

**IDENTIFYING DROUGHT TOLERANT COTTON (*Gossypium
hirsutum* L.) GENOTYPES BY PHYSIOLOGICAL AND
MOLECULAR APPROACHES**

Thesis submitted to the
University of Agricultural Sciences, Dharwad
in partial fulfillment of the requirements for the
Degree of

DOCTOR OF PHILOSOPHY

in

CROP PHYSIOLOGY

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JULY, 2013

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INTRODUCTION

Water deficit is the major abiotic factor limiting plant growth and crop productivity around the world (Kramer, 1983). Approximately one third of the cultivated area of the world suffers from chronically inadequate supplies of water. In all agricultural regions, yields of rain-fed crops are periodically reduced by drought (Kramer, 1983) and these constraints may increase due to changing world climatic trends (Le Houerou, 1996). Advances in irrigation technology have helped reduce the gap between potential and actual yield, but irrigation costs and limited water supplies constrain irrigation throughout the world.

Limited water with low quality hinders the physiological processes and growth of all plants since water is the primary component of actively growing plants ranging from 70-90 per cent of plant fresh mass (Gardner and Gardner, 1984). Due to its predominant role in plant nutrient transport, chemical and enzymatic reactions, cell expansion and transpiration, water stresses result in anatomical and morphological alterations as well as changes in physiological and biochemical processes affecting functions of the plants (Hsiao, 1973; Kramer, 1980).

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 enough to inhibit normal plant function (Hsiao *et al.*, 1973). The effects of water stress on plants depend on the severity and duration of the stress, the growth stage at which plants are subjected to stress and the genotype of the plant (Kramer, 1983).

The effect of water stress is more complex affecting at cellular level to whole plant processes. Cellular water content largely controls stomatal aperture and stomatal conductance directly affects CO₂ diffusion and photosynthetic carbon fixation, which in turn affects metabolic processes such as photosynthesis and respiration.

Cotton, the white gold is also known as king of fibre crops and is the main raw material for textile industry. It is the most important global cash crop and controls economy of many nations. Cotton provides gainful employment to several million people in cultivation, trade, processing, manufacturing and marketing, sustaining directly or indirectly about 10 per cent of the population of India. Taxonomically cotton is described under the order Malvales, family Malvaceae, series hibisceae and the genus *Gossypium*. According to Percy and Wendel (1990) the genus *Gossypium* includes 49 species. Four of these are cultivated viz., *G. hirsutum* and *G. barbadense* which are tetraploid ($2n=2x=52$) and are commonly known as new world cotton, whereas *G. arboreum* and *G. herbaceum* which are diploid ($2n=2x=26$) and are commonly known as old world or Asiatic cotton.

Cotton is an important raw material that meets 65 per cent requirement of the Indian textile industry. The Indian textile industry occupies a significant place in the countries economy with over 1500 mills, four million handlooms, 1.7 million power looms and thousands of garments, hosiery and processing units, providing employment directly or indirectly to about 35 million people (Ashok *et al.*, 2004). Indian government is now looking for many ways to improve the production of cotton to boost the economy. In addition, it is also looking forward to boost production of edible cotton seed oil to help and feed India's growing population of one billion people (James, 2004). In India, cotton is grown under diverse agro-climatic conditions and contributes nearly 65 per cent of total raw material needs of textile industry (Anon., 2011a).

Cotton is cultivated in 70 countries with a total coverage of 32.3 million ha (Anon., 2011b). India ranks first in area covering about 33 per cent of the world cotton area. However, in production it ranks second next to China. In India, cotton was cultivated in an area of 11.17 m ha with a production of 35.61 million bales of seed cotton during 2012-13. Average productivity of cotton in India is 496 kg lint per ha (Anon., 2013). Maharashtra, Gujarat, Andhra Pradesh, Madhya Pradesh, Punjab, Haryana, Karnataka, Rajasthan and Tamil Nadu are the important cotton growing states in India.

