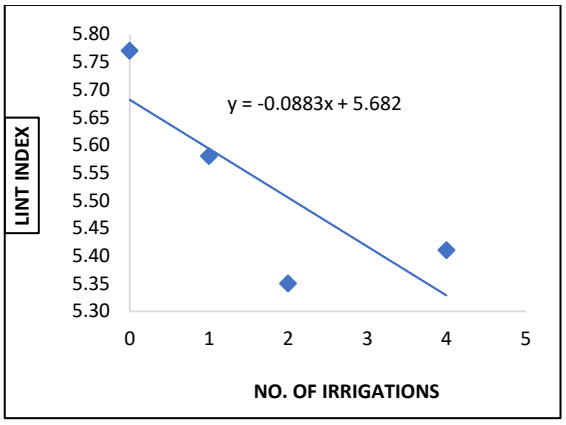




**Figure 72. Relationships between lint index of cotton genotypes and different drought stresses**

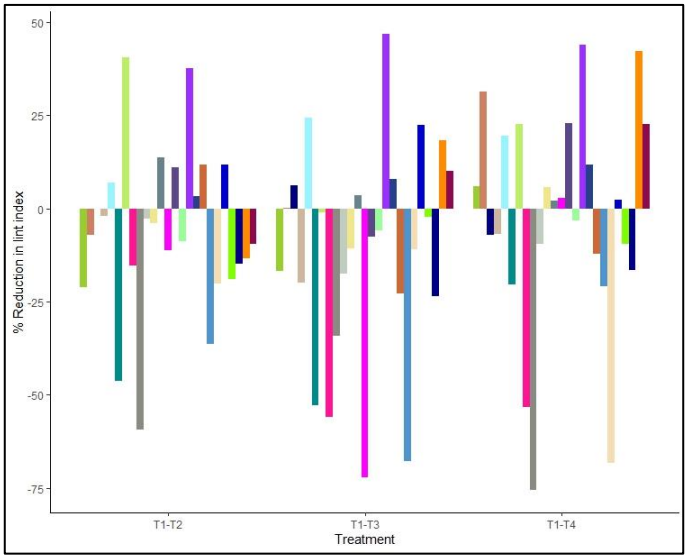



**Figure 73. Reduction percentage of lint index of twenty-five cotton genotypes under different drought stresses compared with control**

The minimum reduction% (-75.48%) was observed in G15 under T4 drought stress (Figure 73, Table 55). Maximum reduction% (46.87%) was observed in G33 under T3 stress (Figure 73). The result showed the positive effect of drought stress on lint index in genotypic dependent manner. Some of the genotypes showed an increase in lint index at severe drought stress. However, the maximum genotypes showed an increase of lint index under the severe drought stress. Shilpa and Chandrasekhar (2020) found that fiber fineness and bundle strength decrease in inferior direction as reduction of soil moisture levels. The reduction in yields could be mainly due to the decrease in lint index, boll weight and seed index rather than a decrease in bolls/plant.

#### 4.3.1.13 Seed cotton yield per hectare

Genotype, treatment and their interaction significantly affected the seed cotton yield per hectare. The highest mean seed cotton yield per hectare (4.43 ton) was observed in T1 drought stress whereas the lowest seed cotton yield per hectare (3.77 ton) was observed in T3 drought stress (Table 56). Among the genotypes, highest seed cotton yield per hectare (5.63 ton) was observed in G43 and lowest (2.95 ton) in G1. Based on the genotype stress interaction, highest Seed cotton yield per hectare (7.04 ton) and lowest (2.33 ton) was observed in G38 under T4 stress, respectively. Based on b values, the best performance was observed in genotype G43 (0.63) followed by G29 (0.48) and lowest in G15 (-0.16). With the increase of drought stress, Seed cotton yield per hectare was decreased as shown in linear regression in Figure 74. The minimum reduction% (-55.10%) was observed in G15 under T4 drought stress (Figure 74, Table 56). Maximum reduction% (50.53%) was observed in G29 under T4 stress (Figure 75). The result showed the negative effect of drought stress on seed cotton yield per hectare in genotypic dependent manner. Some of the genotypes showed a decrease in seed cotton yield per hectare at severe drought stress. However, the maximum genotypes showed a decrease of seed cotton yield per hectare under the severe drought stress. Similar result has been observed in (Bakhsh *et al*., 2019; Kamaran *et al*., 2016; Mahdi *et al*., 2014; Karademir *et al*., 2011). Lint yield was usually reduced due to boll formation because of lower number of flowers and greater boll abortions due to increase in drought stress severity and length during reproductive stage (Pettigrew, 2004; Gerik *et al*., 1996; Grimes, 1969 and Stocton *et al*., 1961).

**Table 56. Seed cotton yield/h (ton) of twenty-five genotypes at different drought treatments**

| Genotype | Seed cotton yield/h at four drought level (ton) | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 3.31 | 3.06 | 2.79 | 2.64 | 2.95 | 7.51 | 15.82 | 20.39 | 14.58 | 0.11 | 13 |
| G2 | 3.90 | 4.06 | 3.63 | 3.39 | 3.74 | -4.22 | 6.91 | 13.13 | 5.27 | 0.03 | 19 |
| G8 | 4.76 | 4.21 | 4.59 | 5.99 | 4.89 | 11.52 | 3.49 | -25.85 | -3.61 | 0.12 | 12 |
| G10 | 3.91 | 3.49 | 3.81 | 4.55 | 3.94 | 10.82 | 2.67 | -16.32 | -0.94 | 0.08 | 16 |
| G11 | 3.38 | 3.17 | 3.39 | 4.05 | 3.50 | 6.13 | -0.19 | -19.82 | -4.63 | 0.04 | 18 |
| G12 | 4.87 | 4.65 | 5.13 | 4.86 | 4.88 | 4.46 | -5.21 | 0.24 | -0.17 | -0.03 | 20 |
| G13 | 4.19 | 3.29 | 3.48 | 4.04 | 3.75 | 21.44 | 17.06 | 3.65 | 14.05 | 0.22 | 7 |
| G14 | 4.94 | 5.26 | 5.14 | 6.25 | 5.40 | -6.62 | -4.18 | -26.56 | -12.45 | -0.03 | 20 |
| G15 | 3.81 | 4.22 | 4.73 | 5.91 | 4.67 | -10.89 | -24.25 | -55.10 | -30.08 | -0.16 | 23 |
| G17 | 3.84 | 3.64 | 2.86 | 3.50 | 3.46 | 5.11 | 25.36 | 8.89 | 13.12 | 0.20 | 9 |
| G18 | 4.13 | 4.16 | 4.99 | 5.16 | 4.61 | -0.76 | -20.84 | -24.90 | -15.50 | -0.15 | 22 |
| G22 | 4.64 | 3.92 | 3.49 | 4.27 | 4.08 | 15.43 | 24.77 | 7.83 | 16.01 | 0.28 | 5 |
| G23 | 4.20 | 4.20 | 2.91 | 2.39 | 3.42 | -0.05 | 30.65 | 43.14 | 24.58 | 0.21 | 8 |
| G29 | 5.04 | 4.50 | 2.52 | 2.49 | 3.64 | 10.81 | 49.98 | 50.53 | 37.10 | 0.48 | 2 |
| G30 | 3.97 | 4.22 | 3.31 | 3.49 | 3.75 | -6.53 | 16.62 | 12.09 | 7.39 | 0.10 | 14 |
| G33 | 4.36 | 3.39 | 2.54 | 2.62 | 3.23 | 22.42 | 41.80 | 39.99 | 34.73 | 0.40 | 3 |
| G34 | 3.66 | 3.74 | 2.67 | 3.41 | 3.37 | -2.01 | 27.20 | 6.77 | 10.65 | 0.19 | 10 |
| G35 | 5.23 | 4.22 | 4.21 | 4.63 | 4.57 | 19.42 | 19.57 | 11.59 | 16.86 | 0.27 | 6 |
| G38 | 3.62 | 3.65 | 3.05 | 2.33 | 3.16 | -0.76 | 15.78 | 35.54 | 16.85 | 0.08 | 17 |
| G39 | 4.82 | 5.60 | 5.00 | 6.65 | 5.52 | -16.18 | -3.80 | -38.01 | -19.33 | -0.05 | 21 |
| G43 | 7.04 | 6.89 | 3.64 | 4.96 | 5.63 | 2.20 | 48.30 | 29.52 | 26.67 | 0.63 | 1 |
| G45 | 4.80 | 5.44 | 4.89 | 5.40 | 5.13 | -13.26 | -1.79 | -12.49 | -9.18 | -0.05 | 21 |
| G46 | 4.25 | 3.92 | 3.99 | 4.62 | 4.19 | 7.96 | 6.28 | -8.61 | 1.88 | 0.09 | 15 |
| G48 | 5.29 | 5.26 | 3.33 | 3.08 | 4.24 | 0.49 | 37.03 | 41.79 | 26.44 | 0.33 | 4 |
| G50 | 4.82 | 4.88 | 4.06 | 4.29 | 4.51 | -1.34 | 15.76 | 11.03 | 8.49 | 0.13 | 11 |
| Mean (T) | 4.43 | 4.28 | 3.77 | 4.20 | | | | | | | |

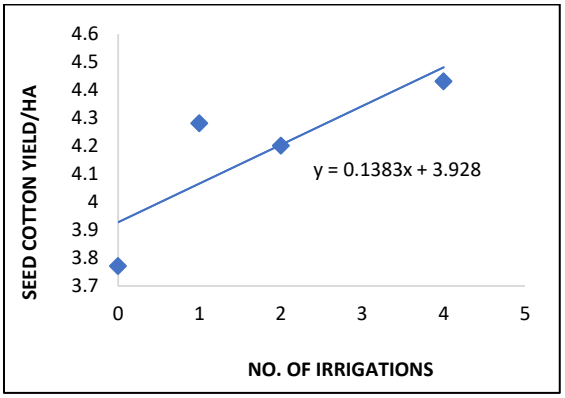



**Figure 74. Relationships between seed cotton yield/ha of cotton genotypes and different drought**

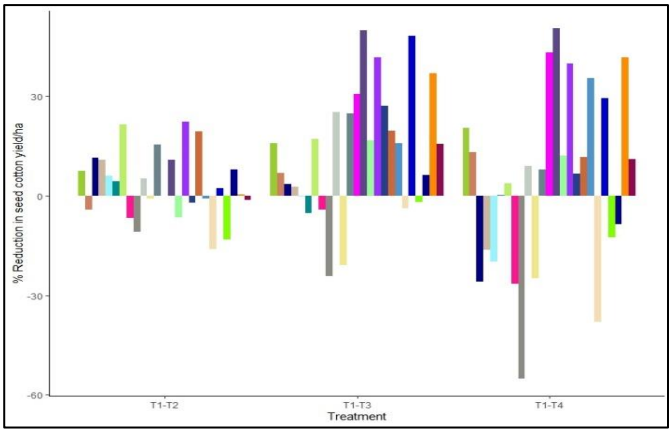



**Figure 75. Reduction percentage of seed cotton yield/ha of twenty-five cotton genotypes under different drought stresses compared with control**

#### 4.3.1.2 Drought Response Index (DRI)

Drought Response Index (DRI) was calculated from the observed phenotypic value of each character. DRI value represents the relative change for each of the character caused by drought treatment. The DRI value was considered as the indicator for drought tolerance. Comparing the DRI value, we have received important information about the drought tolerance in different genotypes of cotton. Finding from this study will provide theoretical bases and practical guidance for distinguishing drought tolerant germplasm resources and breeding for drought tolerant cultivar.

Twenty five cotton genotypes showed a wider range of drought tolerance index (Table 57). DRI value for plant height showed a wide range having maximum DRI (103.7) and minimum (83.5) in G15 and G29, respectively. G29 and G15 showed the minimum (59.5) and maximum (119.0) DRI value for no. of fruiting branches. G29 and G15 showed the minimum (66.4) and maximum (107.9) DRI value for no of bolls per plant. In case of single boll weight, the minimum (74.0) and maximum (120.9) DRI value was observed in G33 and G45 respectively. G11 and G46 showed the minimum (85.5) and maximum (109.0) DRI value for ginning out turn. Minimum (73.9) and maximum (154.2) DRI value for seed index were observed in G33 and G14 respectively. In case of lint index, minimum (57.1) and maximum (156.3) DRI value in G33 and G15 respectively. DRI value for seed cotton yield per hectare showed wider range of value among the genotypes. In case of seed cotton yield per hectare, minimum (62.9) and maximum (130.1) DRI were observed in G29 and G15 respectively.

Based on the average lowest DRI value of each genotype for eight yield contributing traits, genotypes were grouped into four groups such as drought tolerant, moderately tolerant, moderately susceptible and susceptible genotypes (Table 58). 21 genotypes were classified as tolerant genotypes, 3 genotypes showed moderately tolerant and only one genotype showed susceptible based on the average lowest DRI values. Most of the genotypes of cotton showed tolerant to drought stress at Barind tract. Twenty-five cotton genotypes showed a wider range of drought tolerance index (Table 59). DRI value for days to first square initiation showed a wide range having maximum DRI (113.02) and minimum (100.24) in G22 and G48, respectively. G38, G48 and G22 showed the minimum (100.0) and maximum (111.79) DRI value for days to first

**Table 57. Drought Response Index of twenty-five genotypes based on eight morphological characters**

| Genotypes | Plant height | No. of fruiting branches | No. of bolls/plant | Single boll weight | Ginning Out Turn | Seed index | Lint index | Seed cotton yield/ha | Average | Grouping |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 94.6 | 87.0 | 82.3 | 104.7 | 101.5 | 108.4 | 110.7 | 85.4 | 96.8 | T |
| 2 | 88.9 | 83.3 | 87.5 | 108.1 | 90.7 | 106.6 | 91.9 | 94.7 | 94.0 | T |
| 8 | 99.2 | 98.7 | 98.8 | 104.3 | 102.6 | 95.9 | 100.3 | 103.6 | 100.4 | T |
| 10 | 97.0 | 98.3 | 95.9 | 105.0 | 101.2 | 107.9 | 109.5 | 100.9 | 102.0 | T |
| 11 | 94.8 | 96.1 | 92.0 | 114.0 | 85.5 | 107.2 | 83.1 | 104.6 | 97.2 | T |
| 12 | 102.1 | 107.6 | 99.3 | 100.9 | 106.9 | 125.2 | 139.8 | 100.2 | 110.2 | T |
| 13 | 98.9 | 100.0 | 100.7 | 85.3 | 102.4 | 75.0 | 79.2 | 86.0 | 90.9 | T |
| 14 | 100.1 | 98.9 | 93.8 | 119.9 | 95.1 | 154.2 | 141.5 | 112.5 | 114.5 | T |
| 15 | 103.7 | 119.0 | 107.9 | 120.0 | 104.5 | 145.1 | 156.3 | 130.1 | 123.3 | T |
| 17 | 92.6 | 92.6 | 87.6 | 99.1 | 105.3 | 100.7 | 109.9 | 86.9 | 96.8 | T |
| 18 | 103.1 | 107.2 | 106.5 | 108.5 | 92.4 | 117.1 | 102.9 | 115.5 | 106.7 | T |
| 22 | 95.0 | 77.8 | 81.2 | 103.8 | 97.8 | 97.5 | 93.5 | 84.0 | 91.3 | T |
| 23 | 85.1 | 70.2 | 67.8 | 114.0 | 105.4 | 113.7 | 126.8 | 75.4 | 94.8 | T |
| 29 | 83.5 | 59.5 | 66.4 | 95.1 | 98.0 | 93.4 | 91.1 | 62.9 | 81.3 | MT |
| 30 | 90.0 | 78.8 | 80.2 | 115.2 | 93.1 | 120.4 | 106.0 | 92.6 | 97.0 | T |
| 33 | 96.2 | 86.0 | 87.9 | 74.0 | 86.2 | 73.9 | 57.1 | 65.3 | 78.3 | MS |
| 34 | 99.7 | 96.7 | 97.6 | 91.2 | 100.2 | 92.4 | 92.4 | 89.3 | 94.9 | T |
| 35 | 93.6 | 82.1 | 80.4 | 106.1 | 101.6 | 106.4 | 107.8 | 83.1 | 95.1 | T |
| 38 | 89.3 | 69.6 | 69.8 | 120.7 | 104.0 | 133.1 | 141.6 | 83.1 | 101.4 | T |
| 39 | 103.1 | 102.4 | 99.4 | 119.8 | 100.1 | 133.2 | 133.1 | 119.3 | 113.8 | T |
| 43 | 87.5 | 74.1 | 74.1 | 98.1 | 94.4 | 96.9 | 87.8 | 73.3 | 85.8 | MT |
| 45 | 94.5 | 91.0 | 90.4 | 120.9 | 94.0 | 123.0 | 110.2 | 109.2 | 104.1 | T |
| 46 | 102.1 | 102.9 | 96.0 | 102.2 | 109.0 | 102.3 | 118.3 | 98.1 | 103.9 | T |
| 48 | 92.3 | 75.6 | 79.7 | 90.9 | 96.5 | 87.2 | 84.3 | 73.6 | 85.0 | MT |
| 50 | 102.3 | 107.4 | 102.5 | 89.3 | 105.5 | 84.4 | 92.2 | 91.5 | 96.9 | T |

**Table 58. Grouping of 25 genotypes based on DRI values under drought stress**

| Sl No. | Scale | % DRI values | Drought tolerant group | Name of genotypes |
|---|---|---|---|---|
| **1** | I | >90 | Tolerant (T) | G1, G2, G8, G10, G11, G12, G13, G14, G15, G17, G18, G22, G23, G30, G34, G35, G38, G39, G45, G46, G50. |
| **2** | II | 80-90 | Moderately tolerant (MT) | G29, G43, G48 |
| **3** | III | 70-80 | Moderately susceptible (MS) | G33 |
| **4** | IV | <70 | Susceptible (S) | - |

flower initiation.G38 and G1 showed the minimum (98.88) and maximum (110.84) DRI value for days to first boll split. In case of no. of vegetative branches, the minimum (61.90) and maximum (109.52) DRI value was observed in G2 and G22, respectively. G39 and G8 showed the minimum (87.05) and maximum (118.10) DRI value for days to first boll bursting.

Based on the average lowest DRI value of each genotype for five yield contributing traits, genotypes were grouped into four groups such as drought tolerant, moderately tolerant, moderately susceptible and susceptible genotypes (Table 60). All of the genotypes of cotton showed tolerant to drought stress based on the average lowest DRI values at Barind tract.

**Table 59. Drought Response Index of twenty-five genotypes based on five morphological characters**

| genotypes | Days to 1st square initiation | Days to 1st flower initiation | Days to 1st boll split | No. of vegetative branches | Days to 1st boll bursting | average | Grouping |
|---|---|---|---|---|---|---|---|
| 1 | 111.81 | 111.19 | 110.84 | 79.17 | 98.31 | 102.26 | T |
| 2 | 105.99 | 105.41 | 105.22 | 61.90 | 95.25 | 94.75 | T |
| 8 | 107.18 | 103.25 | 102.33 | 100.00 | 118.10 | 106.17 | T |
| 10 | 104.26 | 103.46 | 103.51 | 88.89 | 115.17 | 103.06 | T |
| 11 | 110.40 | 106.71 | 106.63 | 71.43 | 90.61 | 97.16 | T |
| 12 | 111.11 | 107.66 | 103.53 | 91.67 | 105.08 | 103.81 | T |
| 13 | 103.28 | 103.03 | 102.33 | 83.33 | 96.36 | 97.67 | T |
| 14 | 109.41 | 107.59 | 106.75 | 83.33 | 106.62 | 102.74 | T |
| 15 | 108.33 | 106.44 | 106.13 | 77.78 | 105.41 | 100.82 | T |
| 17 | 106.67 | 104.20 | 104.29 | 75.00 | 110.19 | 100.07 | T |
| 18 | 112.20 | 108.51 | 107.11 | 77.78 | 112.78 | 103.67 | T |
| 22 | 113.02 | 111.79 | 109.49 | 109.52 | 116.50 | 112.07 | T |
| 23 | 105.22 | 103.87 | 103.47 | 66.67 | 106.79 | 97.20 | T |
| 29 | 102.17 | 100.92 | 101.85 | 95.24 | 102.65 | 100.57 | T |
| 30 | 104.01 | 102.80 | 102.52 | 95.24 | 110.05 | 102.92 | T |
| 33 | 107.14 | 105.18 | 103.59 | 91.67 | 102.61 | 102.04 | T |
| 34 | 102.01 | 102.81 | 102.53 | 91.67 | 110.46 | 101.90 | T |
| 35 | 106.15 | 104.64 | 105.13 | 86.67 | 110.60 | 102.64 | T |
| 38 | 101.20 | 100.00 | 98.88 | 80.95 | 109.45 | 98.10 | T |
| 39 | 102.64 | 100.21 | 99.81 | 100.00 | 87.05 | 97.94 | T |
| 43 | 107.13 | 104.59 | 103.78 | 91.67 | 99.54 | 101.34 | T |
| 45 | 111.94 | 108.76 | 107.09 | 66.67 | 114.70 | 101.83 | T |
| 46 | 110.93 | 107.21 | 105.95 | 77.78 | 111.38 | 102.65 | T |
| 48 | 100.24 | 100.00 | 99.44 | 100.00 | 100.10 | 99.96 | T |
| 50 | 105.25 | 104.28 | 102.96 | 73.33 | 100.87 | 97.34 | T |

**Table 60. Grouping of 25 genotypes based on DRI values under drought stress**

| Sl No. | Scale | % DRI values | Drought tolerant group | Name of genotypes |
|---|---|---|---|---|
| **1** | I | >90 | Tolerant (T) | G1, G2, G8, G10, G11, G12, G13, G14, G15, G17, G18, G22, G23, G29, G30, G33, G34, G35, G38, G39, G43, G45, G46, G48, G50. |
| **2** | II | 80-90 | Moderately tolerant (MT) | - |
| **3** | III | 70-80 | Moderately susceptible (MS) | - |
| **4** | IV | <70 | Susceptible (S) | - |

#### 4.3.1.3 Genetic variability analysis

The extent of variation among the genotypes in respect of thirteen characters was studied and mean sum of square, phenotypic variance ($\sigma^2p$), genotypic variance ($\sigma^2g$), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ($h^2b$), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) presented in Table 61.

##### 4.3.1.3.1 Plant height

Minimum and maximum value of plant heigth was 131.75 cm and 160.0 cm, respectively which showed the presence of variation in plant height among the genotypes (Table 61). The genotypic and phenotypic variance for this trait was 65.13 and 66.16, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (5.70 and 5.66 respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (98%) with medium genetic advance (16.50) and genetic advance in mean (11.57%). The high heritability coupled with medium genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for cotton plant height had been also reported in Rehman *et al*. (2020). Kapoor and Kaushik (2003), Ahmad *et al*. (2011) and Baloch *et al*. (2015) also found high heritability 94%, 81% and 96.4% correspondingly for plant height. High heritability estimates indicated that selection for plant height can be effective.

**Table 61. Genetic parameters for 13 yield and yield contributing characters of twenty-five cotton genotypes**

| **Genetic parameters** | Plant height | Days to 1st square initiation | Days to 1st flower initiation | Days to 1st boll split | No. of vegetative branches | No. of fruiting branches | No. of bolls/plant | Days to 1st boll bursting | Singles boll weight | Ginning Out Turn | Seed index | Lint index | Seed yield/ha |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Maximum** | 160.00 | 51.00 | 57.75 | 64.00 | 2.75 | 10.50 | 42.25 | 124.00 | 5.92 | 43.99 | 10.10 | 6.47 | 5.80 |
| **Minimum** | 131.75 | 39.75 | 46.75 | 53.25 | 0.50 | 4.50 | 23.75 | 103.00 | 4.55 | 34.09 | 6.95 | 4.58 | 2.91 |
| **GM** | 142.59 | 45.47 | 52.37 | 58.36 | 1.70 | 7.36 | 32.10 | 115.04 | 5.26 | 39.68 | 8.38 | 5.53 | 4.17 |
| **σ2e** | 1.03 | 0.96 | 0.76 | 0.88 | 0.05 | 0.13 | 0.68 | 0.60 | 0.00 | 0.18 | 0.01 | 0.01 | 0.01 |
| **σ2g** | 65.13 | 3.22 | 3.00 | 2.36 | 0.27 | 1.83 | 25.15 | 28.46 | 0.13 | 4.00 | 0.59 | 0.26 | 0.60 |
| **σ2p** | 66.16 | 4.19 | 3.77 | 3.24 | 0.31 | 1.96 | 25.83 | 29.06 | 0.13 | 4.18 | 0.60 | 0.27 | 0.62 |
| **ECV** | 0.71 | 2.16 | 1.67 | 1.61 | 12.68 | 4.96 | 2.58 | 0.67 | 0.33 | 1.07 | 1.05 | 1.82 | 2.68 |
| **GCV** | 5.66 | 3.95 | 3.31 | 2.63 | 30.55 | 18.35 | 15.62 | 4.64 | 6.88 | 5.04 | 9.19 | 9.17 | 18.63 |
| **PCV** | 5.70 | 4.50 | 3.71 | 3.08 | 33.07 | 19.01 | 15.83 | 4.69 | 6.89 | 5.15 | 9.25 | 9.35 | 18.82 |
| **Heritability** | 0.98 | 0.77 | 0.80 | 0.73 | 0.85 | 0.93 | 0.97 | 0.98 | 1.00 | 0.96 | 0.99 | 0.96 | 0.98 |
| **GA (5%)** | 16.50 | 3.25 | 3.19 | 2.70 | 0.99 | 2.69 | 10.19 | 10.88 | 0.74 | 4.03 | 1.58 | 1.02 | 1.58 |
| **GA (% mean)** | 11.57 | 7.14 | 6.09 | 4.62 | 58.11 | 36.49 | 31.76 | 9.45 | 14.16 | 10.16 | 18.81 | 18.53 | 37.99 |
| **SEM** | 0.59 | 0.57 | 0.50 | 0.54 | 0.12 | 0.21 | 0.48 | 0.45 | 0.01 | 0.24 | 0.05 | 0.06 | 0.06 |
| **CD 5%** | 1.66 | 1.61 | 1.43 | 1.54 | 0.35 | 0.60 | 1.36 | 1.27 | 0.03 | 0.69 | 0.15 | 0.16 | 0.18 |
| **CD1%** | 2.22 | 2.15 | 1.91 | 2.06 | 0.47 | 0.80 | 1.81 | 1.70 | 0.04 | 0.93 | 0.19 | 0.22 | 0.24 |

Here, GM= Grand mean; $\sigma^2$g= Genotypic variance; σ2e= environmental variance; σ2p= phenotypic variance; GCV= genotypic coefficient of variation; ECV=Environmental coefficient of variation, PCV= Phenotypic coefficient of variation, GA= genetic advance; SEM=Standard error of mean, CD= Critical differences.

#### 4.3.1.3.2 Days to first square initiation

Minimum and maximum value of days to first square initiation were 39.75 and 51.00, respectively which showed the presence of variation in days to first square initiation among the genotypes (Table 61). The genotypic and phenotypic variance for this trait was 3.22 and 4.19, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (4.50 and 3.95, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were high (77%) with low genetic advance (3.25) and genetic advance in mean (7.14%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for cotton plant height has been also reported in Rehman *et al.* (2020).

#### 4.3.1.3.3 Days to first flower initiation

Minimum and Maximum value of days to first flower initiation were 46.75 and 57.75, respectively which showed the presence of variation in days to first flower initiation among the genotypes (Table 61). The genotypic and phenotypic variance for this trait was 3.00 and 3.77, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (3.71 and 3.31, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of

the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were high (80%) with low genetic advance (3.19) and genetic advance in mean (6.09%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for cotton plant height has been also reported in Rehman *et al*. (2020).

#### 4.3.1.3.4 Days to boll split

Minimum and maximum value of days to boll split were 53.25 and 64.00, respectively which showed the presence of variation in days to first boll split among the genotypes (Table 61). The genotypic and phenotypic variance for this trait was 2.36 and 3.24, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (3.08 and 2.63, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were high (73%) with low genetic advance (2.70) and genetic advance in mean (4.62%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for cotton plant height has been also reported in Rehman *et al*. (2020).

#### 4.3.1.3.5 No. of vegetative branches

Minimum and maximum values of no. of vegetative branches were 0.50 and 2.75, respectively which showed the presence of variation in no. of vegetative branches among the genotypes (Table 61). The genotypic and phenotypic variance for this trait

was 0.27 and 0.31, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were very high (33.07 and 30.55 respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV was high which indicated that environmental influence was major on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be misleading for the improvement of the crop. The heritability estimates for this trait were high (85%) with low genetic advance (0.99) and genetic advance in mean (58.11%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for cotton plant height has been also reported in Rehman *et al*. (2020).

#### 4.3.1.3.6 No. of fruiting branches

Minimum and maximum value of no. of fruiting branches were 4.50 and 10.50, respectively which showed the presence of variation in no. of fruiting branches among the genotypes (Table 61). The genotypic and phenotypic variance for this trait was 1.83 and 1.96, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were medium (19.01 and 18.35, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were high (93%) with low genetic advance (2.69) and genetic advance in mean (36.49%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of

environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and medium phenotypic coefficient of variation for cotton days to boll split has been also reported in Jarwar *et al*. (2018).

#### 4.3.1.3.7 No. of bolls per plant

Minimum and maximum values of no. of bolls per plant were 23.75 and 42.25, respectively which showed the presence of variation in no. of bolls per plant among the genotypes (Table 61). The genotypic and phenotypic variance for this trait was 25.15 and 25.83, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were medium (15.83 and 15.62, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were high (97%) with medium genetic advance (10.19) and genetic advance in mean (31.76%). The high heritability coupled with medium genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. Desalegn *et al*. (2009), Ahmad *et al*. (2011), Baloch *et al*. (2015) and Rathinavel *et al*. (2017) estimated 59%, 88%, 93% and 60.21% high broad sense heritability respectively for bolls per plant. High estimates of heritability revealed that successful and effective selection can be helpful in the improvement of this trait.

#### 4.3.1.3.8 Days to first boll bursting

Minimum and maximum value of days to first boll bursting were 103.0 and 124.0, respectively which showed the presence of variation in days to first boll bursting among the genotypes (Table 61). The genotypic and phenotypic variance for this trait was 28.46 and 29.06, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic

coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (4.69 and 4.64, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were high (98%) with medium genetic advance (10.88) and genetic advance in mean (9.45%). The high heritability coupled with medium genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for days to first boll bursting has been also reported in Rehman *et al*. (2020).

#### 4.3.1.3.9 Single boll weight

Minimum and maximum values of single boll weight were 4.55 and 5.92, respectively which showed the presence of variation in single boll weight among the genotypes (Table 61). The genotypic and phenotypic variance for this trait was 0.13 and 0.13, respectively. The phenotypic and genotypic variance appeared to be same suggested the considerable influence of genotype on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (6.89 and 6.88, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were high (100%) with low genetic advance (0.74) and genetic advance in mean (14.16%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for single boll weight of cotton has been also reported in Rehman *et al*. (2020).

#### 4.3.1.3.10 Ginning out turn

Minimum and maximum values of ginning out turn were 34.09 and 43.99, respectively which showed the presence of variation in ginning out turn among the genotypes (Table 61). The genotypic and phenotypic variance for this trait was 4.0 and 4.18, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (5.15 and 5.04, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were high (96%) with low genetic advance (4.03) and genetic advance in mean (10.16%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for cotton plant height has been also reported in Rehman *et al*. (2020); Devidas *et al*. (2017); Kumar and Katageri (2017); Shahzad *et al*. (2015) and Jarwar *et al*. (2018).

#### 4.3.1.3.11 Seed index

Minimum and maximum values of seed index were 6.95 and 10.10, respectively which showed the presence of variation in seed index among the genotypes (Table 61). The genotypic and phenotypic variance for this trait was 0.59 and 0.60, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (9.25 and 9.19, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that

environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were high (99%) with low genetic advance (1.58) and genetic advance in mean (18.81%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for seed index has been also reported in Rehman *et al*. (2020).

#### 4.3.1.3.12 Lint index

Minimum and maximum values of lint index were 4.58 and 6.47, respectively which showed the presence of variation in lint index among the genotypes (Table 61). The genotypic and phenotypic variance for this trait was 0.26 and 0.27, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (9.35 and 9.17, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were high (96%) with low genetic advance (1.02) and genetic advance in mean (18.53%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for lint index has been also reported in Rehman *et al*. (2020).

#### 4.3.1.3.13 Seed cotton yield per hectare

Minimum and maximum values of seed cotton yield per hectare were 2.91 and 5.80, respectively which showed the presence of variation in seed cotton yield per hectare

among the genotypes (Table 61). The genotypic and phenotypic variance for this trait was 0.60 and 0.62, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were medium (18.82 and 18.63, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV are very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were high (98%) with low genetic advance (1.58) and genetic advance in mean (37.99%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for cotton plant height has been also reported in Rehman *et al*. (2020).

#### 4.3.1.4 Correlation coefficient

Correlation studies along with path analysis provide a better understanding of the association of different characters with yield related traits. Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components as suggested by Sing and Chaudhary 1985. Genotypic and phenotypic correlation coefficients among the different pairs for different genotypes of cotton are given in Table 62 and Table 63 respectively.

In case of genotypic correlation coefficient, plant height showed statistical positive significant correlation with no. of fruiting branches (0.94), no. of bolls per plant (0.95), seed cotton yield per hectare (0.85) and non-significant correlation with days to first square initiation (0.34), days to first flower initiation (0.31), days to first boll split (0.37), no. of vegetative branches (-0.12), days to first boll bursting (-0.35), single boll weight (0.12), ginning out turn (-0.03), seed index (0.06) and lint index (0.002). (Table 62). Days to first square initiation showed statistical positive significant correlation with days to first flower initiation (0.99), days to first boll split (1.0), seed

**Table 62. Genotypic correlation coefficient among the yield and yield contributing characters of cotton genotypes**

| Characters | Plant height | Days to 1st square initiation | Days to 1st flower initiation | Days to 1st boll split | No. of vegetative branches | No. of fruiting branches | No. of bolls/plant | Days to 1st boll bursting | Singles boll weight | Ginning Out Turn | Seed index | Lint index | Seed cotton yield/ha |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Plant height** | | 0.34$^{NS}$ | 0.31$^{NS}$ | 0.37$^{NS}$ | -0.12$^{NS}$ | 0.94** | 0.95** | -0.35$^{NS}$ | 0.12$^{NS}$ | -0.03$^{NS}$ | 0.06$^{NS}$ | 0.002$^{NS}$ | 0.85 ** |
| **Days to 1st square initiation** | | | 0.99** | 1 ** | -0.01$^{NS}$ | 0.36$^{NS}$ | 0.35$^{NS}$ | 0.23$^{NS}$ | 0.27$^{NS}$ | -0.28$^{NS}$ | 0.38$^{NS}$ | 0.10$^{NS}$ | 0.42* |
| **Days to 1st flower initiation** | | | | 0.99 ** | -0.01$^{NS}$ | 0.32$^{NS}$ | 0.32$^{NS}$ | 0.23$^{NS}$ | 0.24$^{NS}$ | -0.27$^{NS}$ | 0.36$^{NS}$ | 0.09$^{NS}$ | 0.38$^{NS}$ |
| **Days to 1st boll split** | | | | | -0.06NS | 0.40 * | 0.38$^{NS}$ | 0.23$^{NS}$ | 0.27$^{NS}$ | -0.30$^{NS}$ | 0.39$^{NS}$ | 0.09$^{NS}$ | 0.44 * |
| **No. of vegetative branches** | | | | | | -0.41* | -0.30$^{NS}$ | 0.34$^{NS}$ | -0.16$^{NS}$ | 0.19$^{NS}$ | 0.03$^{NS}$ | 0.24$^{NS}$ | -0.29$^{NS}$ |
| **No. of fruiting** | | | | | | | 0.99** | -0.39$^{NS}$ | 0.20$^{NS}$ | -0.11$^{NS}$ | 0.07$^{NS}$ | -0.07$^{NS}$ | 0.91 ** |
| **No. of bolls/plant** | | | | | | | | -0.37$^{NS}$ | 0.21$^{NS}$ | -0.05$^{NS}$ | 0.09$^{NS}$ | 0.01$^{NS}$ | 0.92 ** |
| **Days to 1st boll bursting** | | | | | | | | | 0.35$^{NS}$ | -0.33$^{NS}$ | 0.50 ** | 0.20$^{NS}$ | -0.16$^{NS}$ |
| **Singles boll weight** | | | | | | | | | | -0.39 * | 0.80** | 0.41 * | 0.56 ** |
| **Ginning Out Turn** | | | | | | | | | | | -0.44* | 0.49 * | -0.20$^{NS}$ |
| **Seed index** | | | | | | | | | | | | 0.55** | 0.39 * |
| **Lint index** | | | | | | | | | | | | | 0.17$^{NS}$ |
| **Seed yield/ha** | | | | | | | | | | | | | |

**Table 63. Phenotypic correlation coefficient among the yield and yield contributing characters of cotton genotypes**

| Characters | Plant height | Days to 1st square initiation | Days to 1st flower initiation | Days to 1st boll split | No. of vegetative branches | No. of fruiting branches | No. of bolls/plant | Days to 1st boll bursting | Singles boll weight | Ginning Out Turn | Seed index | Lint index | Seed cotton yield/ha |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Plant height** | | 0.30 ** | 0.27 * | 0.32 ** | -0.10 NS | 0.92 ** | 0.93 ** | -0.35 ** | 0.12 NS | -0.03 NS | 0.06 NS | 0.003NS | 0.84 ** |
| **Days to 1st square initiation** | | | 0.98 ** | 0.93 ** | 0.005 NS | 0.29 * | 0.33 ** | 0.19 NS | 0.24 * | -0.23 * | 0.32 ** | 0.08 NS | 0.38 ** |
| **Days to 1st flower initiation** | | | | 0.95 ** | -0.01 NS | 0.26 * | 0.304 ** | 0.19NS | 0.22 NS | -0.23 * | 0.31 ** | 0.08 NS | 0.35 ** |
| **Days to 1st boll split** | | | | | -0.053 NS | 0.32 ** | 0.35 ** | 0.17 NS | 0.23 * | -0.25 * | 0.32 ** | 0.06 NS | 0.39 ** |
| **No. of vegetative branches** | | | | | | -0.39 ** | -0.27 * | 0.31 ** | -0.15NS | 0.18 NS | 0.03 NS | 0.21 NS | -0.27 * |
| **No. of fruiting** | | | | | | | 0.96 ** | -0.37 ** | 0.19 NS | -0.11 NS | 0.06 NS | -0.06 NS | 0.88 ** |
| **No. of bolls/plant** | | | | | | | | -0.36 ** | 0.20 NS | -0.05 NS | 0.08 NS | 0.003 NS | 0.92** |
| **Days to 1st boll bursting** | | | | | | | | | 0.35 ** | -0.32 ** | 0.50 ** | 0.19 NS | -0.16 NS |
| **Singles boll weight** | | | | | | | | | | -0.39 ** | 0.79 ** | 0.40 ** | 0.55 ** |
| **Ginning Out Turn** | | | | | | | | | | | -0.44 ** | 0.50 ** | -0.19 NS |
| **Seed index** | | | | | | | | | | | | 0.54** | 0.38 ** |
| **Lint index** | | | | | | | | | | | | | 0.16 NS |
| **Seed yield/ha** | | | | | | | | | | | | | |

cotton yield per hectare (0.42) and non-significant correlation with no. of vegetative branches (-0.01), no. of fruiting branches (0.36), no. of bolls per plant (0.35), days to first boll bursting (0.23), single boll weight (0.27), ginning out turn (-0.28), seed index (0.38) and lint index (0.10). Days to first flower initiation showed significant positive correlation with days to first boll split (0.99) and non-significant relation with no. of vegetative branches (-0.01), no. of fruiting branches (0.32), no. of bolls per plant (0.32), days to first boll bursting (0.23), single boll weight (0.24), ginning out turn (-0.27), seed index (0.36), lint index (0.09) and) seed cotton yield per hectare (0.38). Days to first boll split showed significant positive correlation with no. of fruiting branches (0.40), seed cotton yield per hectare (0.44) and non-significant correlation with no. of vegetative branches (-0.06), no. of bolls per plant (0.38), days to first boll bursting (0.23), single boll weight (0.27), ginning out turn (-0.30), seed index (0.39) and lint index (0.09). No. of vegetative branches showed negative correlation with no. of fruiting branches (-0.41) and non-significant correlation with no. of bolls per plant (-0.30), days to first boll bursting (0.34), single boll weight (-0.16), ginning out turn (0.19), seed index (0.03), lint index (0.24) and seed cotton yield per hectare (-0.29). No. of fruiting branch showed significant positive correlation with no. of bolls per plant (0.99), seed cotton yield per hectare (0.91) and non-significant correlation with days to first boll bursting (-0.39), single boll weight (0.20), ginning out turn (-0.11), seed index (0.07) and lint index (-0.07). No. of bolls per plant showed significant positive correlation with seed cotton yield per hectare (0.92) and non-significant correlation with days to first boll bursting (-0.37), single boll weight (0.21), ginning out turn (-0.05), seed index (0.09) and lint index (0.01). Number of boll per plant was correlated with boll weight as advocated by Manzoor and Azhar (2000) and seed cotton weight per boll. Days to first boll bursting showed significant correlation with seed index (0.50) and non-significant correlation with single boll weight (0.35), ginning out turn (-0.33), lint index (0.20) and seed cotton yield per hectare (-0.16). Single boll weight showed significant positive correlation with seed index (0.80), lint index (0.41), seed cotton yield per hectare (0.56) and significant negative correlation with ginning out turn (-0.39). Boll weight was positively linked with bolls per plant, sympodial branches per plant, 100 seed weight, staple length and fibre fineness. Jatt *et al*. (2007) revealed that boll weight had positive association with yield of seed cotton. Abdullah *et al*. (2016) and Shaheen and Yaseen (2014) observed that boll weight was positively correlated withfibre length, fibre fineness and sympodial branches per plant.

Ginning out turn showed significant positive correlation with lint index (0.49), negative correlation with seed index (-0.44) and non-significant correlation with seed cotton yield per hectare (-0.20). Seed index showed significant positive correlation with lint index (0.55) and seed cotton yield per hectare (0.39). Seed index had positive linkage with bolls per plant, boll weight and fibre length. Patil (2010), Komala *et al*. (2018), Memon *et al*. (2017), Isong *et al*. (2017), Ashokkumar and Ravikesavan (2010), Shabbir *et al*. (2016) and Méndez *et al*. (2012) depicted similar findings. Lint index showed non-significant correlation with seed cotton yield per hectare (0.17). At the genotypic level, Adeela *et al*. (2021) showed that plant height showed significant positive correlation with number of reproductive branches, number of vegetative branches and root diameter. He also showed that vegetative branches per plant showed non-significant positive correlation with number of reproductive branches which have been observed in our experiment as well. Bolls per plant had positive association with plant height, boll weight, sympodial branches per plant, seed index, seed cotton yield and fibre strength. Ahmad and Azhar (2000), Djaboutou *et al*. (2005), Gul *et al*. (2014), Magadum *et al*. (2012), Alkuddsi *et al*. (2013) and Farooq *et al*. (2014), also found same results. Sympodial branches per plant had positive relationship with plant height, number of bolls per plant, boll weight, seed cotton yield, GOT, staple length and fibre fineness. Pujer *et al*. (2014), Joshi *et al*. (2006), Anandan (2009) indicated that sympodial branches/plant positively correlated with seed cotton yield, plant height, GOT and boll weight. Whereas, Killi *et al*. (2005) found that sympodial branches per plant were positively linked with fibre strength. Rauf *et al*. (2004) also observed that sympodial branches per plant had positive relationship with number of bolls per plant and fibre fineness. Majeedano *et al*. (2014), Joshi *et al*. (2006), Gite *et al*. (2006) and Latif *et al*. (2015) indicated that seed cotton yield was positively linked with plant height, sympodial branches per plant and number of bolls/plant. Monisha *et al*. (2018) determined positive correlation among GOT, fibre strength and seed cotton yield.

In case of phenotypic correlation coefficient, plant height showed statistical positive significant correlation with days to first square initiation (0.30), days to first flower initiation (0.27), days to first boll split (0.32), no. of fruiting branch (0.92), no. of bolls per plant (0.93), seed cotton yield per hectare (0.84), negative significant correlation with days to first boll bursting (-0.35) and non-significant correlation with no. of

vegetative branches (-0.10), single boll weight (0.12), ginning out turn (-0.03), seed index (0.06) and lint index (0.003). (Table 63). Days to first square initiation showed statistical positive significant correlation with days to first flower initiation (0.98), days to first boll split (0.93), no. of fruiting branches (0.29), no. of bolls per plant (0.33), single boll weight (0.24), seed index (0.32) and seed cotton yield per hectare (0.38), negative correlation with ginning out turn (-0.23) and non-significant correlation with no. of vegetative branches (0.005), days to first boll bursting (0.19) and lint index (0.08). Days to first flower initiation showed significant positive correlation with days to first boll split (0.95), no. of fruiting branches (0.26), no. of bolls per plant (0.304), seed index (0.31), seed cotton yield per hectare (0.35), negative correlation with ginning out turn (-0.23) and non-significant relation with no. of vegetative branches (-0.01), days to first boll bursting (0.19), single boll weight (0.22), lint index (0.08). Days to first boll split showed significant positive correlation with no. of fruiting branch (0.32), no. of bolls per plant (0.35), single boll weight (0.23), seed index (0.32), seed cotton yield per hectare (0.39), negative correlation with ginning out turn (-0.25) and non-significant correlation with no. of vegetative branches (-0.053), days to first boll bursting (0.17) and lint index (0.06). No. of vegetative branches showed significant positive correlation with days to first boll bursting (0.31), negative correlation with no. of fruiting branches (-0.39), no. of bolls per plant (-0.27), seed cotton yield per hectare (-0.27) and non-significant correlation with single boll weight (-0.15), ginning out turn (0.18), seed index (0.03) and lint index (0.21). No. of fruiting branches showed significant positive correlation with no. of bolls per plant (0.96), seed cotton yield per hectare (0.88), negative correlation with days to first boll bursting (-0.37) and non-significant correlation with single boll weight (0.19), ginning out turn (-0.11), seed index (0.06) and lint index (-0.06). No. of bolls per plant showed significant positive correlation with seed cotton yield per hectare (0.92), negative correlation with days to first boll bursting (-0.36) and non-significant correlation with single boll weight (0.20), ginning out turn (-0.05), seed index (0.08) and lint index (0.003). Days to first boll bursting showed significant positive correlation with single boll weight (0.35), seed index (0.50), negative correlation with ginning out turn (-0.32) and non-significant correlation with lint index (0.19) and seed cotton yield per hectare (-0.16). Single boll weight showed significant positive correlation with seed index (0.79), lint index (0.40), seed cotton yield per hectare (0.55) and significant negative correlation with ginning out turn (-0.39).

Ginning out turn showed significant positive correlation with lint index (0.50), negative correlation with seed index (-0.44) and non-significant correlation with seed cotton yield per hectare (-0.19). Seed index showed significant positive correlation with lint index (0.54) and seed cotton yield per hectare (0.38). Lint index showed non-significant correlation with seed cotton yield per hectare (0.16). At the genotypic level, Adeela *et al*. (2021) showed that plant height showed significant positive correlation with number of reproductive branches, number of vegetative branches and root diameter. He also showed that vegetative branches per plant showed non-significant positive correlation with number of reproductive branches which have been observed in our experiment as well. According to Grimes *et al*. (1969) there is a positive correlation between the yield and the number of bolls retention, however, the physiochemical or metabolic functions affecting boll formation have not been observed.

#### 4.3.1.5 Path coefficient analysis

Path coefficient is a means of measuring the direct and indirect effects of one variable through the other variables on the end-product. Here seed cotton yield per hectare was considered as effect (dependent variable) and plant height, days to first square initiation, days to first flower initiation, days to first boll split, no. of vegetative branch, no. of fruiting branch, no. of bolls per plant, days to first boll bursting, single boll weight, ginning out turn, seed index and lint index were considered as independent variables. Wright (1921) developed the path coefficient analysis technique and later demonstrated by Deway and Lu (1959) facilitates the partitioning of correlation coefficients into direct and indirect contribution of various characters on seed cotton yield per hectare. It is standardized partial regression coefficient analysis. As such, it measures the direct influence if one variable upon other. Estimation of direct and indirect effect of path coefficient analysis is presented in Table 64 and Table 65.

In case of genotypic path coefficient analysis, plant height had positive direct effect on seed cotton yield per hectare (0.08) which is contributed to result significant positive genotypic correlation (0.85) (Table 64). Plant height had positive indirect effect on days to first flower initiation (0.10), no. of bolls per plant (0.99), single boll weight

**Table 64. Genotypic path coefficient analysis showing the direct (bold) and indirect effect of different characters on seed cotton yield per ha**

| Characters | Plant height | Days to 1st square initiation | Days to 1st flower initiation | Days to 1st boll split | No. of vegetative branches | No. of fruiting branches | No. of bolls/plant | Days to 1st boll bursting | Singles boll weight | Ginning Out Turn | Seed index | Lint index | Genotypic correlation coefficient with Seed cotton yield/ha |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Plant height** | **0.08** | -0.07 | 0.10 | -0.04 | 0.00 | -0.23 | 0.99 | -0.01 | 0.04 | 0.01 | -0.03 | 0.00 | 0.85 ** |
| **Days to 1st square initiation** | 0.03 | **-0.21** | 0.31 | -0.10 | 0.00 | -0.09 | 0.37 | 0.00 | 0.10 | 0.13 | -0.18 | 0.05 | 0.42* |
| **Days to 1st flower initiation** | 0.02 | -0.21 | **0.31** | -0.10 | 0.00 | -0.08 | 0.33 | 0.00 | 0.09 | 0.13 | -0.17 | 0.04 | 0.38 NS |
| **Days to 1st boll split** | 0.03 | -0.21 | 0.31 | **-0.10** | 0.00 | -0.10 | 0.40 | 0.00 | 0.10 | 0.14 | -0.18 | 0.05 | 0.44 * |
| **No. of vegetative branches** | -0.01 | 0.00 | 0.00 | 0.01 | **-0.04** | 0.10 | -0.32 | 0.01 | -0.06 | -0.09 | -0.02 | 0.12 | -0.29 NS |
| **No. of fruiting** | 0.07 | -0.07 | 0.10 | -0.04 | 0.02 | **-0.25** | 1.03 | -0.01 | 0.07 | 0.05 | -0.03 | -0.04 | 0.91 ** |
| **No. of bolls/plant** | 0.07 | -0.07 | 0.10 | -0.04 | 0.01 | -0.24 | **1.04** | -0.01 | 0.08 | 0.03 | -0.04 | 0.00 | 0.92 ** |
| **Days to 1st boll bursting** | -0.03 | -0.05 | 0.07 | -0.02 | -0.01 | 0.10 | -0.39 | **0.02** | 0.13 | 0.16 | -0.24 | 0.10 | -0.16 NS |
| **Singles boll weight** | 0.01 | -0.06 | 0.08 | -0.03 | 0.01 | -0.05 | 0.22 | 0.01 | **0.36** | 0.18 | -0.37 | 0.21 | 0.56 ** |
| **Ginning Out Turn** | 0.00 | 0.06 | -0.09 | 0.03 | -0.01 | 0.03 | -0.06 | -0.01 | -0.14 | **-0.46** | 0.21 | 0.24 | -0.20 NS |
| **Seed index** | 0.00 | -0.08 | 0.11 | -0.04 | 0.00 | -0.02 | 0.10 | 0.01 | 0.29 | 0.21 | **-0.46** | 0.27 | 0.39 * |
| **Lint index** | 0.00 | -0.02 | 0.03 | -0.01 | -0.01 | 0.02 | 0.01 | 0.00 | 0.15 | -0.23 | -0.26 | **0.49** | 0.17 NS |

Residual = 0.0024

**Table 65. Phenotypic path coefficient analysis showing the direct (bold) and indirect effect of different characters on seed cotton yield per ha**

| Characters | Plant height | Days to 1st square initiation | Days to 1st flower initiation | Days to 1st boll split | No. of vegetative branches | No. of fruiting branches | No. of bolls/plant | Days to 1st boll bursting | Singles boll weight | Ginning Out Turn | Seed index | Lint index | Phenotypic correlation coefficient Seed cotton yield/ha |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Plant height** | **-0.01** | -0.02 | 0.03 | -0.02 | 0.00 | 0.03 | 0.80 | 0.00 | 0.04 | 0.01 | -0.03 | 0.00 | 0.84 ** |
| **Days to 1st square initiation** | 0.00 | **-0.07** | 0.12 | -0.04 | 0.00 | 0.01 | 0.28 | 0.00 | 0.09 | 0.11 | -0.15 | 0.04 | 0.38 ** |
| **Days to 1st flower initiation** | 0.00 | -0.07 | **0.12** | -0.05 | 0.00 | 0.01 | 0.26 | 0.00 | 0.08 | 0.11 | -0.15 | 0.04 | 0.35 ** |
| **Days to 1st boll split** | 0.00 | -0.07 | 0.12 | **-0.05** | 0.00 | 0.01 | 0.30 | 0.00 | 0.08 | 0.12 | -0.15 | 0.03 | 0.39 ** |
| **No. of vegetative branches** | 0.00 | 0.00 | 0.00 | 0.00 | **0.02** | -0.01 | -0.23 | 0.00 | -0.06 | -0.08 | -0.02 | 0.11 | -0.27 * |
| **No. of fruiting** | -0.01 | -0.02 | 0.03 | -0.02 | -0.01 | **0.03** | 0.82 | 0.00 | 0.07 | 0.05 | -0.03 | -0.03 | 0.88 ** |
| **No. of bolls/plant** | -0.01 | -0.02 | 0.04 | -0.02 | -0.01 | 0.03 | **0.85** | 0.00 | 0.08 | 0.02 | -0.04 | 0.00 | 0.92** |
| **Days to 1st boll bursting** | 0.00 | -0.01 | 0.02 | -0.01 | 0.01 | -0.01 | -0.31 | **0.00** | 0.13 | 0.15 | -0.23 | 0.10 | -0.16 NS |
| **Singles boll weight** | 0.00 | -0.02 | 0.03 | -0.01 | 0.00 | 0.01 | 0.18 | 0.00 | **0.36** | 0.18 | -0.37 | 0.21 | 0.55 ** |
| **Ginning Out Turn** | 0.00 | 0.02 | -0.03 | 0.01 | 0.00 | 0.00 | -0.05 | 0.00 | -0.14 | **-0.47** | 0.21 | 0.26 | -0.19 NS |
| **Seed index** | 0.00 | -0.02 | 0.04 | -0.02 | 0.00 | 0.00 | 0.08 | 0.00 | 0.29 | 0.21 | **-0.47** | 0.28 | 0.38 ** |
| **Lint index** | 0.00 | -0.01 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.15 | -0.24 | -0.26 | **0.51** | 0.16 NS |