Gossypium hirsutum L and *Gossypium barbadense* L. are the two predominant elite cotton species, usually grown during the summer in arid and semiarid regions exposed to drought, which adversely affects both yield and lint quality (Pettigrew, 2004). Water stress commonly attributed to situations where the water loss exceeds sufficient absorption intensity causing a decrease in plant water content, turgor reduction and consequently, a decrease in cellular expansion and alterations of various essential physiological and biochemical processes that can affect growth and productivity (Pimentel, 2004). Water deficiency causes various responses on plant metabolism, where osmotic

adjustment is an extremely important physiological mechanism for preparing these plants to tolerate hydric stress, where diverse organic compounds accumulate as osmoregulators.

The quantity and quality of the fiber produced in cotton plant crops are directly related to water availability during the different phenological phases of development. Genetically equivalent cotton plant populations, when subjected to water deficits, show reductions in yield up to 50 per cent compared to those that have been irrigated, especially when the stress is imposed during the period between flowering and fructification (Araújo *et al.*, 2003). Thus, the tolerance of cotton genotypes to water deficits has been the target of various studies on both the physiological and the molecular levels (Levi *et al.*, 2009; Lubbers *et al.*, 2007 and Saranga *et al.*, 2004).

There is a considerable diversity observed in cotton for its growth and physiological parameters *viz.*, plant height, number of leaves, specific leaf area, plant dry weight, leaf dry weight and productivity traits *viz.*, number of bolls per plant, boll diameter, staple length, fiber strength, ginning out percentage in relation to varying moisture deficit periods. And also described that juvenile growth stages were more susceptible to water deficit (Mahmood *et al.*, 2006).

Drought, induced by soil and/or atmospheric water deficit, poses the most important environmental constraint to plant survival and crop productivity (Boyer, 1982). Developing drought resistant crop plants is vital to meeting increased demand for agricultural products and mitigating the effects of an anticipated environmental shift towards greater aridity (Parry *et al.*, 2005). This solution, however, requires comprehensive understanding of plant adaptive mechanisms and responses to water stress at their underlying physiological and genetic mechanisms (Muhammad *et al.*, 2011).

Drought tolerance is a quantitative trait, controlled by more than one gene and has a complex inheritance. For the success of any crop improvement programme genetic diversity is a pre-requisite. Molecular markers are useful in the field of genetics and plant breeding programmes to identify loci/QTLs linked for abiotic tolerance traits, biotic stress tolerance traits, marker assisted selection and construction of genetic linkage maps. Marker assisted selection is one of the practical utility it also permit plant breeders to correctly map various interacting genes that condition complex agronomic traits. Molecular markers have been used to identify and characterize QTLs associated with several complex traits plant height and maturity, disease resistance, drought tolerance. In recent days, there are many DNA based molecular markers such as RAPD, RFLP, AFLP, SSR, SNP's, *etc.* which can detect genetic polymorphism at the DNA level. Several types of DNA markers *viz.*, RFLPs, RAPDs, microsatellites, AFLPs, SNPs (Wang *et al.*, 1998; Kanazin *et al.*, 2002) and EST-derived SSR markers (Varshney *et al.*, 2005) have been used widely for linkage mapping. Recently several derivatives of already existing markers have been in use (Rafalski and Tingley, 1999). RAPD technique was successfully used for drought tolerance studies in many crops including cotton (Patil, 2005).

Therefore in present day's scanty rainfall situation and increased area of dry land in Indian subcontinent, there is a need of identifying/developing drought tolerant cotton genotypes suitable to dry environments.

By considering all these points, the present investigation entitled "Identifying drought tolerant cotton (*Gossypium hirsutum* L.) genotypes by physiological and molecular approaches" was undertaken with the following objectives:

1. To assess the genetic variability of cotton genotypes for drought tolerance by biophysical and physiological analysis,
2. To assess the selected cotton genotypes for drought tolerance by biophysical, root architecture, yield and fibre properties
3. To study the genetic polymorphism of selected cotton genotypes using suitable molecular markers (SSR/suitable marker).

REVIEW OF LITERATURE

2.1 Importance of water stress in cotton

Cotton (*Gossypium hirsutum* L.) is the world's leading natural fibre crop. Cotton is grown in about 80 countries but only five countries viz., China India, USA, Pakistan and Brazil accounted for about 81 per cent of the global area. Cotton is cultivated in 70 countries with a total coverage of 32.3 million ha (Anon., 2011b). India ranks first in area (about 33 per cent of the world cotton area). However, in production it ranks second next to China. In India, cotton was cultivated in an area of 11.17 m ha with a production of 35.61 million bales of seed cotton during 2012-13. Average productivity of cotton in India is 496 kg lint per ha (Anon., 2013).

Amongst the abiotic stresses reducing crop productivity, shortage of irrigation water is a primary limiting factor in many regions of the world (Sinclair, 2005). As a result of increasing demand and competition from environmental, industrial and domestic sectors, supply of fresh water to agriculture sector is likely to be reduced in the coming years. It has been reported that most of the crops are sensitive to water stress, particularly during flowering to seed development stage (Salter and Goode, 1967).

Drought is one of the major ecological factors limiting crop production and food quality globally, especially in the arid and semi-arid areas of the world. Recent evaluations have shown that approximately 64 per cent of the world's soils are located in desert or in areas with limited water availability and that 57 per cent of the potentially arable area is located in soils for dry-land crops (FAO, 2000).

Regardless of whether it is irrigated or not, cotton is often exposed to drought, which adversely affects both yield and lint quality (Pettigrew, 2004). Drought, induced by soil and/or atmospheric water deficit, poses the most important environmental constraint to plant survival and crop productivity (Boyer, 1982). With increasing aridity and population growth, water is expected to become even scarcer in the near future (Chaves *et al.*, 2003). Developing drought resistant crop plants is vital to meeting increased demand for agricultural products and mitigating the effects of an anticipated environmental shift towards greater aridity (Parry *et al.*, 2005). This solution, however, requires comprehensive understanding of plant adaptive mechanisms and responses to water stress at their underlying physiological and genetic mechanisms (Muhammad *et al.*, 2011).

There is no certainty as to which adaptive mechanisms are related to higher yields and what selection criteria are to be used for screening cotton cultivars tolerant to water stress conditions (Feres, 1987). However, there are evidences that variability among genotypes exists for stress tolerance. Such variability can simply be measured by evaluating several cultivars under both optimum and water deficit conditions (Fisher and Maurer 1978).

Genetically equivalent cotton plant populations, when submitted to water deficits, show reductions in yield of up to 50 per cent if compared to those that have been irrigated, especially when the stress factor is imposed during the period between flowering and fructification (Araújo *et al.*, 2003). This finding shows the impact of this factor on the physiology and the development of the cotton plant. Thus, the tolerance of cotton genotypes to water deficits has been the target of various studies on both the physiological and the molecular levels (Levi *et al.*, 2009; Lubbers *et al.*, 2007; Saranga *et al.*, 2004).

Significant efforts have been made during the last two decades to improve drought tolerance in cotton using empirical selection for seed cotton yield *per se* as well as analytical approaches. There has been controversy of environment for selection and breeding for yield traits. One approach is to screen germplasm by conducting trials in dry seasons to select productive genotypes. However, these high yielding genotypes under water stress could likely to be low yielding under well-watered environment (Rosielle and Hamblin, 1981). Moreover, the too dry selection sites probably do not reflect the conditions of natural drought which more commonly occur as low water availability in a normally reasonably wet period. Other approach suggests testing of germplasm under stress and non-stress conditions and ranking genotypes for drought tolerance / susceptibility on reduction of the yield (Blum, 1988).

Genotypic variation for physiological attributes had been reported in cotton. Inhibition of photosynthesis and stomatal conductance due to water stress is well documented (Pettigrew, 2004; Athar and Ashraf, 2005). Osmotic adjustment had also been proposed as a potential trait conferring

drought tolerance in cotton (Saranga *et al.*, 2001). Cell membrane stability has been widely exploited as an indicator of tolerance against water stress in wheat (Ashraf *et al.*, 1992), rice (Tripathy *et al.*, 2000) and sorghum (Premachandra *et al.*, 1992). Photochemical activity of photosystem II (PS-II) calculated as F_v/F_m and chlorophyll are reliable indicators for the selection of genotypes/cultivars for drought tolerance in canola (Kausar *et al.*, 2006).