Residual =0.0015

(0.04), ginning out turn (0.01) and negative indirect effect on days to first square initiation (-0.07), days to first boll split (-0.04), no. of fruiting branches (-0.23), days to first boll bursting (-0.01), seed index (-0.03) and no effect on no. of vegetative branches (0.00), lint index (0.00) (Table 68). Days to first square initiation showed negative direct effect (-0.21) on seed cotton yield per hectare with significant positive genotypic correlation (0.42). Days to first square initiation had positive indirect effect on plant height (0.03), days to first flower initiation (0.31), no. of bolls per plant (0.37), single boll weight (0.10), ginning out turn (0.13), lint index (0.05) and negative indirect effect on days to first boll split (-0.10), no. of fruiting branches (-0.09), seed index (-0.18) and no effect on no. of vegetative branches (0.00) and days to first boll bursting (0.00). Days to first flower initiation had positive direct effect on seed cotton yield per hectare (0.31) which was contributed to result on non-significant positive genotypic correlation (0.38). Days to first flower initiation had negative indirect effect on days to first square initiation (-0.21), days to first boll split (-0.10), no. of fruiting branches (-0.08), seed index (-0.17) and positive indirect effect on plant height (0.02), no. of bolls per plant (0.33), single boll weight (0.09), ginning out turn (0.13), lint index (0.04) and no effect on no. of vegetative branches (0.00), days to first boll bursting (0.00). Days to first boll split had negative direct effect on seed cotton yield per hectare (-0.10) which was contributed to result in significant positive genotypic correlation (0.44). Days to first boll split had positive indirect effect on plant height (0.03), days to first flower initiation (0.31), no. of bolls per plant (0.40), single boll weight (0.10), ginning out turn (0.14), lint index (0.05) and negative indirect effect on days to first square initiation (-0.21), no. of fruiting branches (-0.10), seed index (-0.18) and no effect on no. of vegetative branches (0.00) and days to first boll bursting (0.00). No. of vegetative branches had direct negative effect on seed cotton yield per hectare (-0.04) which was contributed non-significant negative genotypic correlation (-0.29). No. of vegetative branches had positive indirect effect on days to first boll split (0.01), no. of fruiting branches (0.10), days to first boll bursting (0.01), lint index (0.12) and indirect negative effect on plant height (-0.01), no. of bolls per plant (-0.32), single boll weight (-0.06), ginning out turn (-0.09), seed index (-0.02) and no effect on days to first square initiation (0.00), days to first flower initiation (0.00). No. of fruiting branches had negative direct effect on seed cotton yield per hectare (-0.25) which was contributed significant positive genotypic correlation (0.91). No. of fruiting branches had positive indirect effect on plant height (0.07), days to first flower

initiation (0.10), no. of vegetative branches (0.02), no. of bolls per plant (1.03), single boll weight (0.07), ginning out turn (0.05) and negative indirect effect on days to first square initiation (-0.07), days to first boll split (-0.04), days to first boll bursting (-0.01), seed index (-0.03) and lint index (-0.04). No. of bolls per plant had positive direct effect on seed cotton yield per hectare (1.04) which was contributed significant positive genotypic correlation (0.92). No. of bolls per plant had positive indirect effect on plant height (0.07), days to first flower initiation (0.10), no. of vegetative branches (0.01), single boll weight (0.08), ginning out turn (0.03) and negative indirect effect on days to first square initiation (-0.07), days to first boll split (-0.04), no. of fruiting branches (-0.24), days to first boll bursting (-0.01), seed index (-0.04) and no effect on lint index (0.00). Days to first boll bursting had positive direct effect on seed cotton yield per hectare (0.02) which was contributed non-significant negative genotypic correlation (-0.16). Days to first boll bursting had positive indirect effect on days to first flower initiation (0.07), no. of fruiting branches (0.10), single boll weight (0.13), ginning out turn (0.16), lint index (0.10) and negative indirect effect on plant height (-0.03), days to first square initiation (-0.05), days to first boll split (-0.02), no. of vegetative branches (-0.01), no. of bolls per plant (-0.39), seed index (-0.24). Single boll weight content had positive direct effect on seed cotton yield per hectare (0.36) which was contributed significant positive genotypic correlation (0.56). Single boll weight had positive indirect effect on plant height (0.01), days to first flower initiation (0.08), no. of vegetative branches (0.01), no. of bolls per plant (0.22), days to first boll bursting (0.01), ginning out turn (0.18), lint index (0.21) and negative indirect effect on days to first square initiation (-0.06), days to first boll split (-0.03), no. of fruiting branches (-0.05), seed index (-0.37). Number of boll per plant and boll weight had negative and non-significant direct effect on seed cotton yield. Similar findings were reported by Alishah *et al*. (2008), Manzoor and Azhar (2000) and Baloch *et al*. (2001). Ginning out turn content had negative direct effect on seed cotton yield per hectare (-0.46) which was contributed non-significant negative genotypic correlation (-0.20). Ginning out turn had positive indirect effect on days to first square initiation (0.06), days to first boll split (0.03), no. of fruiting branches (0.03), seed index (0.21), lint index (0.24) and negative indirect effect on days to first flower initiation (-0.09), no. of vegetative branches (-0.01), no. of bolls per plant (-0.06), days to first boll bursting (-0.01), single boll weight (0.14) and no effect on plant height (0.00). Ahsan *et al*. (2015) observed that GOT had positive and direct effects on yield. Seed index content

had negative direct effect on seed cotton yield per hectare (-0.46) which was contributed significant positive genotypic correlation (0.39). Seed index had positive indirect effect on days to first flower initiation (0.11), no. of bolls per plant (0.10), days to first boll bursting (0.01), single boll weight (0.29), ginning out turn (0.21), lint index (0.27) and negative indirect effect on days to first square initiation (-0.08), days to first boll split (-0.04), no. of fruiting branches (-0.02) and no effect on plant height (0.00), no. of vegetative branches (0.00). Lint index content had positive direct effect on seed cotton yield per hectare (0.49) which was contributed non-significant positive genotypic correlation (0.17). Lint index had positive indirect effect on days to first flower initiation (0.03), no. of fruiting branches (0.02), no. of bolls per plant (0.01), single boll weight (0.15), and negative indirect effect on days to first square initiation (-0.02), days to first boll split (-0.01), no. of vegetative branches (-0.01), ginning out turn (-0.23), seed index (-0.26) and no effect on plant height (0.00), days to first boll bursting (0.00). Similar report has been reported by Adeela *et al.* (2021). Genotypic path coefficient analysis carried out by Chapepa *et al*. (2020) showed that plant height and number of lateral roots have the highest direct effect on cotton yield and number of reproductive branches which has also observed in this study. In this study showed the negative direct effect on number of reproductive branches which has been also observed in Rauf *et al*. (2004). Mahdi *et al*. (2021) concluded that the direct and indirect effects of SCY/P components varied greatly under both environments and LY/P, NB/P and NS/B should be considered as selection indices under normal irrigation, NB/P and NS/B under stress when selection practiced for SCY/P. Farooq *et al*. (2014) found positive direct effect of boll weight on seed cotton yield / plant. Ahsan *et al*. (2015) found that bolls plant1 had maximum direct effect followed by the boll weight, seed index and lint index. Joshi and Patil (2018) found that number of bolls/plants had positive indirect effect on seed cotton yield/plant, seed index, lint index, fiber strength etc. Boll weight was responsible for high yield through seed index and lint index.

In case of phenotypic path coefficient analysis, plant height had negative direct effect on seed cotton yield per hectare (-0.01) which was contributed to result significant positive genotypic correlation (0.84) (Table 65). Plant height had positive indirect effect on days to first flower initiation (0.03), no. of fruiting branches (0.03), no. of bolls per plant (0.80), single boll weight (0.04), ginning out turn (0.01) and negative

indirect effect on days to first square initiation (-0.02), days to first boll split (-0.02), seed index (-0.03) and no effect on no. of vegetative branches (0.00), days to first boll bursting (0.00), lint index (0.00) (Table 65). Days to first square initiation showed negative direct effect (-0.07) on seed cotton yield per hectare with significant positive genotypic correlation (0.38). Days to first square initiation had positive indirect effect on days to first flower initiation (0.12), no. of fruiting branches (0.01), no. of bolls per plant (0.28), single boll weight (0.09), ginning out turn (0.11), lint index (0.04) and negative indirect effect on days to first boll split (-0.04), seed index (-0.15) and no effect on plant height (0.00), no. of vegetative branches (0.00) and days to first boll bursting (0.00). Days to first flower initiation had positive direct effect on seed cotton yield per hectare (0.12) which was contributed to result on significant positive genotypic correlation (0.35). Days to first flower initiation had positive indirect effect on no. of fruiting branches (0.01), ), no. of bolls per plant (0.26), single boll weight (0.08), ginning out turn (0.11), lint index (0.04) and negative indirect effect on days to first square initiation (-0.07), days to first boll split (-0.05), seed index (-0.15) and no effect on plant height (0.00), no. of vegetative branches (0.00), days to first boll bursting (0.00). Days to first boll split had negative direct effect on seed cotton yield per hectare (-0.05) which was contributed to result in significant positive genotypic correlation (0.39). Days to first boll split had positive indirect effect on days to first flower initiation (0.12), no. of fruiting branches (0.01), no. of bolls per plant (0.30), single boll weight (0.08), ginning out turn (0.12), lint index (0.03) and negative indirect effect on days to first square initiation (-0.07), seed index (-0.15) and no effect on plant height (0.00), no. of vegetative branches (0.00), days to first boll bursting (0.00). No. of vegetative branches had direct positive effect on seed cotton yield per hectare (0.02) which was contributed significant negative genotypic correlation (-0.27). No. of vegetative branches had positive indirect effect on lint index (0.11) and indirect negative effect on no. of fruiting branches (-0.01), no. of bolls per plant (-0.23), single boll weight (-0.06), ginning out turn (-0.08), seed index (-0.02) and no effect on plant height (0.00), days to first square initiation (0.00), days to first flower initiation (0.00), days to first boll split (0.00), days to first boll bursting (0.00). No. of fruiting branches had positive direct effect on seed cotton yield per hectare (0.03) which was contributed significant positive genotypic correlation (0.88). No. of fruiting branches had positive indirect effect on days to first flower initiation (0.03), no. of bolls per plant (0.82), single boll weight (0.07), ginning out turn (0.05) and negative

indirect effect on plant height (-0.01), days to first square initiation (-0.02), days to first boll split (-0.02), no. of vegetative branches (-0.01), seed index (-0.03), lint index (-0.03) and no effect on days to first boll bursting (0.00). No. of bolls per plant had positive direct effect on seed cotton yield per hectare (0.85) which was contributed significant positive genotypic correlation (0.92). No. of bolls per plant had positive indirect effect on days to first flower initiation (0.04), no. of fruiting branches (0.03), single boll weight (0.08), ginning out turn (0.02) and negative indirect effect on plant height (-0.01), days to first square initiation (-0.02), days to first boll split (-0.02), no. of vegetative branches (-0.01), seed index (-0.04) and no effect on days to first boll bursting (0.00), lint index (0.00). Days to first boll bursting had no direct effect on seed cotton yield per hectare (0.00) which was contributed non-significant negative genotypic correlation (-0.16). Days to first boll bursting had positive indirect effect on days to first flower initiation (0.02), no. of vegetative branches (0.01), single boll weight (0.13), ginning out turn (0.15), lint index (0.10) and negative indirect effect on days to first square initiation (-0.01), days to first boll split (-0.01), no. of fruiting branches (-0.01), no. of bolls per plant (-0.31), seed index (-0.23) and no effect on plant height (0.00). Single boll weight content had positive direct effect on seed cotton yield per hectare (0.36) which was contributed significant positive genotypic correlation (0.55). Single boll weight had positive indirect effect on days to first flower initiation (0.03), no. of fruiting branches (0.01), no. of bolls per plant (0.18), ginning out turn (0.18), lint index (0.21) and negative indirect effect on days to first square initiation (-0.02), days to first boll split (-0.01), seed index (-0.37) and no effect on plant height (0.00), no. of vegetative branches (0.00), days to first boll bursting (0.00). Ginning out turn content had negative direct effect on seed cotton yield per hectare (-0.47) which was contributed non-significant negative genotypic correlation (-0.19). Ginning out turn had positive indirect effect on days to first square initiation (0.02), days to first boll split (0.01), seed index (0.21), lint index (0.26) and negative indirect effect on days to first flower initiation (-0.03), no. of bolls per plant (-0.05), single boll weight (-0.14) and no effect on plant height (0.00), no. of vegetative branches (0.00), no. of fruiting branches (0.00), days to first boll bursting (0.00). Seed index content had negative direct effect on seed cotton yield per hectare (-0.47) which was contributed significant positive genotypic correlation (0.38). Seed index had positive indirect effect on days to first flower initiation (0.04), no. of bolls per plant (0.08), single boll weight (0.29), ginning out turn (0.21), lint index (0.28) and negative

indirect effect on days to first square initiation (-0.02), days to first boll split (-0.02) and no effect on plant height (0.00), no. of vegetative branches (0.00), no. of fruiting branches (0.00), days to first boll bursting (0.00). Seed index was significantly and positively associated with yield and uniformity ratio as displayed by Ahmed *et al*. (2019), and Rai and Sangwan (2020). Lint index content had positive direct effect on seed cotton yield per hectare (0.51) which was contributed non-significant positive genotypic correlation (0.16). Lint index had positive indirect effect on days to first flower initiation (0.01), single boll weight (0.15) and negative indirect effect on days to first square initiation (-0.01), ginning out turn (-0.24), seed index (-0.26) and no effect on plant height (0.00), days to first boll split (0.00), no. of vegetative branches (0.00), no. of fruiting branches (0.00), no. of bolls per plant (0.00), days to first boll bursting (0.00). Genotypic path coefficient analysis carried out by Chapepa *et al*. (2020) showed that plant height and number of lateral roots have the highest direct effect on cotton yield and number of reproductive branches which has also observed in this study. In this study showed the negative direct effect on number of reproductive branches which has been also observed in Rauf *et al*. (2004). Similar results have been reported by Reddy *et al*. (2019) while Kumbhar *et al*. (2020) reported a significantly positive association of plant height with sympodial branches.

#### 4.3.1.8 Selection of genotypes based on selection index

Selection of cotton genotypes for tolerance to drought stress was undertaken at polytheen house of Godagari, Rajshahi. During the cotton seed growing at field under polytheen house, the data of soil nutrient status was calculated by SRDI laboratory, Rajshahi. After seed sowing of each genotype four droughts build up to without irrigation, one irrigation after 40 days, two irrigation after 40 and 60 days interval with control of seed sowing by irrigation. There was very much rain from July to October during growing season. After maturity of boll, the plant height was count the final plant survival, no. of branches and cotton bolls were noted. So selection based on agromorphological or physiological characters at flowering stage may not be as effective for population improvement as it would be effective on the basis of selection indices for which some more yield contributing as well as morphological characters at drought prone areas are given relative weightage. Discriminant functions is a biometrical technique which provides information about the relative contribution of the various component traits to morphology and aids in the isolation from

**Table 66. Relative selection index scores and ranking of twenty five cotton genotypes based on morphological characters**

| Sl. No. | Genotypes | Variety / line | Selection Index score | Rank |
|---|---|---|---|---|
| **1** | G1 | CB-1 | 21.04 | 21 |
| **2** | G2 | CB-2 | 22.64 | 15 |
| **3** | G8 | CB-8 | 25.63 | 5 |
| **4** | G10 | CB-10 | 23.00 | 14 |
| **5** | G11 | CB-11 | 22.58 | 16 |
| **6** | G12 | CB-12 | 25.34 | 7 |
| **7** | G13 | CB-13 | 22.07 | 18 |
| **8** | G14 | CB-14 | 26.28 | 4 |
| **9** | G15 | CB-15 | 25.22 | 8 |
| **10** | G17 | Ra-3 | 21.56 | 19 |
| **11** | G18 | Ra-4 | 24.24 | 9 |
| **12** | G22 | Ra-16 | 23.19 | 12 |
| **13** | G23 | JA-08/9 | 20.99 | 23 |
| **14** | G29 | JA-13/R | 21.32 | 20 |
| **15** | G30 | SR-15 | 22.07 | 17 |
| **16** | G33 | BC-272 | 19.99 | 24 |
| **17** | G34 | BC-385 | 21.02 | 22 |
| **18** | G35 | BC-394 | 25.35 | 6 |
| **19** | G38 | BC-413 | 19.89 | 25 |
| **20** | G39 | BC-415 | 28.64 | 1 |
| **21** | G43 | BC-433 | 27.71 | 2 |
| **22** | G45 | BC-442 | 26.74 | 3 |
| **23** | G46 | BC-462 | 23.88 | 10 |
| **24** | G48 | BC-510 | 23.03 | 13 |
| **25** | G50 | BC-512 | 23.74 | 11 |

populations of superior genotypes by providing information for indirect selection for yield and fibre quality. On the basis of fitted discriminate functions, selection scores were computed and ranked (Table 66) for all the 25 genotypes. Drought tolerance is a quantitative trait, which means that is inhibited by poly genes and has a complex inheritance. Past research focused on physiological traits such as photosynthesis (Jones *et al*., 1999; Nepomuceno *et al*., 1998; Leidi *et al*., 1993), plant turgor maintenance (Quisenberry *et al*., 1983), water use efficiency (Saranga *et al*., 1999; Quisenberry and McMicheal, 1991), biomass accumulation (Hatfield *et al*., 1987; Quisenberry *et al*., 1981) , root growth and root-shoot ratio (McMichael and Quisenberry, 1991; Cook, 1985; Quisenberry *et al*., 1981), cell membrane stability (Rahman *et al*., 2008) and fruiting pattern (Lopez *et al*., 1995; Sharp and Davies, 1989; Burke *et al*., 1985a). These 25 genotypes having good plant morphology as well as yield contributing characters which may generate primary information regarding suitability of deferent genotypes for drought tolerance. The high yield contributing genotypes were selected acceding to top based on selection scores (Expt-3). These genotypes were used as a plant material for yield contributing characters and selection suitable genotypes for drought prone areas.

### 4.3.2 Fibre quality characters of cotton genotypes under drought stress

Fibre quality characters of twenty-five genotypes were observed under four different drought stress conditions. ANOVA showed the significant effect of genotypes, treatment, and interaction on all ten fibre quality characters (Appendix VII).

#### 4.3.2.1 Uniformity index

Genotype, treatment and their interaction significantly affected the uniformity index. The highest mean uniformity index (84.84%) was observed in T4 drought stress whereas the lowest uniformity index (84.15%) was observed in T3 drought stress (Table 67). Among the genotypes, highest uniformity index (85.28%) was observed in G2 and lowest (83.26%) in G48. Based on the genotype stress interaction, highest uniformity index (85.94%) and lowest (81.02%) was observed in G46 under T4 and G29 under T3 stress, respectively. On the basis of b values, the best performance (highest b value) was observed in genotype G14 (0.88) followed by G29 (0.70) and lowest in G38 (-0.65). With the increase of drought stress, uniformity index was decreased as shown in linear regression in Figure 76. The minimum reduction%

## Table 67. Uniformity index of twenty-five genotypes at different drought treatments

| Genotype | Uniformity index (%) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 85.47 | 84.37 | 85.38 | 85.32 | 85.14 | 1.29 | 0.10 | 0.17 | 0.52 | 0.11 | 11 |
| G2 | 85.34 | 85.12 | 85.06 | 85.59 | 85.28 | 0.26 | 0.34 | -0.29 | 0.10 | 0.08 | 12 |
| G8 | 84.15 | 85.01 | 82.13 | 85.28 | 84.15 | -1.02 | 2.40 | -1.34 | 0.01 | 0.36 | 5 |
| G10 | 84.15 | 83.46 | 85.70 | 85.49 | 84.70 | 0.82 | -1.84 | -1.58 | -0.87 | -0.21 | 22 |
| G11 | 85.04 | 84.12 | 84.26 | 85.59 | 84.75 | 1.07 | 0.92 | -0.65 | 0.45 | 0.25 | 7 |
| G12 | 83.74 | 85.27 | 83.62 | 85.54 | 84.54 | -1.83 | 0.15 | -2.15 | -1.28 | -0.06 | 18 |
| G13 | 85.02 | 84.40 | 85.18 | 85.26 | 84.97 | 0.73 | -0.19 | -0.28 | 0.08 | 0.03 | 15 |
| G14 | 85.33 | 83.75 | 81.46 | 84.20 | 83.69 | 1.85 | 4.54 | 1.33 | 2.58 | 0.88 | 1 |
| G15 | 85.12 | 85.42 | 85.02 | 85.11 | 85.17 | -0.35 | 0.11 | 0.02 | -0.07 | -0.01 | 16 |
| G17 | 85.13 | 83.17 | 85.59 | 84.10 | 84.50 | 2.31 | -0.54 | 1.21 | 0.99 | 0.05 | 13 |
| G18 | 83.29 | 84.21 | 85.56 | 84.28 | 84.33 | -1.10 | -2.73 | -1.19 | -1.68 | -0.51 | 23 |
| G22 | 85.06 | 83.13 | 82.55 | 83.55 | 83.57 | 2.27 | 2.95 | 1.77 | 2.33 | 0.62 | 3 |
| G23 | 83.67 | 84.17 | 84.28 | 85.08 | 84.30 | -0.61 | -0.73 | -1.69 | -1.01 | -0.12 | 20 |
| G29 | 84.83 | 85.00 | 81.02 | 83.07 | 83.48 | -0.20 | 4.48 | 2.07 | 2.12 | 0.70 | 2 |
| G30 | 84.05 | 84.48 | 84.21 | 85.76 | 84.63 | -0.52 | -0.19 | -2.04 | -0.92 | -0.02 | 17 |
| G33 | 85.61 | 85.68 | 84.23 | 85.39 | 85.23 | -0.09 | 1.60 | 0.25 | 0.59 | 0.26 | 6 |
| G34 | 83.52 | 83.36 | 84.25 | 85.27 | 84.10 | 0.20 | -0.87 | -2.10 | -0.92 | -0.08 | 19 |
| G35 | 85.45 | 85.04 | 85.08 | 82.94 | 84.63 | 0.48 | 0.43 | 2.94 | 1.28 | 0.04 | 14 |
| G38 | 81.36 | 85.50 | 83.13 | 83.54 | 83.38 | -5.08 | -2.17 | -2.68 | -3.31 | -0.65 | 24 |
| G39 | 85.06 | 84.19 | 85.29 | 85.56 | 85.02 | 1.03 | -0.26 | -0.58 | 0.06 | 0.04 | 14 |
| G43 | 83.24 | 83.11 | 84.27 | 85.04 | 83.92 | 0.16 | -1.23 | -2.16 | -1.08 | -0.14 | 21 |
| G45 | 85.55 | 84.54 | 85.09 | 85.28 | 85.11 | 1.17 | 0.54 | 0.31 | 0.67 | 0.17 | 9 |
| G46 | 85.10 | 85.25 | 84.49 | 85.94 | 85.20 | -0.18 | 0.71 | -0.99 | -0.15 | 0.13 | 10 |
| G48 | 84.00 | 81.85 | 83.87 | 83.32 | 83.26 | 2.56 | 0.15 | 0.81 | 1.17 | 0.19 | 8 |
| G50 | 85.31 | 85.42 | 82.90 | 85.42 | 84.76 | -0.13 | 2.82 | -0.13 | 0.85 | 0.47 | 4 |
| Mean (T) | 84.54 | 84.36 | 84.15 | 84.84 | | | | | | | |

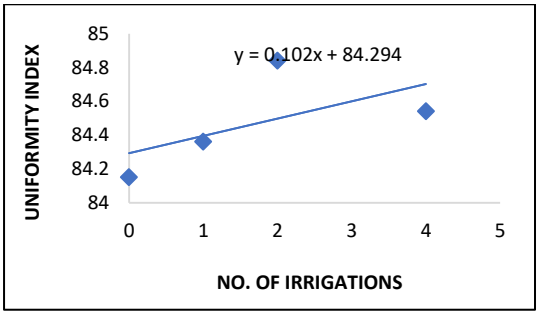



**Figure 76. Relationships between uniformity index of cotton genotypes and different drought stresses**

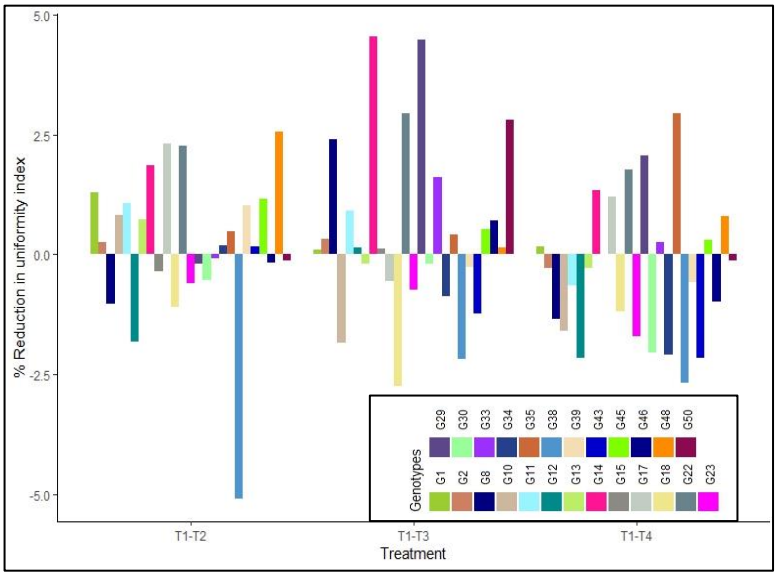



**Figure 77. Reduction percentage of uniformity index of twenty-five cotton genotypes under different drought stresses compared with control**

(-5.08%) was observed in G38 under T2 drought stress (Figure 77, Table 67). Maximum reduction% (4.54%) was observed in G14 under T3 stress (Figure 77). The result showed the negative effect of drought stress on uniformity index in genotypic dependent manner. Some of the genotypes showed an increase in uniformity index at mild and moderate drought stress. However, the maximum genotypes showed a decrease of uniformity index under the severe drought stress. Similar result has been observed in Yagmur *et al*. (2014). Drought stress disturbs fiber development by decreasing leaf water potential, cell expansion, and carbohydrate metabolism, resulting in reduced the quality of developing fiber of upland cotton by lowering the length, uniformity and strength of developing fiber (Witt *et al*., 2020). Drought stress disturbs the fiber cell turgor pressure (Wang *et al*., 2016a; Ullah *et al*., 2017) leading to reduced fiber length, uniformity, and strength.