Some researchers have been characterized the cotton plant by genetic variability for tolerance to water deficits and high temperatures (Quisenberry *et al.*, 1982). Majority of cultivars from modern cotton plants have been developed under irrigated conditions and have undergone intensive screening to increase the yield and quality of the fibre produced, as well as screening to obtain the most adequate genotypes for mechanized harvesting and processing, which are often improved under irrigated conditions. Thus, the screening process under this condition has unintentionally led to a narrowing of genetic variability for stress factors (Rosenow *et al.*, 1983), increasing demand for the supply of water via irrigation. Currently, water availability for use in agriculture is increasingly limited and expensive; creating apriority impetus for research projects that can identify genotypes with more efficient use of water and/or greater tolerance to water-deficit conditions. Thus, identifying physiological traits that can be assessed by rapid, non-destructive manner and characterize accessions in germplasm banks may assist cotton breeding programs in obtaining cultivars that are more tolerant to water deficits or that may even be used in the initial phases of a breeding program.

2.2 Origin of the cotton (genus *Gossypium*)

Cotton plants belong to Malvaceae family and tribe Gossypieae, that includes eight genera (Fryxell, 1968; Fryxell, 1979). Four of these genera (Lebronnecia, Cephalohibiscus, Gossypiodes and Kokia) are small with restricted geographic distributions (Fryxell, 1968; Fryxell, 1979). Other four (Hampea, Cienfuegosia, Thespesia and *Gossypium*) are moderately bigger gener with broder geographic ranges.

The place of origin of the genus *Gossypium* is also enigmatic, however the primary centres of diversity for the genus are west-central and southern Mexico (18 species), north-east Africa and Arabia (14 species) and Australia (17 species). DNA sequence data from the existing *Gossypium* species suggests that the genus arose about 10-20 million years ago (Wendel and Albert, 1992; Seelanan *et al.*, 1997). The wild species of *Gossypium* occur in arid regions of the tropics and subtropics of Africa, Asia, Australia and America. The only cotton variety with spinnable lint that grows wild is *G. herbaceum* var. *africanum* and this is probably the ancestor of all linted cottons in both the Old and New world (Beasley, 1940). Fryxell (1984) considered that the original dissemination and diversification of the genus *Gossypium* occurred in the Mesozoic period under mesophytic conditions and that adaptation to more xerophytic environments in which *Gossypium* spp. characteristically occurs presently began in the early tertiary period. All the species of *Gossypium* have been categorized into different genomic groups on the basis of cytology of the interspecific hybrids (Edwards and Mirza, 1979).

2.3 Cultivated species of cotton and water stress

Generally cotton refers to four species in the genus *Gossypium* under the family Malvaceae, these include the New World allopolyploids *G. hirsutum* L. and *G. barbadense* L. and Old World diploids *G. herbaceum* L. and *G. arboreum* L that were domesticated independently at different times in human history as a source of textile fiber (Brubaker *et al.*, 1999). Three principle groups of cotton were grown primarily for the seed hair that is made into textiles.

Gossypium hirsutum is the most widely cultivated cotton in the world, is known by various common names, including, among others, Acala or Upland cotton, Moco cotton and Cambodia cotton (Johnson, 1926). It has two centers of genetic diversity, southern Mexico- Guatemala and the Caribbean (Wendel and Albert, 1992). The Mesoamerican (Mexico- Guatemala) center of diversity corresponds with the center of morphological diversity and encompasses the only known wild form of *G. hirsutum*, the coastal Yucatan race *yucatanense* populations (Ulloa *et al.*, 2006). Currently, over 90 per cent of the world's cotton derives from *G. hirsutum*. It is productive over a wide range of environments and has a diverse set of fiber properties for many uses. It requires a growing season from 110 to 140 days. The term "upland" refers to the migration of cotton cultivation inland from coastal areas where often first cultivated.