#### 4.3.2.2 Short fibre index

Genotype, treatment and their interaction significantly affected the short fibre index. The highest mean short fibre index (7.74) was observed in T3 drought stress whereas the lowest short fibre index (7.18) was observed in T4 drought stress (Table 68). Among the genotypes, highest short fibre index (8.45) was observed in G29 and lowest (6.92) in G39. Based on the genotype stress interaction, highest short fibre index (10.53) and lowest (6.77) was observed in G29 under T3 and G15 under T2, G39 under T4 stress respectively. On the basis of b values, the best performance (lowest b value) was observed in genotype G14 (-0.67) followed by G29 (-0.47) and highest in G38 (0.70). With the increase of drought stress, short fibre index was increased as shown in linear regression in Figure 78. The minimum reduction% (-44.20%) was observed in G14 under T3 drought stress (Figure 78, Table 68). Maximum reduction% (32.23%) was observed in G38 under T2 stress (Figure 79). The result showed the negative effect of drought stress on short fibre index in genotypic dependent manner. Some of the genotypes showed a decrease in short fibre index at mild and moderate drought stress. However, the maximum genotypes showed an increase of short fibre index under the severe drought stress. Yagmur *et al*. (2014) reported that lint properties such as fiber length, fineness, uniformity, and strength were reduced under limited water levels, except for short fiber index.

## Table 68. Short fibre index (%) of twenty-five genotypes at different drought treatments

| Genotype | Short fiber index at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 6.83 | 7.37 | 6.80 | 6.98 | 7.00 | -7.80 | 0.49 | -2.20 | -3.17 | -0.03 | 14 |
| G2 | 6.90 | 7.03 | 7.07 | 6.83 | 6.96 | -1.93 | -2.42 | 0.97 | -1.13 | -0.05 | 13 |
| G8 | 7.50 | 7.17 | 9.13 | 6.90 | 7.68 | 4.44 | -21.78 | 8.00 | -3.11 | -0.32 | 5 |
| G10 | 7.73 | 8.07 | 7.07 | 6.78 | 7.41 | -4.31 | 8.62 | 12.28 | 5.53 | 0.08 | 18 |
| G11 | 7.13 | 7.40 | 7.30 | 6.80 | 7.16 | -3.74 | -2.34 | 4.67 | -0.47 | -0.07 | 11 |
| G12 | 7.77 | 6.93 | 7.90 | 6.80 | 7.35 | 10.73 | -1.72 | 12.45 | 7.15 | 0.02 | 16 |
| G13 | 7.03 | 7.40 | 7.77 | 6.87 | 7.27 | -5.21 | -10.43 | 2.37 | -4.42 | -0.18 | 7 |
| G14 | 6.90 | 7.77 | 9.95 | 7.52 | 8.03 | -12.56 | -44.20 | -8.94 | -21.90 | -0.67 | 1 |
| G15 | 6.97 | 6.77 | 7.43 | 6.87 | 7.01 | 2.87 | -6.70 | 1.44 | -0.80 | -0.08 | 10 |
| G17 | 6.95 | 7.50 | 6.82 | 7.20 | 7.12 | -7.91 | 1.92 | -3.60 | -3.20 | -0.01 | 15 |
| G18 | 8.00 | 7.48 | 6.80 | 6.90 | 7.30 | 6.46 | 15.00 | 13.75 | 11.74 | 0.25 | 21 |
| G22 | 7.00 | 8.27 | 8.77 | 7.90 | 7.98 | -18.10 | -25.24 | -12.86 | -18.73 | -0.44 | 3 |
| G23 | 7.77 | 7.33 | 7.80 | 6.98 | 7.47 | 5.58 | -0.43 | 10.09 | 5.08 | 0.01 | 15 |
| G29 | 7.80 | 7.10 | 10.53 | 8.37 | 8.45 | 8.97 | -35.04 | -7.26 | -11.11 | -0.47 | 2 |
| G30 | 7.50 | 7.30 | 7.97 | 6.80 | 7.39 | 2.67 | -6.22 | 9.33 | 1.93 | -0.10 | 9 |
| G33 | 6.80 | 6.80 | 7.57 | 6.97 | 7.03 | 0.00 | -11.27 | -2.45 | -4.58 | -0.15 | 8 |
| G34 | 8.03 | 7.50 | 7.37 | 6.87 | 7.44 | 6.64 | 8.30 | 14.52 | 9.82 | 0.15 | 19 |
| G35 | 6.80 | 7.13 | 6.98 | 8.57 | 7.37 | -4.90 | -2.70 | -25.98 | -11.19 | -0.01 | 15 |
| G38 | 10.03 | 6.80 | 7.63 | 7.97 | 8.11 | 32.23 | 23.92 | 20.60 | 25.58 | 0.70 | 22 |
| G39 | 7.03 | 7.03 | 6.86 | 6.77 | 6.92 | 0.00 | 2.46 | 3.79 | 2.09 | 0.03 | 17 |
| G43 | 8.07 | 7.52 | 7.23 | 7.08 | 7.48 | 6.82 | 10.33 | 12.19 | 9.78 | 0.19 | 20 |
| G45 | 6.97 | 7.61 | 7.03 | 7.15 | 7.19 | -9.23 | -0.96 | -2.63 | -4.27 | -0.06 | 12 |
| G46 | 6.97 | 6.90 | 7.30 | 6.80 | 6.99 | 0.96 | -4.78 | 2.39 | -0.48 | -0.07 | 10 |
| G48 | 7.57 | 9.52 | 7.77 | 8.02 | 8.22 | -25.77 | -2.64 | -5.95 | -11.45 | -0.19 | 6 |
| G50 | 6.87 | 7.02 | 8.53 | 6.87 | 7.32 | -2.18 | -24.27 | 0.00 | -8.82 | -0.35 | 4 |
| Mean (T) | 7.40 | 7.39 | 7.74 | 7.18 | | | | | | | |

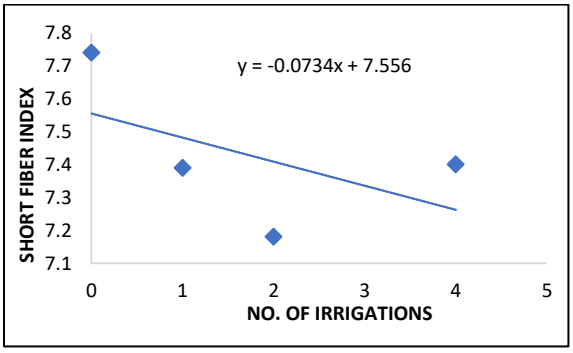



**Figure 78. Relationships between short fibre index of cotton genotypes and different drought stresses**

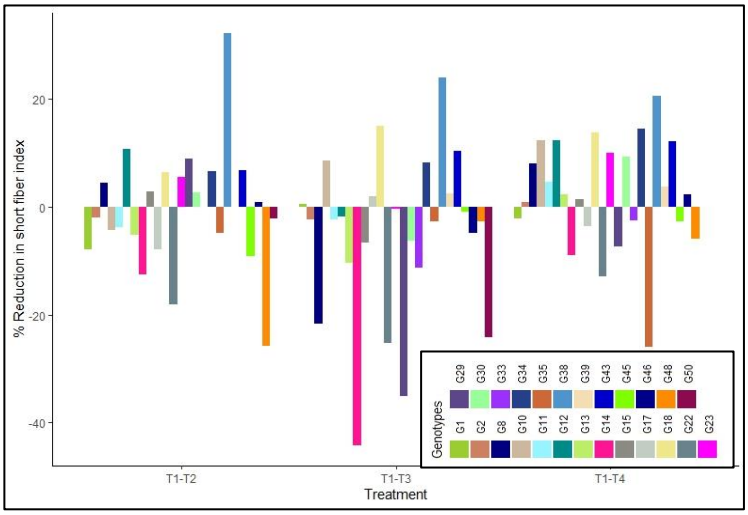



**Figure 79. Reduction percentage of short fibre index of twenty-five cotton genotypes under different drought stresses compared with control**

#### 4.3.2.3 Fibre strength

Genotype, treatment and their interaction significantly affected the fibre strength. The highest mean fibre strength (29.69 g/tex) was observed in T1 drought stress whereas the lowest fibre strength (28.77 g/tex) was observed in T3 drought stress (Table 69). Among the genotypes, highest fibre strength (30.31 g/tex) was observed in G46 and lowest (26.86 g/tex) in G17. Based on the genotype stress interaction, highest fibre strength (31.13 g/tex) was observed in G33 under T1, G46 under T4 and lowest (25.07 g/tex) was observed in G11 under T4, respectively. On the basis of b values, the best performance (highest b value) was observed in genotype G22 (0.71) followed by G29 (0.64) and lowest in G18 (-0.39). With the increase of drought stress, fibre strength was decreased as shown in linear regression in Figure 80. The minimum reduction% (-6.87%) was observed in G38 under T2 drought stress (Figure 81, Table 69). Maximum reduction% (14.57%) was observed in G11 under T4 stress (Figure 81). The result showed the negative effect of drought stress on fibre strength in genotypic dependent manner. Some of the genotypes showed an increase in fibre strength at mild and moderate drought stress. However, the maximum genotypes showed a decrease of fibre strength under the severe drought stress. Similar result has been observed in (Gao *et al*., 2020; Shilpa and Chandrasekhar, 2020). Droughts stress at the secondary wall deposition stage mainly affects fiber thickness and strength which are the main contributors to lint weight (Gao *et al*., 2020). The mature fiber has thicker secondary wall, smaller middle cavity and high strength (Zhang *et al*., 2019). Saleem *et al*., (2015) observed that the genes involved in maintaining high relative water content and cell membrane stability had genetic linkage with those controlling fibre length and strength.

#### 4.3.2.4 Micronnaire

Genotype, treatment and their interaction significantly affected the micronnaire. The highest mean micronnaire (4.25µg/inch) was observed in T3 drought stress whereas the lowest micronnaire (4.16µg/inch) was observed in T2 drought stress (Table 70). Among the genotypes, highest micronnaire (4.89µg/inch) was observed in G35 and lowest (3.42 µg/inch) in G17. Based on the genotype stress interaction, highest micronnaire (5.53µg/inch) was observed in G14 under T4 and lowest (3.18 µg/inch) was observed in G17 under T2, respectively. On the basis of b values, the best

**Table 69. Fiber strength (g/tex) of twenty-five genotypes at different drought treatments**

| Genotype | Fiber strength at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 29.10 | 28.37 | 28.39 | 28.73 | 28.65 | 2.51 | 2.44 | 1.26 | 2.07 | 0.19 | 13 |
| G2 | 28.56 | 28.02 | 27.66 | 28.88 | 28.28 | 1.88 | 3.14 | -1.13 | 1.30 | 0.23 | 11 |
| G8 | 28.65 | 28.72 | 27.30 | 29.11 | 28.44 | -0.24 | 4.70 | -1.62 | 0.95 | 0.28 | 10 |
| G10 | 28.50 | 27.67 | 28.58 | 29.44 | 28.55 | 2.89 | -0.29 | -3.32 | -0.24 | 0.08 | 17 |
| G11 | 29.34 | 28.75 | 28.66 | 25.07 | 27.96 | 2.02 | 2.33 | 14.57 | 6.31 | 0.07 | 18 |
| G12 | 29.84 | 30.06 | 28.79 | 30.04 | 29.68 | -0.76 | 3.52 | -0.69 | 0.69 | 0.20 | 12 |
| G13 | 29.99 | 29.04 | 28.88 | 29.98 | 29.47 | 3.17 | 3.70 | 0.03 | 2.30 | 0.30 | 9 |
| G14 | 30.36 | 29.09 | 28.92 | 29.26 | 29.41 | 4.18 | 4.74 | 3.61 | 4.18 | 0.37 | 7 |
| G15 | 30.65 | 30.38 | 29.51 | 30.01 | 30.14 | 0.88 | 3.70 | 2.09 | 2.22 | 0.23 | 11 |
| G17 | 27.46 | 27.28 | 25.10 | 27.59 | 26.86 | 0.64 | 8.58 | -0.49 | 2.91 | 0.49 | 3 |
| G18 | 29.15 | 29.71 | 30.89 | 29.33 | 29.77 | -1.93 | -5.98 | -0.61 | -2.84 | -0.39 | 21 |
| G22 | 30.83 | 28.35 | 28.11 | 29.08 | 29.09 | 8.04 | 8.80 | 5.68 | 7.51 | 0.71 | 1 |
| G23 | 29.27 | 28.31 | 28.94 | 29.18 | 28.93 | 3.27 | 1.13 | 0.32 | 1.57 | 0.15 | 14 |
| G29 | 30.76 | 29.21 | 27.86 | 28.34 | 29.04 | 5.04 | 9.42 | 7.85 | 7.43 | 0.64 | 2 |
| G30 | 29.40 | 29.05 | 29.25 | 30.58 | 29.57 | 1.18 | 0.50 | -4.03 | -0.78 | 0.09 | 16 |
| G33 | 31.13 | 29.98 | 29.10 | 30.28 | 30.12 | 3.72 | 6.53 | 2.73 | 4.33 | 0.48 | 4 |
| G34 | 29.08 | 27.53 | 29.27 | 29.85 | 28.93 | 5.31 | -0.65 | -2.67 | 0.66 | 0.12 | 15 |
| G35 | 30.95 | 29.70 | 30.21 | 28.78 | 29.91 | 4.05 | 2.39 | 7.01 | 4.48 | 0.19 | 13 |
| G38 | 28.39 | 30.34 | 28.85 | 28.97 | 29.14 | -6.87 | -1.61 | -2.04 | -3.51 | -0.24 | 20 |
| G39 | 30.23 | 28.98 | 30.65 | 30.29 | 30.04 | 4.13 | -1.40 | -0.20 | 0.85 | 0.02 | 19 |
| G43 | 29.06 | 28.74 | 28.97 | 29.79 | 29.14 | 1.12 | 0.32 | -2.50 | -0.35 | 0.07 | 18 |
| G45 | 30.72 | 29.23 | 29.20 | 30.23 | 29.84 | 4.85 | 4.93 | 1.60 | 3.79 | 0.42 | 6 |
| G46 | 30.93 | 30.28 | 28.89 | 31.13 | 30.31 | 2.10 | 6.62 | -0.65 | 2.69 | 0.47 | 5 |
| G48 | 29.14 | 28.54 | 28.48 | 29.29 | 28.86 | 2.04 | 2.27 | -0.53 | 1.26 | 0.19 | 13 |
| G50 | 30.73 | 30.12 | 28.75 | 26.43 | 29.01 | 1.97 | 6.43 | 13.99 | 7.47 | 0.32 | 8 |
| Mean (T) | 29.69 | 29.02 | 28.77 | 29.19 | | | | | | | |

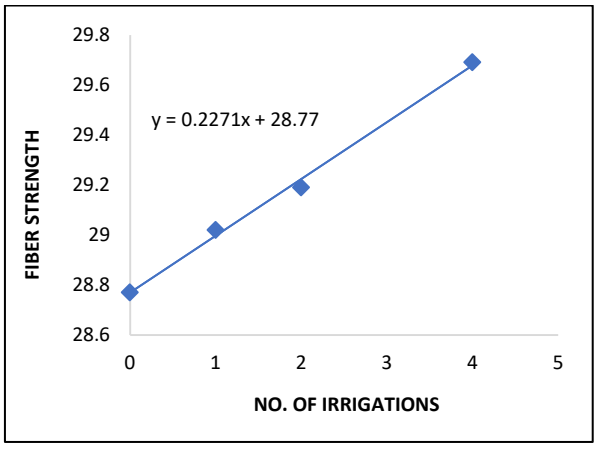



**Figure 80. Relationships betweesn fiber strength of cotton genotypes and different drought stresses**

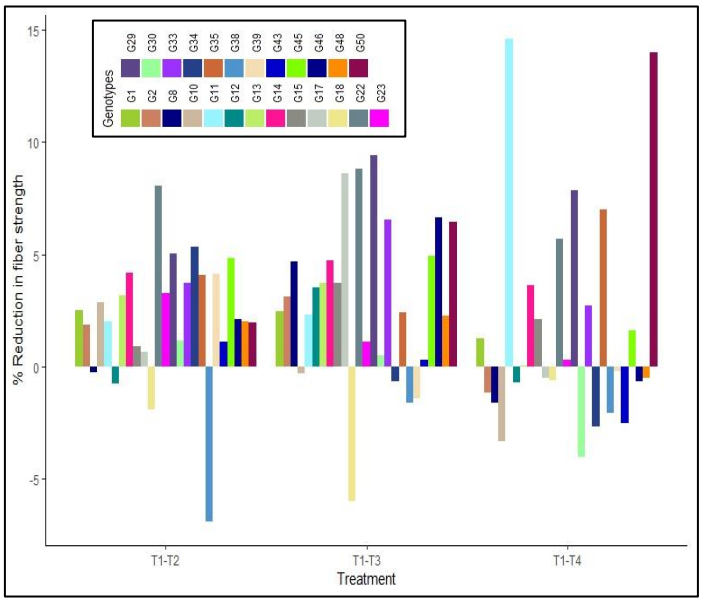



**Figure 81. Reduction percentage of fiber strength of twenty-five cotton genotypes under different drought stresses compared with control**

performance (highest b value) was observed in genotype G23 (0.22) followed by G34 (0.20) and lowest in G45 (-0.30). With the increase of drought stress, micronnaire was decreased as shown in linear regression in Figure 82. The minimum reduction% (-44.39%) was observed in G48 under T2 drought stress (Figure 83, Table 70). Maximum reduction% (22.34%) was observed in G10 under T3 stress (Figure 83). The result showed the negative effect of drought stress on micronnaire in genotypic dependent manner. Some of the genotypes showed an increase in micronnaire at mild and moderate drought stress. However, the maximum genotypes showed a decrease of micronnaire under the severe drought stress. Similar result has been observed in (Eaton and Ergle, 1952; Marani and Amirav, 1971). Drought stress disturbs the fiber cell turgor pressure (Ullah *et al*., 2017; Wang *et al*., 2016a) leading to reduced fiber length, uniformity, and strength; while the increase in fiber micronnaire.

#### 4.3.2.5 Elongation

Genotype, treatment and their interaction significantly affected the elongation. The highest mean elongation (6.48 %) was observed in T1 drought stress whereas the lowest elongation (6.00 %) was observed in T4 drought stress (Table 71). Among the genotypes, highest elongation (6.40 %) was observed in G38 and lowest (6.00 %) in G33. Based on the genotype stress interaction, highest elongation (6.76) was observed in G8 under T1 and lowest (5.80) was observed in G11 under T4, respectively. On the basis of b values, the best performance (highest b value) was observed in genotype G15 (0.12) followed by G46 (0.11) and lowest in G39 (0.03). With the increase of drought stress, elongation was decreased as shown in linear regression in Figure 84. The minimum reduction% (0.10%) was observed in G1 under T2 drought stress (Figure 85, Table 71). Maximum reduction% (12.42%) was observed in G8 under T4 stress (Figure 85). The result showed the negative effect of drought stress on elongation in genotypic dependent manner. None of the genotypes showed an increase in elongation at any drought stress. However, the maximum genotypes showed a decrease of elongation under the severe drought stress. Drought stress reduces the fiber length by reducing the leaf water potential causing a decrease in the rate of fiber elongation. Studies have shown that the force and duration of the cell turgor regulate the fiber elongation process (Gao *et al.,* 2020; Zhao *et al*., 2019a; Tang *et al*., 2017; Wang *et al*., 2016a).

## Table 70. Micronnaire (µg/inch) of twenty-five genotypes at different drought treatments

| Genotype | Micronnaire at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 4.65 | 4.17 | 4.81 | 4.77 | 4.60 | 10.25 | -3.44 | -2.51 | 1.43 | -0.08 | 14 |
| G2 | 4.19 | 3.94 | 4.65 | 3.70 | 4.12 | 5.96 | -10.81 | 11.84 | 2.33 | -0.15 | 17 |
| G8 | 4.22 | 3.81 | 4.24 | 4.08 | 4.09 | 9.87 | -0.39 | 3.39 | 4.29 | 0.01 | 10 |
| G10 | 4.86 | 5.08 | 3.78 | 4.00 | 4.43 | -4.39 | 22.34 | 17.82 | 11.93 | -0.20 | 18 |
| G11 | 3.21 | 3.62 | 3.81 | 3.29 | 3.48 | -12.88 | -18.80 | -2.39 | -11.35 | 0.13 | 5 |
| G12 | 4.65 | 4.18 | 3.99 | 4.46 | 4.32 | 10.04 | 14.13 | 4.02 | 9.40 | 0.12 | 6 |
| G13 | 4.11 | 5.15 | 4.27 | 4.99 | 4.63 | -25.49 | -3.90 | -21.51 | -16.96 | 0.19 | 3 |
| G14 | 4.10 | 4.12 | 4.21 | 5.53 | 4.49 | -0.49 | -2.68 | -34.85 | -12.67 | -0.10 | 15 |
| G15 | 4.03 | 3.81 | 4.08 | 4.02 | 3.98 | 5.38 | -1.32 | 0.17 | 1.41 | -0.06 | 13 |
| G17 | 4.03 | 3.18 | 3.20 | 3.28 | 3.42 | 21.03 | 20.61 | 18.46 | 20.03 | 0.10 | 7 |
| G18 | 3.86 | 3.91 | 4.06 | 4.02 | 3.96 | -1.29 | -5.18 | -3.97 | -3.48 | -0.12 | 16 |
| G22 | 4.82 | 4.10 | 4.52 | 4.00 | 4.36 | 15.00 | 6.36 | 17.14 | 12.83 | 0.02 | 9 |
| G23 | 5.14 | 4.81 | 4.21 | 4.66 | 4.70 | 6.49 | 18.09 | 9.34 | 11.31 | 0.22 | 1 |
| G29 | 4.27 | 3.43 | 5.09 | 3.98 | 4.19 | 19.69 | -19.22 | 6.72 | 2.40 | -0.10 | 15 |
| G30 | 4.81 | 3.95 | 4.18 | 4.40 | 4.33 | 17.88 | 13.17 | 8.52 | 13.19 | 0.17 | 4 |
| G33 | 3.91 | 3.98 | 4.03 | 3.57 | 3.87 | -1.79 | -3.07 | 8.86 | 1.33 | -0.01 | 11 |
| G34 | 4.58 | 4.16 | 3.97 | 3.73 | 4.11 | 9.10 | 13.39 | 18.49 | 13.66 | 0.20 | 2 |
| G35 | 4.77 | 4.23 | 5.27 | 5.28 | 4.89 | 11.39 | -10.55 | -10.76 | -3.31 | 0.01 | 10 |
| G38 | 3.87 | 4.38 | 4.33 | 4.46 | 4.26 | -13.17 | -11.88 | -15.06 | -13.37 | -0.04 | 12 |
| G39 | 3.41 | 4.25 | 4.26 | 4.76 | 4.17 | -24.41 | -24.90 | -39.36 | -29.56 | -0.10 | 15 |
| G43 | 3.86 | 3.78 | 4.41 | 3.83 | 3.97 | 2.16 | -14.15 | 0.86 | -3.71 | 0.17 | 4 |
| G45 | 4.28 | 4.17 | 3.72 | 4.26 | 4.11 | 2.65 | 13.08 | 0.55 | 5.43 | -0.30 | 19 |
| G46 | 3.94 | 4.06 | 4.22 | 4.18 | 4.10 | -3.22 | -7.20 | -6.10 | -5.50 | 0.03 | 8 |
| G48 | 3.57 | 5.15 | 4.57 | 4.77 | 4.52 | -44.39 | -28.22 | -33.74 | -35.45 | -0.04 | 12 |
| G50 | 4.55 | 4.54 | 4.48 | 3.73 | 4.33 | 0.22 | 1.68 | 18.08 | 6.66 | -0.04 | 12 |
| Mean (T) | 4.23 | 4.16 | 4.25 | 4.23 | | | | | | | |

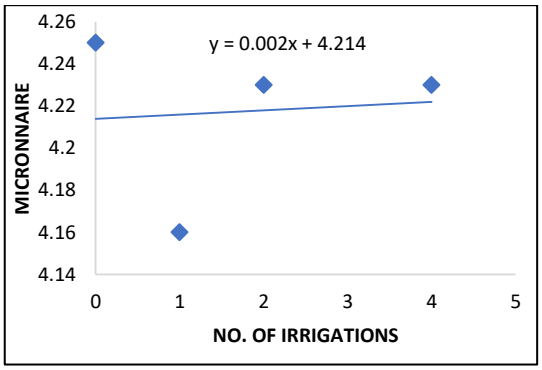



**Figure 82. Relationships betweesn micronnair of cotton genotypes and different drought stresses**

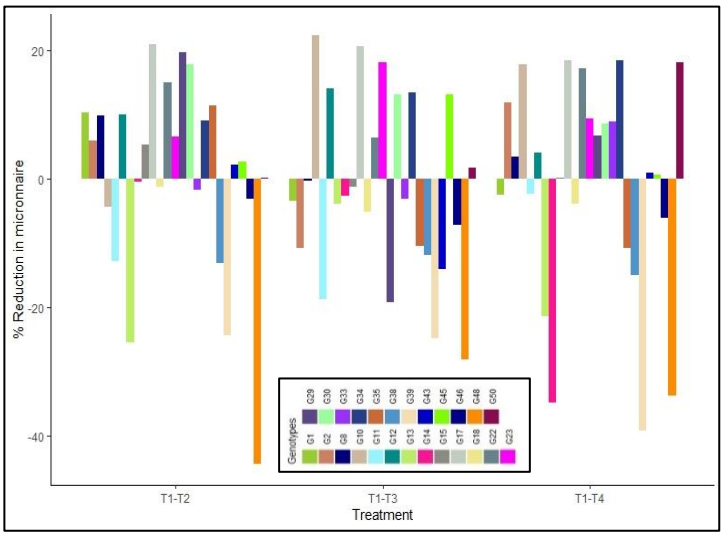



**Figure 83. Reduction percentage of micronnaire of twenty-five cotton genotypes under different drought stresses compared with control**

**Table 71. Elongation (%) of twenty-five genotypes at different drought treatments**

| Genotype | Elongation at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 6.40 | 6.39 | 6.06 | 5.95 | 6.20 | 0.10 | 5.21 | 7.03 | 4.12 | 0.04 | 9 |
| G2 | 6.34 | 6.19 | 6.14 | 5.89 | 6.14 | 2.47 | 3.26 | 7.20 | 4.31 | 0.04 | 9 |
| G8 | 6.76 | 6.44 | 6.25 | 5.92 | 6.35 | 4.73 | 7.59 | 12.42 | 8.25 | 0.10 | 3 |
| G10 | 6.44 | 6.30 | 6.10 | 5.87 | 6.18 | 2.18 | 5.23 | 8.80 | 5.40 | 0.05 | 8 |
| G11 | 6.26 | 6.20 | 6.01 | 5.80 | 6.07 | 0.96 | 4.05 | 7.40 | 4.14 | 0.06 | 7 |
| G12 | 6.41 | 6.27 | 6.11 | 5.93 | 6.18 | 2.24 | 4.73 | 7.49 | 4.82 | 0.10 | 3 |
| G13 | 6.49 | 6.29 | 6.10 | 5.85 | 6.19 | 3.08 | 6.06 | 9.86 | 6.33 | 0.05 | 8 |
| G14 | 6.53 | 6.36 | 6.15 | 6.01 | 6.26 | 2.70 | 5.87 | 7.96 | 5.51 | 0.08 | 5 |
| G15 | 6.61 | 6.38 | 6.12 | 5.99 | 6.28 | 3.38 | 7.42 | 9.28 | 6.69 | 0.12 | 1 |
| G17 | 6.44 | 6.21 | 5.93 | 5.85 | 6.10 | 3.57 | 7.92 | 9.17 | 6.89 | 0.08 | 5 |
| G18 | 6.49 | 6.30 | 6.18 | 6.00 | 6.24 | 2.93 | 4.68 | 7.45 | 5.02 | 0.06 | 7 |
| G22 | 6.55 | 6.31 | 6.17 | 5.97 | 6.25 | 3.56 | 5.75 | 8.81 | 6.04 | 0.08 | 5 |
| G23 | 6.42 | 6.32 | 6.13 | 5.93 | 6.20 | 1.61 | 4.52 | 7.58 | 4.57 | 0.10 | 3 |
| G29 | 6.66 | 6.50 | 6.29 | 6.12 | 6.39 | 2.45 | 5.65 | 8.10 | 5.40 | 0.07 | 6 |
| G30 | 6.49 | 6.38 | 6.21 | 5.99 | 6.27 | 1.75 | 4.31 | 7.70 | 4.59 | 0.06 | 7 |
| G33 | 6.21 | 6.04 | 5.91 | 5.84 | 6.00 | 2.68 | 4.88 | 6.01 | 4.53 | 0.09 | 4 |
| G34 | 6.36 | 6.26 | 6.04 | 5.91 | 6.14 | 1.68 | 5.03 | 7.07 | 4.59 | 0.05 | 8 |
| G35 | 6.54 | 6.37 | 6.21 | 6.04 | 6.29 | 2.60 | 4.95 | 7.55 | 5.03 | 0.05 | 8 |
| G38 | 6.68 | 6.50 | 6.36 | 6.06 | 6.40 | 2.74 | 4.79 | 9.23 | 5.59 | 0.06 | 7 |
| G39 | 6.45 | 6.34 | 6.20 | 6.00 | 6.25 | 1.76 | 3.88 | 7.03 | 4.22 | 0.03 | 10 |
| G43 | 6.37 | 6.33 | 6.18 | 6.10 | 6.25 | 0.68 | 3.03 | 4.29 | 2.67 | 0.06 | 7 |
| G45 | 6.53 | 6.29 | 6.09 | 6.26 | 6.29 | 3.72 | 6.84 | 4.13 | 4.90 | 0.05 | 8 |
| G46 | 6.59 | 6.35 | 6.04 | 6.19 | 6.29 | 3.59 | 8.30 | 6.07 | 5.99 | 0.11 | 2 |
| G48 | 6.49 | 6.29 | 6.29 | 6.37 | 6.36 | 3.03 | 3.03 | 1.75 | 2.60 | 0.07 | 6 |
| G50 | 6.53 | 6.37 | 6.09 | 6.25 | 6.31 | 2.45 | 6.64 | 4.19 | 4.43 | 0.06 | 7 |
| Mean (T) | 6.48 | 6.32 | 6.13 | 6.00 | | | | | | | |

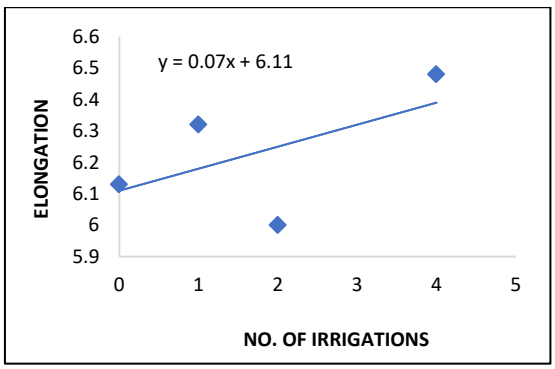



**Figure 84. Relationships betweesn elongation of cotton genotypes and different drought stresses**

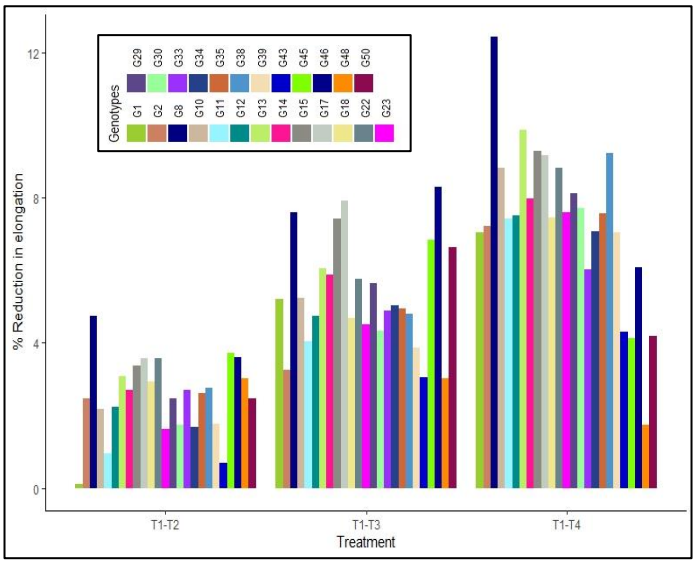



**Figure 85. Reduction percentage of elongation of twenty-five cotton genotypes under different drought stresses compared with control**

#### 4.3.2.6 Maturity ratio

Genotype, treatment and their interaction significantly affected the maturity ratio. The highest mean maturity ratio (0.87) was observed in T1 drought stress whereas the lowest maturity ratio (0.84) was observed in T3 drought stress (Table 72). Among the genotypes, highest maturity ratio (0.87) was observed in G12, G13, G35 and lowest (0.84) in G11, G34. Based on the genotype stress interaction, highest maturity ratio (0.89) was observed in G35 and G38 under T1 and lowest (0.79) was observed in G34 under T3, respectively. On the basis of b values, the best performance (highest b value) was observed in genotype G33 (0.016) followed by G13, G18 (0.013) and lowest in G45 (0.003). With the increase of drought stress, maturity ratio was decreased as shown in linear regression in Figure 86. The minimum reduction% (-1.15%) was observed in G14 under T4 drought stress (Figure 87, Table 72). Maximum reduction% (8.46%) was observed in G34 under T3 stress (Figure 87). The result showed the negative effect of drought stress on maturity ratio in genotypic dependent manner. Some of the genotypes showed an increase in maturity ratio at mild and moderate drought stress. However, the maximum genotypes showed a decrease of maturity ratio under the severe drought stress.

#### 4.3.2.7 Moisture content/regain

Genotype, treatment and their interaction significantly affected the moisture content. The highest mean moisture content (6.29 %) was observed in T2 drought stress whereas the lowest moisture content (6.17 %) was observed in T1 and T3 drought stress (Table 73). Among the genotypes, highest moisture content (6.62 %) was observed in G11 and lowest (5.55 %) in G33. Based on the genotype stress interaction, highest moisture content (6.93 %) and lowest (5.12 %) was observed in G50 under T1 stress respectively. On the basis of b values, the best performance (lowest b value) was observed in genotype G13 (-0.29) followed by G12 (-0.15) and highest in G39 (0.25). With the increase of drought stress, moisture content was increased as shown in linear regression in Figure 88. The minimum reduction% (-26.09%) was observed in G50 under T4 drought stress (Figure 89, Table 73). Maximum reduction% (18.82%) was observed in G2 under T4 stress (Figure 89). The result showed the negative effect of drought stress on moisture content in genotypic dependent manner.

## Table 72. Maturity ratio of twenty-five genotypes at different drought treatments

| Genotype | Maturity ratio at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 0.87 | 0.85 | 0.86 | 0.87 | 0.86 | 2.29 | 1.53 | 0.76 | 1.53 | 0.007 | 8 |
| G2 | 0.87 | 0.86 | 0.85 | 0.86 | 0.86 | 0.77 | 2.31 | 0.77 | 1.28 | 0.007 | 8 |
| G8 | 0.86 | 0.85 | 0.84 | 0.86 | 0.85 | 1.55 | 1.94 | 0.00 | 1.16 | 0.007 | 8 |
| G10 | 0.87 | 0.87 | 0.83 | 0.85 | 0.86 | 0.76 | 4.58 | 2.29 | 2.54 | 0.010 | 5 |
| G11 | 0.86 | 0.84 | 0.83 | 0.84 | 0.84 | 2.32 | 3.47 | 3.09 | 2.96 | 0.009 | 6 |
| G12 | 0.88 | 0.86 | 0.86 | 0.87 | 0.87 | 2.64 | 3.02 | 1.51 | 2.39 | 0.008 | 7 |
| G13 | 0.87 | 0.87 | 0.85 | 0.87 | 0.87 | 0.00 | 1.92 | -0.38 | 0.51 | 0.013 | 2 |
| G14 | 0.87 | 0.86 | 0.85 | 0.88 | 0.86 | 1.15 | 1.54 | -1.15 | 0.51 | 0.007 | 8 |
| G15 | 0.87 | 0.86 | 0.84 | 0.87 | 0.86 | 1.15 | 3.44 | 0.76 | 1.78 | 0.010 | 5 |
| G17 | 0.87 | 0.86 | 0.82 | 0.87 | 0.85 | 1.15 | 5.38 | 0.00 | 2.18 | 0.010 | 5 |
| G18 | 0.88 | 0.85 | 0.84 | 0.86 | 0.86 | 3.42 | 3.80 | 1.90 | 3.04 | 0.013 | 2 |
| G22 | 0.88 | 0.86 | 0.85 | 0.86 | 0.86 | 2.27 | 3.41 | 1.89 | 2.53 | 0.004 | 9 |
| G23 | 0.88 | 0.85 | 0.84 | 0.86 | 0.86 | 3.03 | 4.92 | 1.89 | 3.28 | 0.012 | 3 |
| G29 | 0.87 | 0.83 | 0.84 | 0.85 | 0.85 | 5.34 | 4.20 | 3.05 | 4.20 | 0.004 | 9 |
| G30 | 0.86 | 0.84 | 0.81 | 0.86 | 0.85 | 2.32 | 5.79 | 0.39 | 2.83 | 0.010 | 5 |
| G33 | 0.88 | 0.83 | 0.84 | 0.86 | 0.85 | 6.06 | 4.92 | 2.27 | 4.42 | 0.016 | 1 |
| G34 | 0.87 | 0.85 | 0.79 | 0.84 | 0.84 | 2.31 | 8.46 | 2.69 | 4.49 | 0.011 | 4 |
| G35 | 0.89 | 0.85 | 0.85 | 0.88 | 0.87 | 4.49 | 4.87 | 1.12 | 3.50 | 0.004 | 9 |
| G38 | 0.89 | 0.86 | 0.84 | 0.86 | 0.86 | 2.63 | 5.26 | 3.38 | 3.76 | 0.012 | 3 |
| G39 | 0.87 | 0.86 | 0.84 | 0.86 | 0.86 | 1.91 | 3.44 | 1.15 | 2.16 | 0.007 | 8 |
| G43 | 0.88 | 0.86 | 0.83 | 0.87 | 0.86 | 2.26 | 6.42 | 1.13 | 3.27 | 0.011 | 4 |
| G45 | 0.87 | 0.85 | 0.82 | 0.86 | 0.85 | 2.31 | 5.00 | 1.15 | 2.82 | 0.003 | 10 |
| G46 | 0.88 | 0.86 | 0.84 | 0.87 | 0.86 | 3.02 | 4.53 | 1.89 | 3.14 | 0.010 | 5 |
| G48 | 0.88 | 0.87 | 0.85 | 0.87 | 0.86 | 1.14 | 3.42 | 1.14 | 1.90 | 0.004 | 9 |
| G50 | 0.88 | 0.85 | 0.83 | 0.87 | 0.86 | 3.03 | 5.30 | 1.52 | 3.28 | 0.007 | 8 |
| Mean (T) | 0.87 | 0.85 | 0.84 | 0.86 | | | | | | | |

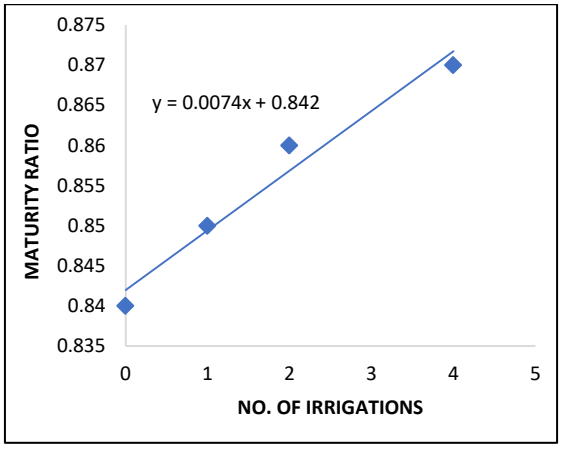



**Figure 86. Relationships betweesn maturity ratio of cotton genotypes and different drought stresses**

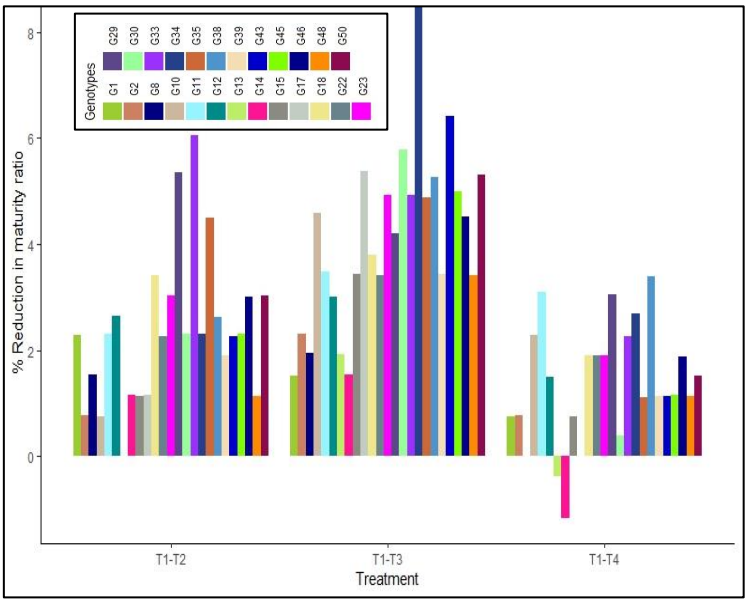



**Figure 87. Reduction percentage of maturity ratio of twenty-five cotton genotypes under different drought stresses compared with control**

## Table 73. Moisture content of twenty-five genotypes at different drought treatments

| Genotype | Moisture (%) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 6.18 | 5.96 | 6.49 | 6.65 | 6.32 | 3.67 | -4.96 | -7.49 | -2.93 | 0.03 | 14 |
| G2 | 6.61 | 6.52 | 6.03 | 5.36 | 6.13 | 1.36 | 8.68 | 18.82 | 9.62 | -0.01 | 11 |
| G8 | 6.45 | 6.39 | 6.64 | 6.06 | 6.39 | 0.83 | -3.00 | 5.95 | 1.26 | 0.15 | 17 |
| G10 | 5.76 | 6.49 | 6.33 | 6.62 | 6.30 | -12.74 | -10.02 | -15.06 | -12.60 | 0.15 | 17 |
| G11 | 6.62 | 6.65 | 6.66 | 6.54 | 6.62 | -0.35 | -0.60 | 1.21 | 0.08 | -0.06 | 7 |
| G12 | 6.64 | 6.73 | 5.83 | 6.57 | 6.44 | -1.46 | 12.15 | 1.05 | 3.92 | -0.15 | 2 |
| G13 | 5.90 | 6.22 | 6.51 | 6.46 | 6.27 | -5.54 | -10.46 | -9.55 | -8.52 | -0.29 | 1 |
| G14 | 6.50 | 6.44 | 6.90 | 5.37 | 6.30 | 0.97 | -6.05 | 17.38 | 4.10 | -0.02 | 10 |
| G15 | 5.62 | 5.80 | 5.50 | 6.11 | 5.76 | -3.26 | 2.08 | -8.66 | -3.28 | 0.19 | 18 |
| G17 | 6.46 | 6.35 | 5.53 | 6.08 | 6.11 | 1.75 | 14.44 | 5.93 | 7.37 | 0.09 | 16 |
| G18 | 6.28 | 6.51 | 6.43 | 5.89 | 6.28 | -3.55 | -2.39 | 6.21 | 0.09 | -0.13 | 4 |
| G22 | 5.95 | 6.28 | 6.03 | 6.64 | 6.23 | -5.60 | -1.29 | -11.65 | -6.18 | -0.05 | 8 |
| G23 | 6.45 | 6.48 | 6.75 | 6.75 | 6.61 | -0.41 | -4.65 | -4.65 | -3.24 | 0.09 | 16 |
| G29 | 5.98 | 5.78 | 6.16 | 6.79 | 6.18 | 3.40 | -2.95 | -13.60 | -4.38 | -0.11 | 5 |
| G30 | 6.90 | 6.26 | 6.64 | 6.31 | 6.53 | 9.18 | 3.72 | 8.46 | 7.12 | -0.10 | 6 |
| G33 | 5.33 | 5.87 | 5.72 | 5.28 | 5.55 | -10.00 | -7.31 | 1.00 | -5.44 | 0.06 | 15 |
| G34 | 6.35 | 6.63 | 5.74 | 5.17 | 5.97 | -4.46 | 9.61 | 18.64 | 7.93 | 0.01 | 12 |
| G35 | 5.74 | 6.62 | 6.13 | 6.67 | 6.29 | -15.40 | -6.80 | -16.21 | -12.80 | 0.09 | 16 |
| G38 | 6.72 | 6.17 | 6.14 | 6.45 | 6.37 | 8.09 | 8.64 | 4.02 | 6.91 | -0.13 | 4 |
| G39 | 6.11 | 6.33 | 5.95 | 6.66 | 6.26 | -3.55 | 2.56 | -9.06 | -3.35 | 0.25 | 19 |
| G43 | 5.52 | 5.98 | 6.77 | 5.57 | 5.96 | -8.39 | -22.71 | -0.91 | -10.67 | -0.06 | 7 |
| G45 | 6.23 | 6.40 | 5.70 | 6.19 | 6.13 | -2.73 | 8.40 | 0.59 | 2.09 | -0.14 | 3 |
| G46 | 5.96 | 5.97 | 6.49 | 6.18 | 6.15 | -0.28 | -8.95 | -3.75 | -4.33 | -0.05 | 8 |
| G48 | 6.93 | 6.71 | 5.76 | 6.67 | 6.52 | 3.17 | 16.88 | 3.85 | 7.96 | -0.03 | 9 |
| G50 | 5.12 | 5.62 | 5.39 | 6.46 | 5.65 | -9.63 | -5.20 | -26.09 | -13.64 | 0.02 | 13 |
| Mean (T) | 6.17 | 6.29 | 6.17 | 6.22 | | | | | | | |

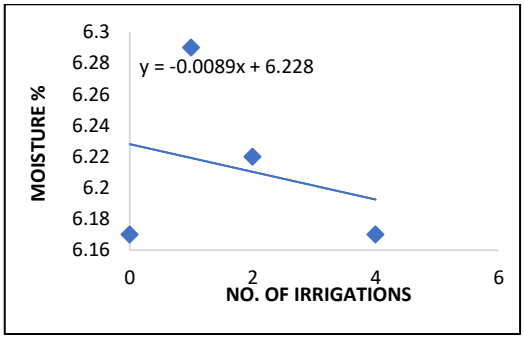



**Figure 88. Relationships betweesn moisture content of cotton genotypes and different drought stresses**

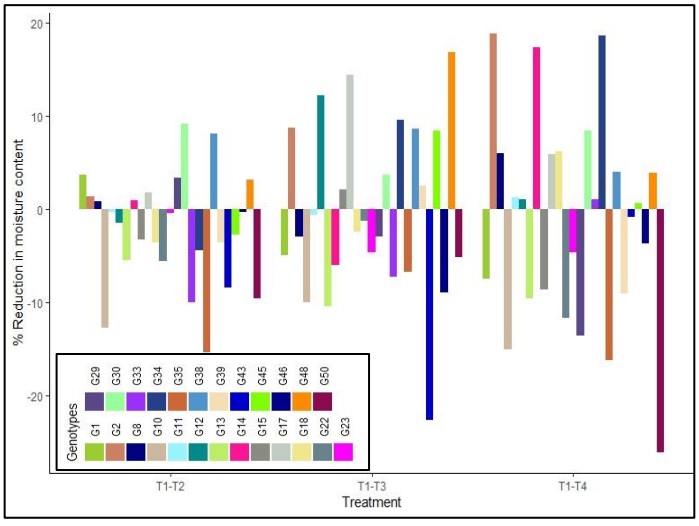



**Figure 89. Reduction percentage of moisture content of twenty-five cotton genotypes under different drought stresses compared with control**

Some of the genotypes showed a decrease in moisture content at mild and moderate drought stress. However, the maximum genotypes showed an increase of moisture content under the severe drought stress. Drought stress disturbs fiber development by decreasing leaf water potential, cell expansion, and carbohydrate metabolism, resulting in reduced the quality of developing fiber of upland cotton (Witt *et al*., 2020).

#### 4.3.2.8 Reflectance degree

Genotype and treatment significantly affected the reflectance degree and their interaction was non-significant. The highest mean reflectance degree (77.55 %) was observed in T1 drought stress whereas the lowest reflectance degree (74.43 %) was observed in T3 drought stress (Table 74). Among the genotypes, highest reflectance degree (78.33 %) was observed in G13 and lowest (70.19 %) in G11. Based on the genotype stress interaction, highest reflectance degree (80.33 %) was observed in G46 under T1 and lowest (69.40 %) was observed in G11 under T2, respectively. On the basis of b values, the best performance (highest b value) was observed in genotype G29 (1.14) followed by G30 (1.12) and lowest in G8 (0.46). With the increase of drought stress, reflectance degree was decreased as shown in linear regression in Figure 90. The minimum reduction% (0.05%) was observed in G1 under T4 drought stress (Figure 91, Table 74). Maximum reduction% (5.71%) was observed in G14 under T3 stress (Figure 91). The result showed the negative effect of drought stress on reflectance degree in genotypic dependent manner. None of the genotypes showed an increase in reflectance degree at any drought stress. However, the maximum genotypes showed a decrease of reflectance degree under the severe drought stress.

#### 4.3.2.9 Yellowness

Genotype, treatment and their interaction significantly affected the yellowness. The highest mean yellowness (16.48) was observed in T3 drought stress whereas the lowest yellowness (14.30) was observed in T1 drought stress (Table 75). Among the genotypes, highest yellowness (16.99) was observed in G38 and lowest (13.63) in G1. Based on the genotype stress interaction, highest yellowness (17.73) and lowest (10.67) was observed in G8 under T1 and G13 under T4 stress, respectively. On the basis of b values, the best performance (lowest b value) was observed in genotype G22 (-1.69) followed by G1 (-1.38) and highest in G14 (0.23). With the increase of

## Table 74. Reflectance degree (%) of twenty-five genotypes at different drought treatments

| Genotype | Reflectance degree at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 71.50 | 70.37 | 69.63 | 71.47 | 70.74 | 1.59 | 2.61 | 0.05 | 1.41 | 0.72 | 13 |
| G2 | 77.57 | 76.07 | 75.17 | 76.60 | 76.35 | 1.93 | 3.09 | 1.25 | 2.09 | 0.50 | 20 |
| G8 | 78.67 | 76.30 | 75.30 | 76.67 | 76.73 | 3.01 | 4.28 | 2.54 | 3.28 | 0.46 | 22 |
| G10 | 73.33 | 71.27 | 70.13 | 71.70 | 71.61 | 2.82 | 4.36 | 2.23 | 3.14 | 0.80 | 8 |
| G11 | 71.23 | 69.40 | 69.43 | 70.70 | 70.19 | 2.57 | 2.53 | 0.75 | 1.95 | 0.92 | 5 |
| G12 | 77.50 | 76.50 | 75.53 | 76.90 | 76.61 | 1.29 | 2.54 | 0.77 | 1.53 | 0.77 | 10 |
| G13 | 80.07 | 77.27 | 76.57 | 79.40 | 78.33 | 3.50 | 4.37 | 0.83 | 2.90 | 0.75 | 12 |
| G14 | 80.00 | 76.60 | 75.43 | 77.57 | 77.40 | 4.25 | 5.71 | 3.04 | 4.33 | 0.95 | 4 |
| G15 | 79.60 | 76.10 | 75.30 | 77.40 | 77.10 | 4.40 | 5.40 | 2.76 | 4.19 | 0.69 | 15 |
| G17 | 74.30 | 72.30 | 71.50 | 72.73 | 72.71 | 2.69 | 3.77 | 2.11 | 2.86 | 0.62 | 17 |
| G18 | 77.33 | 75.73 | 73.30 | 76.40 | 75.69 | 2.07 | 5.22 | 1.21 | 2.83 | 0.65 | 16 |
| G22 | 77.63 | 75.63 | 73.57 | 76.47 | 75.83 | 2.58 | 5.24 | 1.50 | 3.11 | 0.82 | 7 |
| G23 | 78.27 | 76.30 | 75.27 | 77.63 | 76.87 | 2.51 | 3.83 | 0.81 | 2.39 | 0.91 | 6 |
| G29 | 77.53 | 75.87 | 75.33 | 76.77 | 76.38 | 2.15 | 2.84 | 0.99 | 1.99 | 1.14 | 1 |
| G30 | 79.17 | 76.53 | 75.53 | 77.63 | 77.22 | 3.33 | 4.59 | 1.94 | 3.28 | 1.12 | 2 |
| G33 | 74.13 | 72.27 | 71.53 | 73.10 | 72.76 | 2.52 | 3.51 | 1.39 | 2.47 | 0.79 | 9 |
| G34 | 77.10 | 74.93 | 73.93 | 76.00 | 75.49 | 2.81 | 4.11 | 1.43 | 2.78 | 0.56 | 19 |
| G35 | 79.70 | 77.67 | 76.57 | 78.43 | 78.09 | 2.55 | 3.93 | 1.59 | 2.69 | 0.58 | 18 |
| G38 | 79.17 | 77.53 | 75.47 | 76.50 | 77.17 | 2.06 | 4.67 | 3.37 | 3.37 | 0.76 | 11 |
| G39 | 79.13 | 77.30 | 76.10 | 77.70 | 77.56 | 2.32 | 3.83 | 1.81 | 2.65 | 0.71 | 14 |
| G43 | 78.40 | 76.10 | 75.47 | 77.37 | 76.83 | 2.93 | 3.74 | 1.32 | 2.66 | 0.75 | 12 |
| G45 | 79.03 | 77.23 | 76.57 | 78.13 | 77.74 | 2.28 | 3.12 | 1.14 | 2.18 | 0.92 | 5 |
| G46 | 80.33 | 76.30 | 76.20 | 78.67 | 77.88 | 5.02 | 5.15 | 2.07 | 4.08 | 0.75 | 12 |
| G48 | 78.73 | 77.20 | 75.67 | 77.67 | 77.32 | 1.95 | 3.90 | 1.35 | 2.40 | 0.47 | 21 |
| G50 | 79.27 | 77.47 | 76.13 | 78.27 | 77.78 | 2.27 | 3.95 | 1.26 | 2.50 | 1.10 | 3 |
| Mean (T) | 77.55 | 75.45 | 74.43 | 76.31 | | | | | | | |

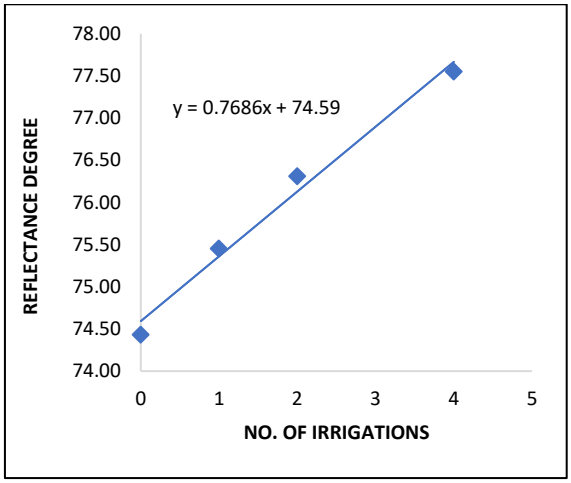



**Figure 90. Relationships between reflectance degree of cotton genotypes and different drought stresses**

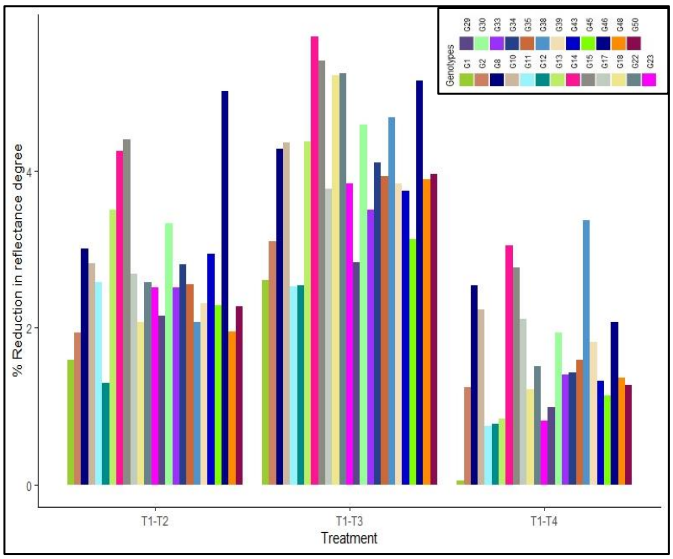



**Figure 91. Reduction percentage of reflectance degree of twenty-five cotton genotypes under different drought stresses compared with control**

## Table 75. Yellowness of twenty-five genotypes at different drought treatments

| Genotype | Yellowness at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 12.60 | 12.30 | 14.40 | 15.23 | 13.63 | 2.38 | -14.29 | -20.90 | -10.93 | -1.38 | 2 |
| G2 | 11.10 | 12.10 | 17.20 | 15.33 | 13.93 | -9.01 | -54.95 | -38.14 | -34.03 | -1.24 | 3 |
| G8 | 10.67 | 15.63 | 17.67 | 15.37 | 14.83 | -46.56 | -65.63 | -44.06 | -52.08 | -0.81 | 8 |
| G10 | 13.43 | 17.27 | 17.47 | 14.27 | 15.61 | -28.54 | -30.02 | -6.20 | -21.59 | -0.17 | 17 |
| G11 | 11.33 | 15.50 | 16.43 | 16.30 | 14.89 | -36.76 | -45.00 | -43.82 | -41.86 | -0.41 | 11 |
| G12 | 11.80 | 12.07 | 16.23 | 15.17 | 13.82 | -2.26 | -37.57 | -28.53 | -22.79 | -1.11 | 5 |
| G13 | 16.37 | 15.97 | 16.50 | 10.67 | 14.88 | 2.44 | -0.81 | 34.83 | 12.15 | 0.14 | 23 |
| G14 | 10.73 | 17.23 | 13.63 | 16.63 | 14.56 | -60.56 | -27.02 | -54.97 | -47.52 | 0.23 | 24 |
| G15 | 16.30 | 15.97 | 15.83 | 15.83 | 15.98 | 2.04 | 2.86 | 2.86 | 2.59 | -0.03 | 19 |
| G17 | 16.27 | 16.60 | 16.23 | 16.10 | 16.30 | -2.05 | 0.20 | 1.02 | -0.27 | -0.33 | 13 |
| G18 | 15.93 | 17.10 | 17.53 | 16.20 | 16.69 | -7.32 | -10.04 | -1.67 | -6.35 | -0.46 | 10 |
| G22 | 17.67 | 16.90 | 16.60 | 15.93 | 16.78 | 4.34 | 6.04 | 9.81 | 6.73 | -1.69 | 1 |
| G23 | 16.17 | 15.83 | 16.03 | 16.30 | 16.08 | 2.06 | 0.82 | -0.82 | 0.69 | 0.03 | 20 |
| G29 | 12.50 | 12.40 | 17.50 | 17.37 | 14.94 | 0.80 | -40.00 | -38.93 | -26.04 | -0.97 | 6 |
| G30 | 14.37 | 12.30 | 15.13 | 14.67 | 14.12 | 14.39 | -5.34 | -2.09 | 2.32 | -0.31 | 14 |
| G33 | 15.40 | 15.93 | 17.50 | 15.73 | 16.14 | -3.46 | -13.64 | -2.16 | -6.42 | -0.34 | 12 |
| G34 | 12.63 | 13.70 | 14.33 | 15.73 | 14.10 | -8.44 | -13.46 | -24.54 | -15.48 | -0.85 | 7 |
| G35 | 16.40 | 16.40 | 17.73 | 16.27 | 16.70 | 0.00 | -8.13 | 0.81 | -2.44 | -1.18 | 4 |
| G38 | 16.93 | 17.33 | 17.50 | 16.20 | 16.99 | -2.36 | -3.35 | 4.33 | -0.46 | -0.27 | 15 |
| G39 | 12.47 | 16.43 | 17.50 | 11.23 | 14.41 | -31.82 | -40.37 | 9.89 | -20.77 | -0.75 | 9 |
| G43 | 16.50 | 16.47 | 15.63 | 15.33 | 15.98 | 0.20 | 5.25 | 7.07 | 4.18 | 0.06 | 21 |
| G45 | 14.73 | 15.70 | 16.20 | 16.40 | 15.76 | -6.56 | -9.95 | -11.31 | -9.28 | -0.16 | 18 |
| G46 | 15.90 | 15.93 | 17.57 | 16.77 | 16.54 | -0.21 | -10.48 | -5.45 | -5.38 | 0.06 | 21 |
| G48 | 13.13 | 12.33 | 17.40 | 14.50 | 14.34 | 6.09 | -32.49 | -10.41 | -12.27 | -0.26 | 16 |
| G50 | 16.23 | 16.07 | 16.20 | 17.60 | 16.53 | 1.03 | 0.21 | -8.42 | -2.40 | 0.11 | 22 |
| Mean (T) | 14.30 | 15.26 | 16.48 | 15.49 | | | | | | | |

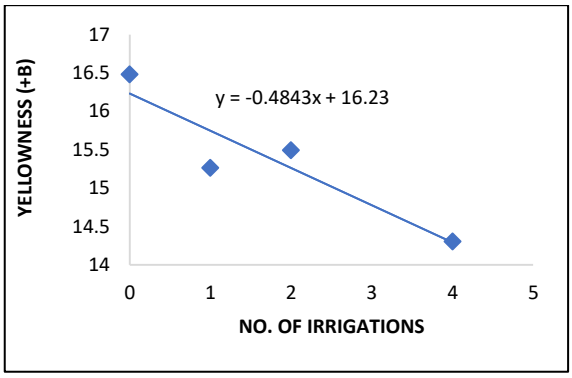



**Figure 92. Relationships betweesn yellowness (+b) content of cotton genotypes and different drought stresses**

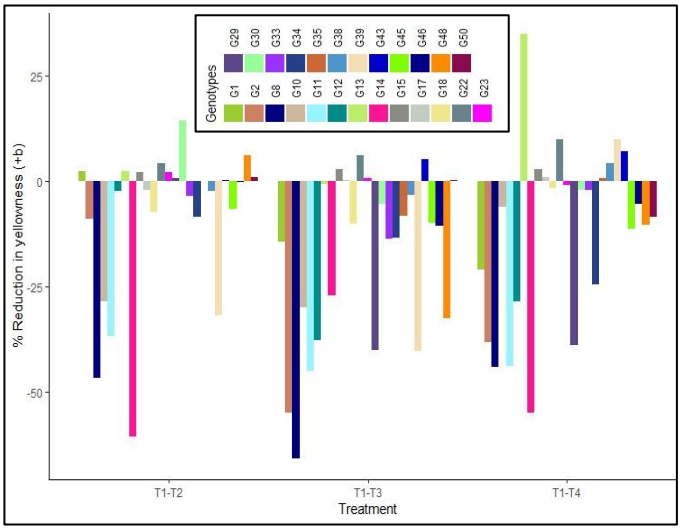



**Figure 93. Reduction percentage of yellowness (+b) of twenty-five cotton genotypes under different drought stresses compared with control**

drought stress, yellowness was increased as shown in linear regression in Figure 92. The minimum reduction% (-65.63%) was observed in G8 under T3 drought stress (Figure 93, Table 75). Maximum reduction% (34.83%) was observed in G13 under T4 stress (Figure 93). The result showed the negative effect of drought stress on yellowness in genotypic dependent manner. Maximum genotypes showed a decrease in yellowness at moderate drought stress. However, some of the genotypes showed an increase of yellowness under the severe drought stress.

#### 4.3.2.10 Fibre length

Genotype, treatment and their interaction significantly affected the fibre length. The highest mean fibre length (31.91 mm) was observed in T4 drought stress whereas the lowest fibre length (30.55 mm) was observed in T3 drought stress (Table 76). Among the genotypes, highest fibre length (32.71 mm) was observed in G33 and lowest (29.66 mm) in G29. Based on the genotype stress interaction, highest fibre length (33.97 mm) was observed in G33 under T2 and lowest (27.15 mm) was observed in G29 under T3, respectively. On the basis of b values, the best performance (highest b value) was observed in genotype G29 (1.08) followed by G34 (0.78) and lowest in G11 (-0.81). With the increase of drought stress, fibre length was decreased as shown in linear regression in Figure 94. The minimum reduction% (-20.14%) was observed in G38 under T2 drought stress (Figure 95, Table 76). Maximum reduction% (14.42%) was observed in G14 under T3 stress (Figure 95). The result showed the negative effect of drought stress on fibre length in genotypic dependent manner. Some of the genotypes showed an increase in fibre length at any drought stress. However, the maximum genotypes showed a decrease of fibre length under the severe drought stress. Similar result has been observed in (Ullah *et al*., 2017; Saleem *et al*., 2015; Yagmur *et al*., 2014). Dhindsa *et al*. (1975) observed that cotton fiber was a process primarily dependent on turgor and carbohydrate supply, the reductions in plant water status and photosynthesis that occur under drought stress condition would result in reduction in fiber growth. Cosgrove *et al*. (1993) who reported that increased volume of growing plant cells depends on the water uptake by the vacuole. Osmotic stress, at fiber initiation and elongation, reduces the fiber cell division leading to a smaller number of total fiber cells (Zhang *et al*., 2020) and shortens the fiber length.

## Table 76. Fiber length of twenty-five genotypes at different drought treatments

| Genotype | Fiber length (mm) at four drought level | | | | | % Reduction | | | | Regression coefficient b value | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | T1 | T2 | T3 | T4 | Mean (G) | T1-T2 | T1-T3 | T1-T4 | mean | | |
| G1 | 32.92 | 30.70 | 32.67 | 32.54 | 32.21 | 6.75 | 0.77 | 1.17 | 2.90 | -0.12 | 19 |
| G2 | 32.23 | 31.64 | 31.35 | 33.41 | 32.16 | 1.83 | 2.75 | -3.66 | 0.31 | 0.25 | 10 |
| G8 | 30.47 | 31.16 | 28.38 | 32.34 | 30.59 | -2.26 | 6.84 | -6.15 | -0.53 | -0.04 | 14 |
| G10 | 30.09 | 29.69 | 31.09 | 33.47 | 31.09 | 1.33 | -3.35 | -11.26 | -4.42 | -0.80 | 22 |
| G11 | 31.05 | 30.40 | 30.45 | 33.54 | 31.36 | 2.11 | 1.93 | -8.00 | -1.32 | -0.81 | 23 |
| G12 | 30.18 | 32.35 | 29.85 | 33.05 | 31.36 | -7.17 | 1.12 | -9.51 | -5.19 | -0.07 | 16 |
| G13 | 31.27 | 30.59 | 30.23 | 32.17 | 31.06 | 2.17 | 3.33 | -2.90 | 0.87 | -0.10 | 17 |
| G14 | 32.35 | 30.00 | 27.68 | 30.42 | 30.11 | 7.24 | 14.42 | 5.95 | 9.20 | 0.67 | 4 |
| G15 | 31.45 | 32.84 | 31.35 | 31.60 | 31.81 | -4.43 | 0.31 | -0.49 | -1.54 | -0.34 | 21 |
| G17 | 31.57 | 31.13 | 33.52 | 32.18 | 32.10 | 1.39 | -6.19 | -1.94 | -2.25 | -0.05 | 15 |
| G18 | 29.54 | 30.54 | 33.42 | 31.29 | 31.20 | -3.39 | -13.13 | -5.94 | -7.49 | 0.60 | 5 |
| G22 | 31.43 | 29.33 | 28.72 | 29.77 | 29.81 | 6.67 | 8.61 | 5.27 | 6.85 | 0.41 | 6 |
| G23 | 29.93 | 29.34 | 30.29 | 31.49 | 30.26 | 1.98 | -1.20 | -5.19 | -1.47 | -0.11 | 18 |
| G29 | 31.25 | 31.06 | 27.15 | 29.20 | 29.66 | 0.59 | 13.12 | 6.55 | 6.75 | 1.08 | 1 |
| G30 | 30.43 | 30.81 | 31.29 | 33.79 | 31.58 | -1.24 | -2.81 | -11.04 | -5.03 | 0.12 | 12 |
| G33 | 33.76 | 33.97 | 30.50 | 32.62 | 32.71 | -0.64 | 9.66 | 3.37 | 4.13 | -0.14 | 20 |
| G34 | 29.84 | 29.26 | 31.13 | 32.29 | 30.63 | 1.94 | -4.31 | -8.22 | -3.53 | 0.78 | 2 |
| G35 | 32.63 | 31.20 | 31.47 | 29.03 | 31.08 | 4.40 | 3.55 | 11.03 | 6.33 | 0.26 | 9 |
| G38 | 27.53 | 33.07 | 29.45 | 29.66 | 29.93 | -20.14 | -6.97 | -7.72 | -11.61 | 0.25 | 10 |
| G39 | 31.31 | 30.65 | 32.45 | 33.22 | 31.91 | 2.13 | -3.64 | -6.08 | -2.53 | 0.27 | 8 |
| G43 | 29.33 | 29.13 | 30.21 | 31.26 | 29.98 | 0.67 | -3.00 | -6.58 | -2.97 | 0.77 | 3 |
| G45 | 31.10 | 31.36 | 31.29 | 31.55 | 31.32 | -0.83 | -0.60 | -1.45 | -0.96 | 0.29 | 7 |
| G46 | 31.41 | 32.04 | 30.90 | 33.94 | 32.07 | -1.98 | 1.63 | -8.03 | -2.79 | 0.02 | 13 |
| G48 | 30.21 | 27.92 | 29.99 | 31.14 | 29.82 | 7.58 | 0.75 | -3.07 | 1.75 | 0.23 | 11 |
| G50 | 32.41 | 31.50 | 29.00 | 32.67 | 31.39 | 2.79 | 10.51 | -0.80 | 4.17 | -0.10 | 17 |
| Mean (T) | 31.03 | 30.87 | 30.55 | 31.91 | | | | | | | |

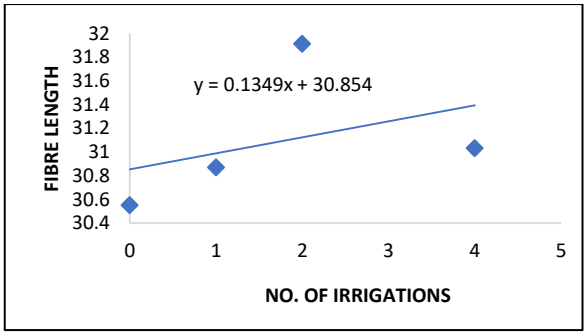



**Figure 94. Relationships betweesn fiber length of cotton genotypes and different drought stresses**

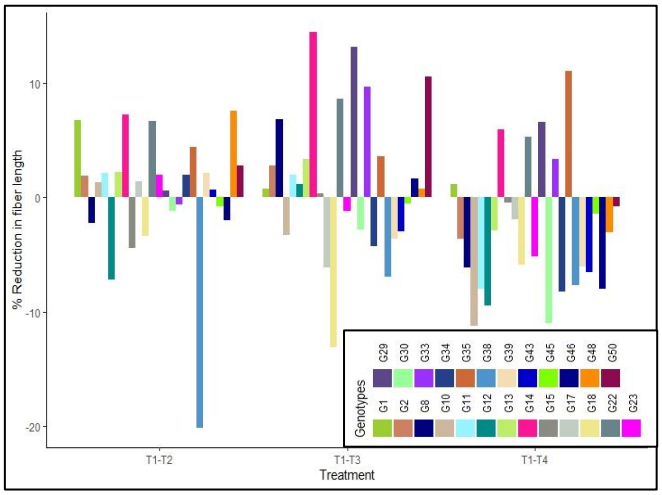



**Figure 95. Reduction percentage of fiber length of twenty-five cotton genotypes under different drought stresses compared with control**

#### 4.3.2.2 Drought Response Index (DRI)

Drought Response Index (DRI) was calculated from the observed phenotypic value of each character. DRI value represents the relative change for each of the character caused by drought treatment. The DRI value was considered as the indicator for drought tolerance. Comparing the DRI value, we had received important information about the drought tolerance in different genotypes of cotton. Finding from this study will provide theoretical bases and practical guidance for distinguishing drought tolerant germplasm resources and breeding for drought tolerant cultivar.

Twenty five cotton genotypes showed a wider range of drought tolerance index (Table 77). DRI value for uniformity index showed a wide range having maximum DRI (103.3) and minimum (97.4) in G38 and G14, respectively. G38 and G14 showed the minimum (74.4) and maximum (121.9) DRI value for short fibre index. G22, G50 and G38 showed the minimum (92.5) and maximum (103.5) DRI value for fibre strength. In case of micronnaire, the minimum (80.0) and maximum (135.5) DRI value was observed in G17 and G48, respectively. G8 and G48 showed the minimum (91.8) and maximum (97.4) DRI value for elongation. Minimum (95.5) and maximum (99.5) DRI value for maturity ratio were observed in G34 and G13, G14, respectively. In case of moisture content, minimum (90.4) and maximum (113.6) DRI value in G2 and G50 respectively. DRI value for reflectance degree showed wider range of value among the genotypes. In case of reflectance degree, minimum (95.7) and maximum (98.6) DRI were observed in G14 and G1 respectively. G13 and G8 showed the minimum (87.8) and maximum (152.1) DRI value for yellowness. Minimum (90.8) and maximum (111.6) DRI value for fibre length were observed in G14 and G38, respectively.

Based on the average highest DRI value of each genotype for ten fibre quality traits, genotypes were grouped into two groups such as drought tolerant and moderately tolerant genotypes (Table 78). All of the genotypes of cotton showed tolerant to drought stress based on the average DRI values.

**Table 77. Drought Response Index of twenty-five genotypes based on ten fiber quality characters**

| Genotypes | Uniformity index | Short fibre index | Fibre strength | Mironnaire | Elongation | Maturity ratio | Moisture content | Reflectance degree | yellowness | Fibre length | average | group |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| G1 | 99.5 | 103.2 | 97.9 | 98.6 | 95.9 | 98.5 | 102.9 | 98.6 | 110.9 | 97.1 | 100.3 | Tolerant |
| G2 | 99.9 | 101.1 | 98.7 | 97.7 | 95.7 | 98.7 | 90.4 | 97.9 | 134.0 | 99.7 | 101.4 | Tolerant |
| G8 | 100.0 | 103.1 | 99.1 | 95.7 | 91.8 | 98.8 | 98.7 | 96.7 | 152.1 | 100.5 | 103.7 | Tolerant |
| G10 | 100.9 | 94.5 | 100.2 | 88.1 | 94.6 | 97.5 | 112.6 | 96.9 | 121.6 | 104.4 | 101.1 | Tolerant |
| G11 | 99.6 | 100.5 | 93.7 | 111.4 | 95.9 | 97.0 | 99.9 | 98.1 | 141.9 | 101.3 | 103.9 | Tolerant |
| G12 | 101.3 | 92.8 | 99.3 | 90.6 | 95.2 | 97.6 | 96.1 | 98.5 | 122.8 | 105.2 | 99.9 | Tolerant |
| G13 | 99.9 | 104.4 | 97.7 | 117.0 | 93.7 | 99.5 | 108.5 | 97.1 | 87.8 | 99.1 | 100.5 | Tolerant |
| G14 | 97.4 | 121.9 | 95.8 | 112.7 | 94.5 | 99.5 | 95.9 | 95.7 | 147.5 | 90.8 | 105.2 | Tolerant |
| G15 | 100.1 | 100.8 | 97.8 | 98.6 | 93.3 | 98.2 | 103.3 | 95.8 | 97.4 | 101.5 | 98.7 | Tolerant |
| G17 | 99.0 | 103.2 | 97.1 | 80.0 | 93.1 | 97.8 | 92.6 | 97.1 | 100.3 | 102.2 | 96.2 | Tolerant |
| G18 | 101.7 | 88.3 | 102.8 | 103.5 | 95.0 | 97.0 | 99.9 | 97.2 | 106.3 | 107.5 | 99.9 | Tolerant |
| G22 | 97.7 | 118.7 | 92.5 | 87.2 | 94.0 | 97.5 | 106.2 | 96.9 | 93.3 | 93.1 | 97.7 | Tolerant |
| G23 | 101.0 | 94.9 | 98.4 | 88.7 | 95.4 | 96.7 | 103.2 | 97.6 | 99.3 | 101.5 | 97.7 | Tolerant |
| G29 | 97.9 | 111.1 | 92.6 | 97.6 | 94.6 | 95.8 | 104.4 | 98.0 | 126.0 | 93.2 | 101.1 | Tolerant |
| G30 | 100.9 | 98.1 | 100.8 | 86.8 | 95.4 | 97.2 | 92.9 | 96.7 | 97.7 | 105.0 | 97.1 | Tolerant |
| G33 | 99.4 | 104.6 | 95.7 | 98.7 | 95.5 | 95.6 | 105.4 | 97.5 | 106.4 | 95.9 | 99.5 | Tolerant |
| G34 | 100.9 | 90.2 | 99.3 | 86.3 | 95.4 | 95.5 | 92.1 | 97.2 | 115.5 | 103.5 | 97.6 | Tolerant |
| G35 | 98.7 | 111.2 | 95.5 | 103.3 | 95.0 | 96.5 | 112.8 | 97.3 | 102.4 | 93.7 | 100.6 | Tolerant |
| G38 | 103.3 | 74.4 | 103.5 | 113.4 | 94.4 | 96.2 | 93.1 | 96.6 | 100.5 | 111.6 | 98.7 | Tolerant |
| G39 | 99.9 | 97.9 | 99.2 | 129.6 | 95.8 | 97.8 | 103.3 | 97.3 | 120.8 | 102.5 | 104.4 | Tolerant |
| G43 | 101.1 | 90.2 | 100.4 | 103.7 | 97.3 | 96.7 | 110.7 | 97.3 | 95.8 | 103.0 | 99.6 | Tolerant |
| G45 | 99.3 | 104.3 | 96.2 | 94.6 | 95.1 | 97.2 | 97.9 | 97.8 | 109.3 | 101.0 | 99.3 | Tolerant |
| G46 | 100.2 | 100.5 | 97.3 | 105.5 | 94.0 | 96.9 | 104.3 | 95.9 | 105.4 | 102.8 | 100.3 | Tolerant |
| G48 | 98.8 | 111.5 | 98.7 | 135.5 | 97.4 | 98.1 | 92.0 | 97.6 | 112.3 | 98.2 | 104.0 | Tolerant |
| G50 | 99.1 | 108.8 | 92.5 | 93.3 | 95.6 | 96.7 | 113.6 | 97.5 | 102.4 | 95.8 | 99.6 | Tolerant |

**Table 78. Grouping of 25 genotypes based on DRI values under drought stress**

| Sl No. | Scale | % DRI values | Drought tolerant group | Name of genotypes |
|---|---|---|---|---|
| **1** | I | >90 | Tolerant (T) | G1, G2, G8, G10, G11, G12, G13, G14, G15, G17, G18, G22, G23, G29, G30, G33, G34, G35, G38, G39, G43, G45, G46, G48, G50. |
| **2** | II | 80-90 | Moderately tolerant (MT) | - |
| **3** | III | 70-80 | Moderately susceptible (MS) | - |
| **4** | IV | <70 | Susceptible (S) | - |

#### 4.3.2.3 Genetic variability analysis

The extent of variation among the genotypes in respect of ten characters was studied and mean sum of square, phenotypic variance ($\sigma^2p$), genotypic variance ($\sigma^2g$), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ($h^2b$), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) presented in Table 79.

##### 4.3.2.3.1 Uniformity index

Minimum and maximum values of uniformity index were 83.12% and 85.40% respectively which showed the presence of variation in uniformity index among the genotypes (Table 79). The genotypic and phenotypic variance for this trait was 0.39 and 0.41, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (0.76 and 0.74, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (95%) with low genetic advance (1.26) and genetic advance in mean (1.49%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for cotton uniformity index has been also reported in Shakeel *et al*. (2015).

##### 4.3.2.3.2 Short fibre index

Minimum and maximum values of short fibre index were 6.83 and 8.50, respectively which showed the presence of variation in short fibre index among the genotypes (Table 79). The genotypic and phenotypic variance for this trait was 0.17 and 0.19, respectively. The phenotypic variance appeared to be high compared to the genotypic

**Table 79. Genetic parameters for 10 fiber quality characters of twenty-five cotton genotypes**

| Genetic parameters | Uniformity index | Short fibre index | Fibre strength | Mironnaire | Elongation | Maturity ratio | Moisture content | Reflectance degree | yellowness | Fibre length |
|---|---|---|---|---|---|---|---|---|---|---|
| **Maximum** | 85.40 | 8.50 | 30.79 | 5.06 | 6.43 | 0.88 | 6.74 | 78.93 | 17.35 | 32.87 |
| **Minimum** | 83.12 | 6.83 | 26.76 | 3.40 | 6.00 | 0.84 | 5.43 | 70.10 | 13.40 | 29.46 |
| **GM** | 84.47 | 7.43 | 29.17 | 4.22 | 6.23 | 0.86 | 6.21 | 75.93 | 15.38 | 31.09 |
| **σ2e** | 0.02 | 0.02 | 0.14 | 0.00 | 0.00 | 0.00 | 0.01 | 1.04 | 0.05 | 0.02 |
| **σ2g** | 0.39 | 0.17 | 0.57 | 0.12 | 0.01 | 0.00 | 0.07 | 5.26 | 1.15 | 0.77 |
| **σ2p** | 0.41 | 0.19 | 0.71 | 0.12 | 0.01 | 0.00 | 0.08 | 6.30 | 1.20 | 0.79 |
| **ECV** | 0.17 | 1.90 | 1.28 | 1.18 | 0.29 | 0.51 | 1.20 | 1.35 | 1.46 | 0.42 |
| **GCV** | 0.74 | 5.62 | 2.60 | 8.08 | 1.56 | 1.17 | 4.33 | 3.02 | 6.97 | 2.83 |
| **PCV** | 0.76 | 5.94 | 2.90 | 8.17 | 1.59 | 1.17 | 4.49 | 3.31 | 7.12 | 2.86 |
| **Heritability** | 0.95 | 0.90 | 0.80 | 0.98 | 0.97 | 1.00 | 0.93 | 0.83 | 0.96 | 0.98 |
| **GA (5%)** | 1.26 | 0.82 | 1.40 | 0.69 | 0.20 | 0.02 | 0.53 | 4.32 | 2.16 | 1.79 |
| **GA (% mean)** | 1.49 | 10.98 | 4.79 | 16.47 | 3.17 | 2.40 | 8.60 | 5.68 | 14.06 | 5.77 |
| **SEM** | 0.08 | 0.08 | 0.22 | 0.03 | 0.01 | 0.00 | 0.04 | 0.59 | 0.13 | 0.08 |
| **CD 5%** | 0.24 | 0.23 | 0.62 | 0.08 | 0.03 | 0.01 | 0.12 | 1.68 | 0.37 | 0.22 |
| **CD1%** | 0.32 | 0.31 | 0.82 | 0.11 | 0.04 | 0.01 | 0.16 | 2.24 | 0.49 | 0.29 |

Here, GM= Grand mean; $\sigma^2$g= Genotypic variance; σ2e= environmental variance; σ2p= phenotypic variance; GCV= genotypic coefficient of variation; ECV=Environmental coefficient of variation, PCV= Phenotypic coefficient of variation, GA= genetic advance; SEM=Standard error of mean, CD= Critical differences.

variance suggested the considerable influence of environment on the expression ofgenes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (5.94 and 5.62 respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (90%) with low genetic advance (0.82) and genetic advance in mean (10.98%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for cotton uniformity index has been also reported in Shakeel *et al*. (2015).

#### 4.3.2.3.3 Fibre strength

Minimum and maximum values of fibre strength were 26.76 g/tex and 30.79 g/tex, respectively which showed the presence of variation in fibre strength among the genotypes (Table 79). The genotypic and phenotypic variance for this trait was 0.57 and 0.71, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (2.90 and 2.60 respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (80%) with low genetic advance (1.40) and genetic advance in mean (4.79%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be

rewarding. Heritability was maximum for micronaire and fiber strength with low genetic advance as revealed by Nawaz *et al*. (2019). Shilpa and Chandrasekhar (2020) found that fiber bundle strength decrease in inferior direction as reduction of soil moisture levels.

#### 4.3.2.3.4 Micronnaire

Minimum and maximum values of micronnaire were 3.40 µg/inch and 5.06 µg/inch, respectively which showed the presence of variation in micronnaire among the genotypes (Table 79). The genotypic and phenotypic variance for this trait was 0.12 and 0.12, respectively. The phenotypic variance and the genotypic variance appeared to be same to suggest no influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (8.17 and 8.08 respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (98%) with low genetic advance (0.69) and genetic advance in mean (16.47%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. Heritability was maximum for micronaire and fiber strength with low genetic advance as revealed by Nawaz *et al*. (2019). Shilpa and Chandrasekhar (2020) found that fiber fineness decrease in inferior direction as reduction of soil moisture levels.

#### 4.3.2.3.5 Elongation

Minimum and maximum values of elongation were 6.00% and 6.43%, respectively which showed the presence of variation in elongation among the genotypes (Table 79). The genotypic and phenotypic variance for this trait was 0.01 and 0.01, respectively. The phenotypic variance and the genotypic variance appeared to be same to suggest no influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of

variation (GCV) were low (1.59 and 1.56, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (97%) with low genetic advance (0.20) and genetic advance in mean (3.17%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low phenotypic coefficient of variation for cotton uniformity index has been also reported in Shakeel *et al*. (2015).

#### 4.3.2.3.6 Maturity ratio

Minimum and maximum values of maturity ratio were 0.84 and 0.88, respectively which showed the presence of variation in maturity ratio among the genotypes (Table 79). The genotypic and phenotypic variance for this trait was 0.00 and 0.00, respectively. The phenotypic, genotypic and environmental variance appeared to be same to suggest no influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (1.17 and 1.17, respectively). PCV and GCV was same value which suggested that the appeared variation was due to the genotypes. However, the difference between the PCV and GCV was none which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (100%) with low genetic advance (0.02) and genetic advance in mean (2.40%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low genetic advance for cotton maturity ratio has been also reported in Shar *et al*. (2015).

#### 4.3.2.3.7 Moisture content/regain

Minimum and maximum values of moisture content were 5.43% and 6.74%, respectively which showed the presence of variation in moisture content among the genotypes (Table 79). The genotypic and phenotypic variance for this trait was 0.07 and 0.08, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (4.49 and 4.33, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (93%) with low genetic advance (0.53) and genetic advance in mean (8.60%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low genetic advance for cotton moisture content has been also reported in Nawaz *et al*. (2019).

#### 4.3.2.3.8 Reflectance degree

Minimum and maximum values of reflectance degree were 70.10% and 78.93%, respectively which showed the presence of variation in reflectance degree among the genotypes (Table 79). The genotypic and phenotypic variance for this trait was 5.26 and 6.30, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (3.31 and 3.02, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the

genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (83%) with low genetic advance (4.32) and genetic advance in mean (5.68%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding.

#### 4.3.2.3.9 Yellowness

Minimum and maximum values of yellowness were 13.40 and 17.35, respectively which showed the presence of variation in yellowness among the genotypes (Table 79). The genotypic and phenotypic variance for this trait was 1.15 and 1.20, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low (7.12 and 6.97, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (96%) with low genetic advance (2.16) and genetic advance in mean (14.06%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding.

#### 4.3.2.3.10 Fibre length

Minimum and maximum values of fibre length were 29.46 mm and 32.87 mm, respectively which showed the presence of variation in fibre length among the genotypes (Table 79). The genotypic and phenotypic variance for this trait was 0.77 and 0.79, respectively. The phenotypic variance appeared to be high compared to the genotypic variance suggested the considerable influence of environment on the expression of genes controlling for this trait. The phenotypic coefficient of variation

(PCV) and genotypic coefficient of variation (GCV) were low (2.86 and 2.83, respectively). PCV was higher than GCV which suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the difference between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. The heritability estimates for this trait were very high (98%) with low genetic advance (1.79) and genetic advance in mean (5.77%). The high heritability coupled with low genetic advance indicated the non-additive gene action. The high heritability was due to the favorable influence of environment rather than the genotypes and selection based on this trait will not be rewarding. High heritability and low genetic advance for cotton moisture content has been also reported in Nawaz *et al*. (2019), Azhar and Ajmal (1999), Rao and Gopinath (2013) and Shahzad *et al*. (2015).

#### 4.3.2.4 Correlation coefficient

Correlation studies along with path analysis provide a better understanding of the association of different characters with fibre quality traits. Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components as suggested by Sing and Chaudhary1985. Genotypic and phenotypic correlation coefficients among the different pairs for different genotypes of cotton are given in Table 80 and Table 81, respectively. In case of genotypic correlation coefficient, uniformity index showed statistical positive significant correlation with fibre length (0.91), negative significant correlation with short fibre index (-0.95), elongation (-0.51) and non-significant correlation with fibre strength (0.22), micronnaire (-0.15), maturity ratio (-0.02), moisture content (-0.32), reflectance degree (-0.19) and yellowness (-0.09). (Table 80). Short fibre index showed statistical positive significant correlation with elongation (0.61), negative significant correlation with fibre length (-0.91) and non-significant correlation with fibre strength (-0.11), micronnaire (0.30), maturity ratio (0.02), moisture content (0.30), reflectance degree (0.26) and yellowness (0.04). Fibre strength showed significant positive correlation with reflectance degree (0.57) and non-significant relation with micronnaire (0.35), elongation (0.26), maturity ratio (0.30), moisture content (-0.25), yellowness (0.16) and fibre length (0.09).

**Table 80. Genotypic correlation coefficient among 10 fiber quality characters of cotton genotypes**

| Characters | Uniformity index | Short fibre index | Fibre strength | Mironnaire | Elongation | Maturity ratio | Moisture content | Reflectance degree | yellowness | Fibre length |
|---|---|---|---|---|---|---|---|---|---|---|
| **Uniformity index** | | -0.95** | 0.22 $^{NS}$ | -0.15$^{NS}$ | -0.51 ** | -0.02$^{NS}$ | -0.32 $^{NS}$ | -0.19 $^{NS}$ | -0.09 $^{NS}$ | 0.91 ** |
| **Short fiber index** | | | -0.11 $^{NS}$ | 0.30 $^{NS}$ | 0.61 ** | 0.02 $^{NS}$ | 0.30 $^{NS}$ | 0.26 $^{NS}$ | 0.04 $^{NS}$ | -0.91** |
| **Fiber strength** | | | | 0.35 $^{NS}$ | 0.26 $^{NS}$ | 0.30 $^{NS}$ | -0.25 $^{NS}$ | 0.57 ** | 0.16 $^{NS}$ | 0.09$^{NS}$ |
| **Micronnaire** | | | | | 0.39 * | 0.54 ** | 0.29 $^{NS}$ | 0.42 * | -0.12 $^{NS}$ | -0.32$^{NS}$ |
| **Elongation** | | | | | | 0.25 $^{NS}$ | 0.18 $^{NS}$ | 0.66 ** | 0.16 $^{NS}$ | -0.57** |
| **Maturity ratio** | | | | | | | 0.103 $^{NS}$ | 0.36 $^{NS}$ | 0.18 $^{NS}$ | -0.07$^{NS}$ |
| **Moisture content** | | | | | | | | -0.04 $^{NS}$ | -0.33 $^{NS}$ | -0.35$^{NS}$ |
| **Reflectance degree** | | | | | | | | | 0.14 $^{NS}$ | -0.34 $^{NS}$ |
| **Yellowness** | | | | | | | | | | -0.10 $^{NS}$ |
| **Fiber length** | | | | | | | | | | |

**Table 81. Phenotypic correlation coefficient among 10 fiber quality characters of cotton genotypes**

| Characters | Uniformity index | Short fibre index | Fibre strength | Mironnaire | Elongation | Maturity ratio | Moisture content | Reflectance degree | yellowness | Fibre length |
|---|---|---|---|---|---|---|---|---|---|---|
| **Uniformity index** | | -0.89 ** | 0.20$^{NS}$ | -0.14 $^{NS}$ | -0.49 ** | -0.01 $^{NS}$ | -0.29 ** | -0.17 $^{NS}$ | -0.08$^{NS}$ | 0.88 ** |
| **Short fiber index** | | | -0.10$^{NS}$ | 0.27 * | 0.57 ** | 0.01 $^{NS}$ | 0.27 * | 0.22 $^{NS}$ | 0.04 $^{NS}$ | -0.85 ** |
| **Fiber strength** | | | | 0.31 ** | 0.23 * | 0.21 $^{NS}$ | -0.20 $^{NS}$ | 0.48 ** | 0.15 $^{NS}$ | 0.08 NS |
| **Micronnaire** | | | | | 0.38 ** | 0.47 ** | 0.27 * | 0.39 ** | -0.11$^{NS}$ | -0.32 ** |
| **Elongation** | | | | | | 0.21 $^{NS}$ | 0.16 $^{NS}$ | 0.58 ** | 0.16 $^{NS}$ | -0.56 ** |
| **Maturity ratio** | | | | | | | 0.06 $^{NS}$ | 0.25 * | 0.15 $^{NS}$ | -0.06 $^{NS}$ |
| **Moisture content** | | | | | | | | -0.03 $^{NS}$ | -0.31 ** | -0.33 ** |
| **Reflectance degree** | | | | | | | | | 0.11 $^{NS}$ | -0.30 ** |
| **Yellowness** | | | | | | | | | | -0.10 $^{NS}$ |
| **Fiber length** | | | | | | | | | | |

Micronnaire showed significant positive correlation with elongation (0.39), maturity ratio (0.54), reflectance degree (0.42) and non-significant correlation with moisture content (0.29), yellowness (-0.12) and fibre length (-0.32). Elongation showed statistical positive significant correlation with reflectance degree (0.66), negative significant correlation with fibre length (-0.57) and non-significant correlation with maturity ratio (0.25), moisture content (0.18), yellowness (0.16). Maturity ratio showed non-significant correlation with moisture content (0.103), reflectance degree (0.36), yellowness (0.18) and fibre length (-0.07). Moisture content showed non-significant correlation with reflectance degree (-0.04), yellowness (-0.33) and fibre length (-0.35). Reflectance degree showed non-significant correlation with yellowness (0.14) and fibre length (-0.34). Yellowness showed non-significant correlation with fibre length (-0.10). At the genotypic level, Adeela *et al*. (2021) showed that plant height showed significant positive correlation with number of reproductive branches, number of vegetative branches and root diameter. He also showed that vegetative branches per plant showed non-significant positive correlation with number of reproductive branches which have been observed in our experiment as well. Fiber length was positively linked with plant height, boll weight, GOT, seed index, fibre fineness and seed cotton yield. Fiber length had negative correlation with fibre strength. Ali and Awan (2009) and Echekwu (2001) indicated that fiber length was negatively associated with fibre strength. Ali and Awan (2009), Zeng and Meredith (2009), Tang and Xiao (2014) and Yaqoob *et al*. (2016) found positive linkage between fibre fineness and fibre strength. Abbas *et al*. (2013) and Altaher and Singh (2003) revealed that fibre fineness had positive linkage with plant height, sympodial branches per plant. Abdullah *et al*. (2016) reported that fibre fineness was positively correlated with boll weight. Heritability value for fibre fineness was 70.42%. Hendawi *et al*. (1999) and Lu *et al*. (2002) estimated 67% and 73% heritability respectively for fibre fineness.

In case of phenotypic correlation coefficient, uniformity index showed statistical positive significant correlation with fibre length (0.88), negative significant correlation with short fibre index (-0.89), elongation (-0.49), moisture content (-0.29) and non-significant correlation with fibre strength (0.20), micronnaire (-0.14), maturity ratio (-0.01), reflectance degree (-0.17) and yellowness (-0.08). (Table 81). You may add discussion for root length here. Short fibre index showed statistical positive significant

correlation with micronnaire (0.27), elongation (0.57), moisture content (0.27), negative significant correlation with fibre length (-0.85) and non-significant correlation with fibre strength (-0.10), maturity ratio (0.01), reflectance degree (0.22) and yellowness (0.04). Fibre strength showed significant positive correlation with micronnaire (0.31), elongation (0.23), reflectance degree (0.48) and non-significant relation with maturity ratio (0.21), moisture content (-0.20), yellowness (0.15) and fibre length (0.08). Micronnaire showed significant positive correlation with elongation (0.38), maturity ratio (0.47), moisture content (0.27), reflectance degree (0.39), negative significant correlation with fibre length (-0.32) and non-significant correlation with yellowness (-0.11). Elongation showed statistical positive significant correlation with reflectance degree (0.58), negative significant correlation with fibre length (-0.56) and non-significant correlation with maturity ratio (0.21), moisture content (0.16), yellowness (0.16). Maturity ratio showed statistical positive significant correlation with reflectance degree (0.25) and non-significant correlation with moisture content (0.06), yellowness (0.15) and fibre length (-0.06). Moisture content showed negative significant correlation with yellowness (-0.31), fibre length (-0.33) and non-significant correlation with reflectance degree (-0.03). Reflectance degree showed negative significant correlation with fibre length (-0.30) and non-significant correlation with yellowness (0.11). Yellowness showed non-significant correlation with fibre length (-0.10). At the phenotypic level, Adeela *et al*. (2021) showed that plant height showed significant positive correlation with number of reproductive branches, number of vegetative branches and root diameter. They also showed that vegetative branches per plant showed non-significant positive correlation with number of reproductive branches which have been observed in our experiment as well. Rehman *et al*. (2020) revealed that seed cotton yield had significant positive correlation with plant height, number of bolls per plant, number of sympodial branches per plant, GOT, staple length and fibre strength. Staple length and fibre strength were negatively linked with each other.

#### 4.3.2.5 Path coefficient analysis

Path coefficient is a means of measuring the direct and indirect effects of one variable through the other variables on the end-product. Here fibre length was considered as effect (dependent variable) and uniformity index, short fibre index, fibre strength, micronnaire, elongation, maturity ratio, moisture content, reflectance degree and

yellowness were considered as independent variables. Wright (1921) developed the path coefficient analysis technique and later demonstrated by Deway and Lu (1959) facilitates the partitioning of correlation coefficients into direct and indirect contribution of various characters on fibre length. It is standardized partial regression coefficient analysis. As such, it measures the direct influence if one variable upon other. Estimation of direct and indirect effect of path coefficient analysis is presented in Table 82 and Table 83.

In case of genotypic path coefficient analysis, uniformity index had positive direct effect on fibre length (0.682) which was contributed to result significant positive genotypic correlation (0.91) (Table 82). Uniformity index had positive indirect effect on short fibre index (0.164), fibre strength (0.009), micronnaire (0.028), moisture content (0.026), reflectance degree (0.037), yellowness (0.009) and negative indirect effect on elongation (-0.035), maturity ratio (-0.002) (Table 90). Short fibre index showed negative direct effect (-0.172) on fibre length with significant negative genotypic correlation (-0.91). Short fibre index had positive indirect effect on elongation (0.042), maturity ratio (0.003) and negative indirect effect on uniformity index (-0.650), fibre strength (-0.005), micronnaire (-0.052), moisture content (-0.025), reflectance degree (-0.050), yellowness (-0.004). Fibre strength had positive direct effect on fibre length (0.041) which was contributed to result on non-significant positive genotypic correlation (0.09). Fibre strength had negative indirect effect on micronnaire (-0.061), reflectance degree (-0.109), yellowness (-0.015) and positive indirect effect on uniformity index (0.152), short fibre index (0.020), elongation (0.018), maturity ratio (0.031), moisture content (0.021). Micronnaire had negative direct effect on fibre length (-0.173) which was contributed to result in non-significant negative genotypic correlation (-0.32). Micronnaire had positive indirect effect on fibre strength (0.015), elongation (0.027), maturity ratio (0.056), yellowness (0.011) and negative indirect effect on uniformity index (-0.109), short fibre index (-0.052), moisture content (-0.024), reflectance degree (-0.081). Elongation had direct positiveeffect on fibre length (0.067) which was contributed significant negative genotypic correlation (-0.57). Elongation had positive indirect effect on fibre strength (0.011), maturity ratio (0.026) and indirect negative effect on uniformity index (-0.352), short fibre index (-0.106), micronnaire (-0.068), moisture content (-0.015), reflectance degree (-0.126) and yellowness (-0.015). Maturity ratio had positive

**Table 82. Genotypic path coefficient analysis showing the direct (bold) and indirect effect of different characters on fiber length of cotton**

| Characters | Uniformity index | Short fibre index | Fibre strength | Mironnaire | Elongation | Maturity ratio | Moisture content | Reflectance degree | yellowness | Genotypic correlation coefficient with Fibre length |
|---|---|---|---|---|---|---|---|---|---|---|
| **Uniformity index** | **0.682** | 0.164 | 0.009 | 0.028 | -0.035 | -0.002 | 0.026 | 0.037 | 0.009 | 0.91 ** |
| **Short fiber index** | -0.650 | **-0.172** | -0.005 | -0.052 | 0.042 | 0.003 | -0.025 | -0.050 | -0.004 | -0.91** |
| **Fiber strength** | 0.152 | 0.020 | **0.041** | -0.061 | 0.018 | 0.031 | 0.021 | -0.109 | -0.015 | $0.09^{NS}$ |
| **Micronnaire** | -0.109 | -0.052 | 0.015 | **-0.173** | 0.027 | 0.056 | -0.024 | -0.081 | 0.011 | $-0.32^{NS}$ |
| **Elongation** | -0.352 | -0.106 | 0.011 | -0.068 | **0.067** | 0.026 | -0.015 | -0.126 | -0.015 | -0.57** |
| **Maturity ratio** | -0.014 | -0.005 | 0.012 | -0.093 | 0.017 | **0.104** | -0.008 | -0.069 | -0.016 | $-0.07^{NS}$ |
| **Moisture content** | -0.221 | -0.052 | -0.010 | -0.051 | 0.013 | 0.010 | **-0.081** | 0.009 | 0.030 | $-0.35^{NS}$ |
| **Reflectance degree** | -0.135 | -0.046 | 0.024 | -0.074 | 0.045 | 0.038 | 0.004 | **-0.189** | -0.013 | $-0.34^{NS}$ |
| **Yellowness** | -0.065 | -0.008 | 0.007 | 0.022 | 0.011 | 0.019 | 0.027 | -0.027 | **-0.091** | $-0.10^{NS}$ |

**Table 83. Phenotypic path coefficient analysis showing the direct (bold) and indirect effect of different characters on fiber length of cotton**

| Characters | Uniformity index | Short fibre index | Fibre strength | Mironnaire | Elongation | Maturity ratio | Moisture content | Reflectance degree | yellowness | Pheenotypic correlation coefficient Fibre length |
|---|---|---|---|---|---|---|---|---|---|---|
| **Uniformity index** | **0.544** | 0.237 | 0.013 | 0.004 | 0.060 | 0.000 | 0.020 | 0.003 | 0.003 | 0.88 ** |
| **Short fiber index** | -0.484 | **-0.266** | -0.006 | -0.008 | -0.071 | 0.000 | -0.019 | -0.004 | -0.001 | -0.85 ** |
| **Fiber strength** | 0.109 | 0.026 | **0.065** | -0.009 | -0.030 | -0.075 | 0.014 | -0.009 | -0.005 | 0.08 NS |
| **Micronnaire** | -0.079 | -0.074 | 0.020 | **-0.027** | -0.047 | -0.091 | -0.018 | -0.007 | 0.004 | -0.32 ** |
| **Elongation** | -0.265 | -0.153 | 0.015 | -0.010 | **-0.126** | 0.000 | -0.012 | -0.011 | -0.005 | -0.56 ** |
| **Maturity ratio** | 0.000 | 0.000 | 0.015 | -0.008 | 0.000 | **0.000** | 0.000 | -0.005 | -0.003 | -0.06 NS |
| **Moisture content** | -0.164 | -0.074 | -0.013 | -0.007 | -0.022 | 0.000 | **-0.068** | 0.001 | 0.010 | -0.33 ** |
| **Reflectance degree** | -0.098 | -0.059 | 0.031 | -0.011 | -0.073 | -0.075 | 0.002 | **-0.019** | -0.003 | -0.30 ** |
| **Yellowness** | -0.047 | -0.012 | 0.010 | 0.003 | -0.021 | -0.029 | 0.021 | -0.002 | **-0.031** | -0.10 NS |

direct effect on fibre length (0.104) which was contributed non-significant negative genotypic correlation (-0.07). Maturity ratio had positive indirect effect on fibre strength (0.012), elongation (0.017) and negative indirect effect on uniformity index (-0.014), short fibre index (-0.005), micronnaire (-0.093), moisture content (-0.008), reflectance degree (-0.069) and yellowness (-0.016). Moisture content had negative direct effect on fibre length (-0.081) which was contributed non-significant negative genotypic correlation (-0.35). Moisture content had positive indirect effect on elongation (0.013), maturity ratio (0.010), reflectance degree (0.009), yellowness (0.030) and negative indirect effect on uniformity index (-0.221), short fibre index (-0.052), fibre strength (-0.010), micronnaire (-0.051). Reflectance degree had negative direct effect on fibre length (-0.189) which was contributed non-significant negative genotypic correlation (-0.34). Reflectance degree had positive indirect effect on fibre strength (0.024), elongation (0.045), maturity ratio (0.038), moisture content (0.004) and negative indirect effect on uniformity index (-0.135), short fibre index (-0.046), micronnaire (-0.074), yellowness (-0.013). Yellowness had negative direct effect on fibre length (-0.091) which was contributed non-significant negative genotypic correlation (-0.10). Yellowness had positive indirect effect on fibre strength (0.007), micronnaire (0.022), elongation (0.011), maturity ratio (0.019), moisture content (0.027) and negative indirect effect uniformity index (-0.065), short fibre index (-0.008), reflectance degree (-0.027). Genotypic path coefficient analysis carried out by Adeela *et al*. (2021) revealed that seed cotton yield had a significant positive association with plant height, the number of monopodial or vegetative branches, the number of sympodial (reproductive) branches, ginning out turn (GOT), the number of bolls, seed per boll, seed index, uniformity index, the number of sympodial branches, reflectance and seed index at the genotypic level while a significant positive relationship was observed with plant height, the number of sympodial branches, boll number, and GOT. They also negative significant relation was observed for short fiber index at genotypic level.

In case of phenotypic path coefficient analysis, uniformity index had positive direct effect on fibre length (0.544) which was contributed to result significant positive genotypic correlation (0.88) (Table 83). Uniformity index had positive indirect effect on short fibre index (0.237), fibre strength (0.013), micronnaire (0.004), elongation (0.060), moisture content (0.020), reflectance degree (0.003), yellowness (0.003) and

no indirect effect on maturity ratio (0.000) (Table 83). Short fibre index showed negative direct effect (-0.266) on fibre length with significant negative genotypic correlation (-0.85). Short fibre index had negative indirect effect on uniformity index (-0.484), fibre strength (-0.006), micronnaire (-0.008), elongation (-0.071), moisture content (-0.019), reflectance degree (-0.004), yellowness (-0.001) and no indirect effect on maturity ratio (0.000). Fibre strength had positive direct effect on fibre length (0.065) which was contributed to result on non-significant positive genotypic correlation (0.08). Fibre strength had negative indirect effect on micronnaire (-0.009), elongation (-0.030), maturity ratio (-0.075), reflectance degree (-0.009), yellowness (-0.005) and positive indirect effect on uniformity index (0.109), short fibre index (0.026), moisture content (0.014). Micronnaire had negative direct effect on fibre length (-0.027) which was contributed to result in significant negative genotypic correlation (-0.32). Micronnaire had positive indirect effect on fibre strength (0.020), yellowness (0.004) and negative indirect effect on uniformity index (-0.079), short fibre index (-0.074), elongation (-0.047), maturity ratio (-0.091), moisture content (-0.018) and reflectance degree (-0.007). Elongation had direct negative effect on fibre length (-0.126) which was contributed significant negative genotypic correlation (-0.56). Elongation had positive indirect effect on fibre strength (0.015) and indirect negative effect on uniformity index (-0.265), short fibre index (-0.153), micronnaire (-0.010), moisture content (-0.012), reflectance degree (-0.011), yellowness (-0.005) and no indirect effect on maturity ratio (0.000). Maturity ratio had no direct effect on fibre length (0.000) which was contributed non-significant negative genotypic correlation (-0.06). Maturity ratio had positive indirect effect on fibre strength (0.015) and negative indirect effect on micronnaire (-0.008), reflectance degree (-0.005), yellowness (-0.003) and no indirect effect on uniformity index (0.000), short fibre index (0.000), elongation (0.000), moisture content (0.000). Moisture content had negative direct effect on fibre length (-0.068) which was contributed significant negative genotypic correlation (-0.33). Moisture content had positive indirect effect on reflectance degree (0.001), yellowness (0.010) and negative indirect effect on uniformity index (-0.164), short fibre index (-0.074), fibre strength (-0.013), micronnaire (-0.007), elongation (-0.022) and no indirect effect on maturity ratio (0.000). Reflectance degree had negative direct effect on fibre length (-0.019) which was contributed significant negative genotypic correlation (-0.30). Reflectance degree had positive indirect effect on fibre strength (0.031), moisture content (0.002) and negative indirect effect on

uniformity index (-0.098), short fibre index (-0.059), micronnaire (-0.011), elongation (-0.073), maturity ratio (-0.075), yellowness (-0.003). Yellowness had negative direct effect on fibre length (-0.031) which was contributed non-significant negative genotypic correlation (-0.10). Yellowness had positive indirect effect on fibre strength (0.010), micronnaire (0.003), moisture content (0.021) and negative indirect effect uniformity index (-0.047), short fibre index (-0.012), elongation (-0.021), maturity ratio (-0.029) and reflectance degree (-0.002).

#### 4.3.2.5 Selection of genotypes based on selection index

Selection of cotton genotypes for tolerance to drought stress was undertaken at polytheen house of Godagari, Rajshahi. During the cotton seed growing at field under polytheen house, the data of soil nutrient status was calculated by SRDI laboratory, Rajshahi. After seed sowing of each genotype four droughts build up to without irrigation, one irrigation after 40 days, two irrigation after 40 and 60 days interval with control of seed sowing by irrigation. After maturity of cotton boll, seed cotton was collected. So selection based on soil and plant morphology characters at drought prone areas may not be as effective for population improvement as it would be effective on the basis of selection indices for which some more fibre quality characters are given relative weightage. Discriminant functions is a biometrical technique which provides information about the relative contribution of the various component traits to fibre quality and aids in the isolation from populations of superior genotypes by providing information for indirect selection for yield and fibre quality. On the basis of fitted discriminate functions, selection scores were computed for all the 25 genotypes and ranked (Table 84). These 25 genotypes having good fibre quality characters may generate primary information regarding suitability of deferent genotypes for drought tolerance. The high fiber quality contributing genotypes were selected acceding to top based on selection scores (Expt-3). These genotypes were used as a plant material for fiber quality characters and selection suitable genotypes for drought prone areas.

**Table 84. Relative selection index scores and ranking of twenty five cotton genotypes based on fiber quality characters**

| Sl. No. | Genotypes | Variety / line | Selection Index score | Rank |
|---|---|---|---|---|
| **1** | G1 | CB-1 | 2394.51 | 20 |
| **2** | G2 | CB-2 | 2256.60 | 25 |
| **3** | G8 | CB-8 | 2428.18 | 16 |
| **4** | G10 | CB-10 | 2366.75 | 23 |
| **5** | G11 | CB-11 | 2378.29 | 22 |
| **6** | G12 | CB-12 | 2390.99 | 21 |
| **7** | G13 | CB-13 | 2345.67 | 24 |
| **8** | G14 | CB-14 | 2481.88 | 8 |
| **9** | G15 | CB-15 | 2467.57 | 10 |
| **10** | G17 | Ra-3 | 2459.37 | 11 |
| **11** | G18 | Ra-4 | 2519.81 | 2 |
| **12** | G22 | Ra-16 | 2489.45 | 7 |
| **13** | G23 | JA-08/9 | 2435.70 | 14 |
| **14** | G29 | JA-13/R | 2420.36 | 18 |
| **15** | G30 | SR-15 | 2431.47 | 15 |
| **16** | G33 | BC-272 | 2472.99 | 9 |
| **17** | G34 | BC-385 | 2515.63 | 3 |
| **18** | G35 | BC-394 | 2425.43 | 17 |
| **19** | G38 | BC-413 | 2502.22 | 5 |
| **20** | G39 | BC-415 | 2439.94 | 13 |
| **21** | G43 | BC-433 | 2511.10 | 4 |
| **22** | G45 | BC-442 | 2441.08 | 12 |
| **23** | G46 | BC-462 | 2498.93 | 6 |
| **24** | G48 | BC-510 | 2531.45 | 1 |
| **25** | G50 | BC-512 | 2419.64 | 19 |

# CHAPTER V
# SUMMARY AND CONCLUSION

Drought is the widest spread of the adverse soil problems which affects crop production. Cotton is now grown in marginal land due to pressure of food crops. To increase the cotton growing area towards the drought prone areas, there needed to develop drought stress tolerant cotton variety. The tolerance is a relative term depending mainly upon the intensity and duration of drought and relative performance of genotypes. The knowledge on genetics of drought tolerance is a pre-requisite in designing effective breeding programme to develop cotton varieties with higher ability to cope with drought stress. In order to identify high yielding drought stress tolerant cotton variety, the present investigation was carried out with three separate experiments during the period from April 2017 to March 2020 at the pot experiment of poly house at Sher e bangla Agricultural University and field experimental plot of Godagari, Rajshahi. The research works are summarized here.

Through morphological experiment at early flowering stage, fifty cotton genotypes were studied to know the genotypic variation of morphological characters for drought tolerance and their inter relationship. Significant genotypic variation for morphological characters viz. Root length, shoot length, shoot-root length ratio, root diameter, number of lateral root, total biomass of root, number of vegetative branch, number of reproductive branch were observed. Among all genotypes G12 had the highest number of reproductive branches at early flowering stage and the highest shoot lenght and it was followed by G19, G29, G36, G42, G45, G48 and G50. Genotype G5 had the minimum number of reproductive branch and lowest shoot length. Genotype G36 under T3 drought stress showed the highest reduction percentages on the number of reproductive branches and minimum values was in the genotypes in G12, G24, G29 and G45 under T4 stress, respectively. High phenotypic and genotypic variance was found in shoot length with high heritability, medium genetic advance. Low magnitude of genotypic and phenotypic variance was observed in number of vegetative branches with low heritability. High genotypic coefficient of variation was found in number of vegetative branches and total biomass of root. Heritability values in broad sense were relatively high for all most all characters except number of vegetative branches.

In the present study, the values of genotypic correlation coefficient were higher than phenotypic correlation coefficient for all the characters, indicating a strong inherent relationship among the characters which indicated the selection for drought tolerance would be effective based on these characters. According to Path analysis shoot length exhibited highest positive direct effect on number of reproductive branches. This was followed by root diameter, shoot root length ratio and total biomass of root. Rest of characters showed negative and negligible direct effect on number of reproductive branches. The path coefficient suggested that shoot length and root diameter were the major contributors to number of reproductive branches and selection for high plant heigth, number of reproductive branches, root diameter, root lenght would give better response for yield improvement in cotton.

Hierarchical cluster analysis of 50 cotton genotypes carried out taking eight morphological characters during growing season. The wards method of clustering was adopted using Euclidean distances genotypes were grouped into 8 clusters. Form the result, the largest cluster V with 12 cotton genotypes followed by cluster II with 10 genotypes and cluster III with 10 genotypes. The smallest cluster was observed in cluster I, cluster IV, and cluster VII with two genotypes in each cluster. The clustering pattern of the genotypes indicated that developing from the same locations or common eco-geographic origin did not form a single cluster. The genotypes belonging different locations were included in the same cluster, indicated that genotypic distribution and genetic divergence did not follow same trend. Here interestingly, the genotypes with high shoot length with high number of reproductive branches clustered together. On the other hand, genotypes with root diameter, number of lateral root, total biomass of root, number of vegetative branches were remained together. It was observed that inter group distances were always higher than those of intra group distances. The highest intra clusteric distance was found in cluster VIII and lowest was in cluster I. On the other hand, highest inter cluster distance was measured in between cluster V and cluster VI iIndicated maximum genetic diversity between those two clusters. From the cluster mean values, the cluster-IV had the highest mean value for shoot length and number of reproductive branch. On the other hand, the lowest mean value of number of vegetative branch was found among the genotypes in cluster I. These indicate the presence of drought tolerant genotypes in cluster IV and drought stress tolerance genotypes in the cluster VII. The result of PCA revealed that all the

characters did not contribute equally to the total diversity, in vector-I the important characters responsible for genetic divergence in the major axis of differentiation were shoot length, root diameter, total biomass of root, shoot root length ratio and in vector II root length, shoot root length ratio and number of lateral root played significant role. For effective selection in the pot screening of 50 upland cotton genotypes for their tolerance of drought stress, selection score was computed for all the 50 genotypes on the basis of fitted discriminate functions analysis. Based on relative selection index (RSI) and drought response index (DRI) Ra-16 and BC-442 could be selected as tolerant genotype to drought at early flowering stage.

Through physiological experiments at early flowering stage, fifty cotton genotypes were studied to know the genotypic variation for physiological characters related to drought tolerance and their inter relationship. Significant genotypic variation for physiological characters viz. soil moisture content, relative water content, water saturation deficit, water retension capacity, water uptake capacity, total chlorophyll content, nitrogen concentration, membrane stability index, proline content and pollen viability were observed. Among all genotypes G14 was the highest ranked genotype for pollen viability followed by water retension capacity and water uptake capacity and it was followed by G27, G35, G49, G43, G42, G45, G48 and G50. On the other hand, genotype G19 and G5 had the minimum pollen viability. SR-16 was the highest ranked genotype for proline content. BC-394 was also higher ranked genotype for proline content as well as for water saturation deficit and relative water content.

Genotype G19 and G5 under T4 drought stress showed the highest reduction percentages on the pollen viability and relative water content and minimum values was found in the genotypes G27, G32 under T3 and G47, G4 under T1 stress, respectively. High phenotypic and genotypic variance was found in membrane stability index. Low magnitude of genotypic and phenotypic variance was observed in total chlorophyll content, nitrogen concentration, water uptake capacity and water retension capacity. High genotypic coefficient of variation was found in water uptake capacity, water saturation deficit and proline content. Heritability values in broad sense were relatively high for all most all characters. High heritability coupled with high genetic advanced in percent of mean was recorded for water saturation deficit, water retention capasity, water uptake capacity, membrane stability index and proline content indicating additive gene action controlling these traits and selection based on

these traits will be rewarding. In the present study, the values of genotypic correlation coefficient were higher than phenotypic correlation coefficient for all the characters, indicating a strong inherent relationship among the characters which indicates the selection for drought tolerance would be effective based on these characters. There remained a significant positive correlation between the pollen viability and total chlorophyll as well as nitrogen content. Path analysis evinced that the important characters that had highest direct and indirect effect on pollen viability. It also showed positive direct effect of chlorophyll and nitrogen content on pollen viability. Relative water content exhibited highest positive direct effect on pollen viability. This was followed by water saturation deficit, nitrogen concentration, water uptake capacity, soil moisture content and proline content. Rest of characters showed negative and negligible direct effect on pollen viability. The path coefficient suggested that relative water content, water saturation deficit and proline content were the major contributors to pollen viability and selection for high relative water content, total chlorophyll, membrane stability index, proline content and pollen viability would give better response for yield and fiber quality improvement in cotton. For effective selection in the pot screening of 50 upland cotton genotypes for their tolerance of drought stress, selection score were computed for all the 50 genotypes on the basis of fitted discriminate functions analysis. Based on RSI and DRI, BC-512, Ra-3, BC-413, CB-14, BC-385 and BC-394 could be selected as drought tolerant genotypes based on physiological study at early flowering stage.

The twenty-five top ranking genotypes based on selection score of morphological and physiological study at early flowering stage, and two lowest ranked genotypes as negative control were selected for further trial of the genotypes for drought tolerance at drought prone area (Barind tract). These genotypes were studied to know the genotypic variation for yield contributing and fibre quality characters related to drought tolerance and their inter relationship. Significant genotypic variation for yield and yield contributing characters viz. plant height, days to first square initiation, days to first flower initiation, days to first boll split, number of vegetative branches, number of fruiting branches, number of bolls per plant, days to first boll bursting, single boll weight, ginning out turn, seed index, lint index and seed cotton yield per hectare were observed. Significant genotypic variation for fibre quality characters viz. uniformity index, short fibre index, fibre strength, micronnaire, elongation, maturity ratio,

moisture content/regain, reflectance degree, yellowness, and fibre length were observed. Among twenty-five selected genotypes from previous two experiments, G43 (BC-433) had the highest rank for seed cotton yield per hectare followed by G29 (JA-13/R), G33 (BC-272) and G48 (BC-510) and genotype G15 and G18 were the minimum seed cotton yield per hectare. On the other hand, genotypes G29 had the long fibre length after harvesting and it was followed by G34, G43, G14, G18, G22, G45 and genotype G10 and G11 were the short fibre length. Genotype G14 under T3 drought stress showed the highest reduction percentages on the fibre length and on G38 under T2 seed cotton yield per hectare and minimum values was in the genotypes in G38 under T2 and G15 under T2 stress, respectively. The lowest days to first boll bursting rank was found in CB-8 followed by Ra-16 and CB-10. The highest rank for Ginning Out Turn (GOT) was found in BC-272 followed by CB-11 and BC-442.

High phenotypic and genotypic variance was found in plant heigth and reflectance degree. Low magnitude of genotypic and phenotypic variance was observed in single boll weigth, lint index, number of vegetative branch and uniformity index, moisture content. High genotypic coefficient of variation was found in number of vegetative branch and micronnaire. Heritability values in broad sense were relatively high for all most all characters. High heritability coupled with high genetic advance at percent of mean was found for the traits, no. of vegetative and fruiting brunches, no. of bolls per plant, seed cotton yield per hectare indicating additing gene action controlling these traits and selection would be effective. The values of genotypic correlation coefficient were higher than phenotypic correlation coefficient for all the characters, indicating a strong inherent relationship among the characters which indicates the selection for drought tolerance would be effective based on these characters. Significant positive correlation with yield was found for the characters plant height, days to first square initiation, days to first boll split, no. of fruiting branch, no. of bolls per plant, single boll weight and seed index. Path analysis evinced that the important characters that had highest direct and indirect effect on seed cotton yield and fiber length. Path analysis revealed positive direct effect of plant height, no. of bolls per plant and single boll weight on yield. The path coefficient suggested that days to firs boll split, number of bolls per plant, single boll weigth, ginning out turn, number of fruiting branch and fibre strength, micronnaire, reflectance degree, yellowness were the major contributors to seed cotton yield and fibre length. Selection for maximum fruiting

branches, number of bolls per plant, single boll weigth, ginning out turn, minimum days to first boll split and bursting and fibre length, strength, uniformity index, micronnaire, reflectance degree and yellowness would give better response for yield and fiber quality improvement in cotton. Based on RSI and DRI values BC-415 is best ranking genoype for yield followed by BC-433 and BC-442, CB-14, CB-8 and BC-394.

Regarding quality traits, genotypes JA-13/R had the longest fibre length, reflectance degree and fibre strength followed by BC-385, BC-433, CB-14, Ra-4, Ra-16 and BC-442. RA-08/9 had the highest micronnaire followed by BC-385 and CB-13. Ra-16 had the highest fibre strength followed by JA-13/R, Ra-3. Uniformity index had significant positive correlation with fibre length both at genotypic and phenotypic level. Path analysis also showed positive direct effect of uniformity index on fibre length. Based on SRI and DRI value, BC-510 is the highest ranking genotype followed by Ra-4, BC-385, BC-433, BC-413 and BC-462. Five genotypes as BC-415, BC-433, BC-442 and CB-14 for highest yield and three genotypes as BC-510, Ra-4, BC-385, BC-433, BC-413 and BC-462 for best quality fibre could be recommended to the farmers' of northern region of Bangladesh.

Considering morphological, physiological, yield and fibre quality characteristics in breeding and other crop improvement programs will give a clear understanding of drougth stress related events and eventually will lead us to develop crop varieties superior in drought stress tolerance by genetic manipulation. Genotype G8 (CB-8), G12 (CB-12), G15 (CB-15) and G35 (BC-394) could be recommended as candidate of drought tolerant cotton genotypes and genotypes G14 (CB-14), G39 (BC-415), G43 (BC-433), G45 (BC-442) could be recommended to the farmers for cultivation in northern region of Bangladesh. For fibre quality, genotype G43 (BC-433), G38 (BC-413) could be recommended for further trial and G18 (Ra-4), G34 (BC-385), G48 (BC-510) could be recommended for cultivation. For earliness of seed cotton harvesting, G46 (BC-462), G15 (CB-15), G18 (Ra-4) and G14 (CB-14) could be recommended for further trial. Based on days to first square initiation, days to first flower initiation, days to first boll split and days to first boll bursting, BC-462 required further trial for earliness under drought prone areas.

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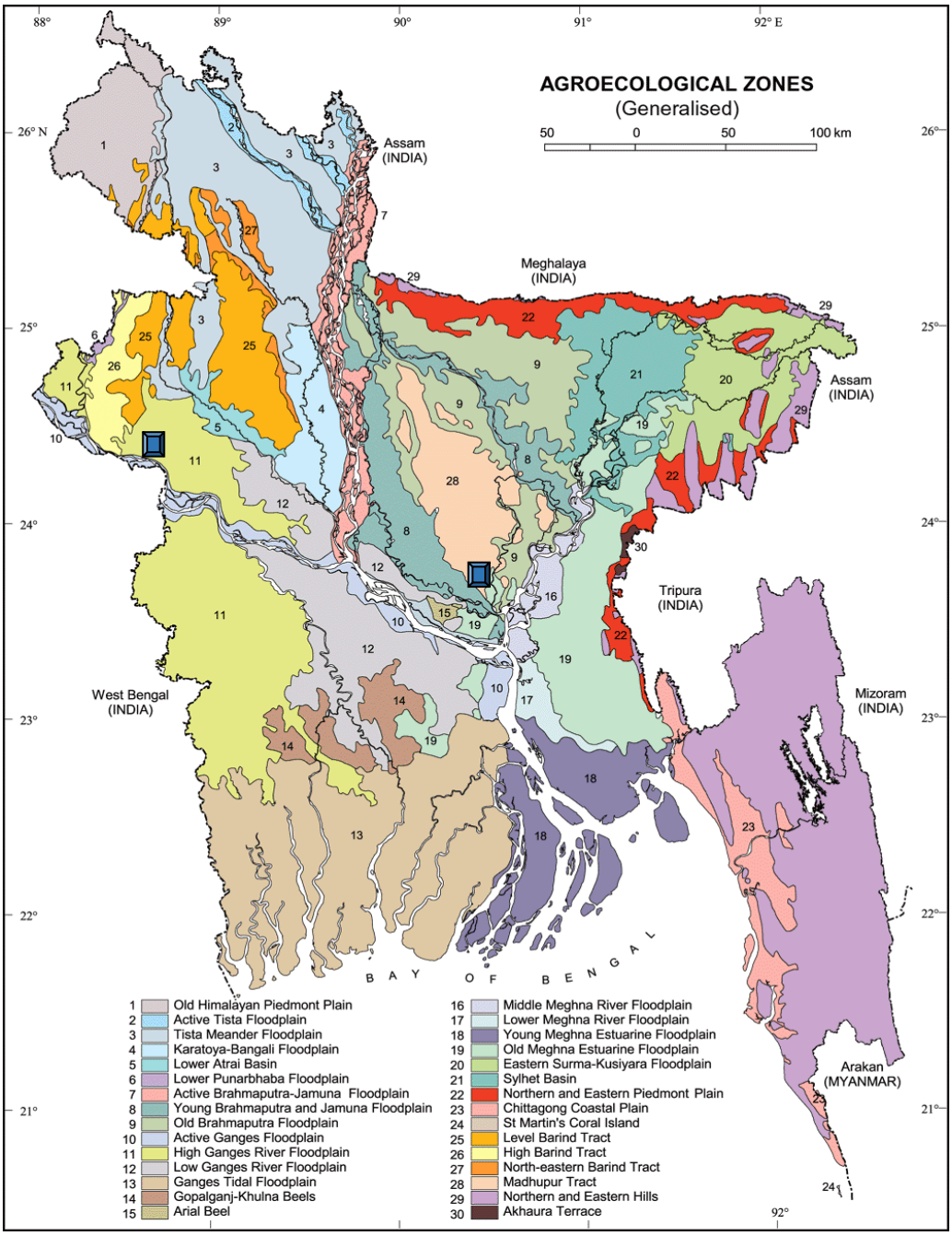
## Appendix I. Map showing the experimental site for experiment 1, 2 and 3



**Appendix II. The mechanical and chemical characteristics of soil of the experimental site (Sher-e-Bangla Agricultural University, Agargaon, Dhaka) as observed prior to experimentation (0 - 15 cm depth)**

**Mechanical composition:**

| Particle size | constitution |
|---|---|
| Sand | 40% |
| Silt | 40% |
| Clay | 20% |
| Texture | Loamy |

**Chemical composition:**

| **Soil characters** | **Value** |
|---|---|
| Organic matter | 1.44 % |
| Potassium | 0.15 meq/100 g soil |
| Calcium | 3.60 meq/100 g soil |
| Magnesium | 1.00 meq/100 g soil |
| Total nitrogen | 0.072 |
| Phosphorus | 22.08 µg/g soil |
| Sulphur | 25.98 µg/g soil |
| Boron | 0.48 µg/g soil |
| Copper | 3.54 µg/g soil |
| Iron | 262.6 µg/g soil |
| Manganese | 164 µg/g soil |
| Zinc | 3.32 µg/g soil |

**Source:** Soil Resources Development Institute (SRDI), Krishi Khamar Sarhak, Dhaka

**Appendix III. The chemical characteristics of soil of the experimental site (Godagari, Rajshahi) as observed prior to experimentation (0 - 15 cm depth)**

**Chemical composition:**

| Soil characters | Value | Nutrition status |
|---|---|---|
| Organic matter | 1.49 % | Low |
| Potassium | 0.93 meq/100 g soil | Optimum/Sufficient |
| Total nitrogen | 0.09 % | Very low |
| Phosphorus | 72.50 µg/g soil | Optimum/Sufficient |
| Sulphur | 11 µg/g soil | Low |
| Boron | 1.46 µg/g soil | Optimum/Sufficient |
| Zinc | 5.19 µg/g soil | Optimum/Sufficient |
| pH | 5.8 | Mild acidic |

Source: Soil Resource Development Institute, Chapai Nawabgonj, Bangladesh

**Appendix IV. Analysis of variance (ANOVA) for eight agromorphogenic traits of fifty genotypes under four drought treatments**

| Sources of variances | df | MS value | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | Root length | Shoot length | Shoot/root | Root diameter | Total biomass of root | No. of lateral roots | No. of vegetative branches | No. of reproductive branches |
| **Genotypes (G)** | 49 | 32.02** | 729** | 5.35** | 3.7** | 6.11** | 145.19** | 1.57** | 10.45** |
| **Treatment (T)** | 3 | 278.42** | 53292** | 175.88** | 464.7** | 306.33** | 298.24** | 9.00** | 135.65** |
| **Interaction (G × T)** | 147 | 28.10** | 635** | 6.13** | 4.7** | 5.49** | 144.88** | 1.03** | 11.34** |
| **Error** | 400 | 0.99 | 16 | 0.18 | 0.4 | 0.21 | 3.42 | 0.42 | 0.60 |

** Significant at 1% level,
* Significant at 5% level.
NS Non-significant.
df = Degree of freedom.

**Appendix V. Analysis of variance (ANOVA) for ten physiological traits of fifty genotypes under four drought treatments**

| Sources of variances | df | MS value | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Soil moisture content | Relative water content | Water saturation deficit | Water retention capacity | Water uptake capacity | Total chlorophyll | Nitrogen content | Membrane stability index | Pollen viability | Proline content |
| **Genotypes (G)** | 49 | 26.1** | 315.9** | 315.9** | 5.05** | 0.28** | 0.13** | 0.09** | 480.8** | 55.1 | 138.3 |
| **Treatment (T)** | 3 | 9992.8** | 7120.9** | 7120.9** | 84.89** | 1.65** | 5.21** | 3.84** | 7311.5** | 9692.7 | 6333.3 |
| **Interaction (G × T)** | 147 | 11.94** | 193.2** | 193.2** | 2.69** | 0.22** | 0.13** | 0.09** | 65.6** | 18.71 | 56.9 |
| **Error** | 400 | 0.27 | 11.3 | 11.3 | 0.09 | 0.02 | 0.01 | 0.006 | 0.25 | 0.26 | 0.54 |

** Significant at 1% level,
*Significant at 5% level.
NS Non-significant.
df = Degree of freedom.

**Appendix VI. Analysis of variance (ANOVA) for 13 morphological traits of twenty-five genotypes under four drought treatments**

| Sources of variations | Df | MS value | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Plant height | Days to 1st square initiation | Days to 1st flower initiation | Days to f1st boll split | No. of vegetative branches | No. of fruiting branches | No. bolls/plant | Days to 1st boll bursting | Single boll weight | Ginning out turn | Seed index | Lint index | Seed cotton yield/h |
| Genotypes | 24 | 785.7** | 42.5** | 39.1** | 31.8** | 3.4** | 22.4** | 304.5** | 343.9** | 1.5** | 48.7** | 7.1** | 3.1** | 7.2** |
| Treatment | 3 | 1843.2** | 327.9** | 293.2** | 260.4** | 4.2** | 25.6** | 555.7** | 1321.3** | 1.0** | 61.7** | 4.7** | 2.7** | 6.1** |
| G*T | 72 | 183.2** | 13.7** | 13.6** | 12.9** | $0.2^{NS}$ | 3.6** | 49.4** | 129.2** | 0.9** | 15.2** | 4.2** | 2.6** | 1.3** |
| Error | 200 | 4.1 | 3.2 | 3.1 | 3.3 | 0.2 | 0.5 | 2.4 | 2.5 | 0.002 | 0.9 | 0.04 | 0.06 | 0.04 |

** Significant at 1% level,
*Significant at 5% level.
NS Non-significant.
df = Degree of freedom.

**Appendix VII. Analysis of variance (ANOVA) for 10 fiber quality traits of fifty genotypes under four drought treatments**

| Sources of variations | df | MS value | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Uniformity index | Short fibre index | Fibre strength | Mironnaire | Elongation | Maturity ratio | moisture | Reflectance degree | yellowness | Fibre length |
| Genotypes | 24 | 4.76** | 2.17** | 7.44** | 1.40** | 0.12** | 0.0007** | 0.89** | 67.30** | 14.01** | 9.35** |
| Treatment | 3 | 6.42** | 3.93** | 11.31** | 0.13** | 3.27** | 0.017** | 0.22** | 131.52** | 59.84** | 25.18** |
| G*T | 72 | 2.86** | 1.34** | 2.27** | 0.53** | 0.02** | 0.0002** | 0.48** | $0.62^{NS}$ | 7.66** | 5.15** |
| Error | 200 | 0.14 | 0.06 | 0.33 | 0.01 | 0.001 | 0.00005 | 0.02 | 1.17 | 0.13 | 0.13 |

** Significant at 1% level,
*Significant at 5% level.
NS Non-significant.
df = Degree of freedom.