Since plants anchor in nature, they are exposed to environmental factors and often frequently suffer from one or combination of abiotic stresses such as water (deficit or excess), temperature (low

or high), ions (deficit or excess), light (deficit or excess) that generally causes reduction in growth and development. For instance, 59 per cent and 64 per cent losses in yield corn due to abiotic stresses in temperate and tropical areas respectively (Edmeadcs *et al.*, 2001). Among the various abiotic stress conditions, water deficiency is the most devastating factor and about one third of the worlds arable land suffers from chronically inadequate supplies of water for agriculture (Boyer, 1982). The consistently expanding world population will require more water for domestic, municipal and industrial needs, as well as larger amounts of food and fiber however, diminishing water supplies in many regions across the world. Hence, developing stress resistant crop plants is vital to meet increased demand for food and fiber (Parry *et al.*, 2005). The development of stress resistant crops has been hindered by low heritability of complex traits such as yield by lack of knowledge of physiological parameters that reflect genetic potential for improved productivity under water deficit. Water stress commonly attributed to situations where the water loss exceeds sufficient absorption intensity causing a decrease in plant water content, turgor reduction and consequently, a decrease in cellular expansion and alterations of various essential physiological and biochemical processes that can effect growth and productivity (Pimentel, 2004).

Compbell *et al.* (2012) examined the $G \times E$ interactions and trait correlations present in the 70-yr Pee Dee cotton germplasm enhancement program. They found that there was significant $G \times E$ interactions exist for several agronomic and fibre quality performance traits that are mostly due to changes in magnitude. A negative genotypic correlation was still persist between lint percent/lint yield and fibre length/fibre strength. However, thy concluded that apparently the breeding methods and selection criteria used over 70 year have lessened the negative relationship between agronomic performance and fibre quality over time to some degrees.

In recent years, however, new insights in drought tolerance have been attained through crop physiology and genomic studies which have presented breeders and producers with new knowledge and tools for plant improvement (Tuberosa and Salvi, 2006). Impact of water stress on physiological and biochemical processes in cotton are reviewed below.

2.4 Impact of water stress on specific physiological traits in cotton

2.4.1 Plant height

Plant height plays an important role in determining the morphological frame work relating to plant type and canopy development in cotton. It is one of the important characters of growth and yield of cotton and is influenced by both genetic and environmental factors. Jagvir Singh *et al.* (2003) reported that plant height was less in Bt hybrid especially in MECH-184 Bt (90.7 cm) as compared to its non-Bt counterpart (104.7 cm). Kim *et al.* (1987) observed that plant height is positively correlated with the number of fruiting branches, yield, boll weight and lint percentage. Ansari *et al.* (1989) reported that yield per plant is positively correlated with plant height and number of bolls. Basu and Bhat (1987) observed that plant height and number of monopodial branches have no influence on harvest index unlike number of sympodial branches and seed cotton yield. Ansari *et al.* (1989) observed that the yield per plant was correlated with plant height and boll number, but not with the number of monopodial branches.

Marani *et al.* (1985) found that water stress had a strong effect on vegetative growth. Rate of increase in plant height and leaf area declined when dry leaf water potential was lower than -1.4 MPa and they were ceased to almost zero at 2.0 to -2.5 MPa. Gao and Jei (1989) reported that changes in leaf production is associated with changes in plant height. Chen *et al.* (1991) reported that plant height and sympodial branches per plant were significantly correlated with each other and negatively correlated with first pick in cotton harvest.

Patterson (1988) reported that stress reduced plant height, leaf number, leaf area, total DM, stomatal conductance, transpiration, NAR and leaf area duration in all species, in comparison with well watered controls. Water stress decreased partitioning of plant biomass into leaves and increased partitioning into roots.

Patil (2011) studied the effect of water stress on performance of the cotton genotypes, the study revealed that, water stress reduced plant height, number of leaves, leaf area, total dry matter, stomatal conductance, transpiration, NAR and leaf area duration in all the genotypes under water stressed condition compared with well watered control.

2.4.2 Number of leaves per plant

If moisture stress occurs during vegetative stage causes less leaf growth and leaf area (Boyer, 1973; Pace *et al.*, 1999) leading to smaller leaves and increasing leaf senescence and abscission (Marani *et al.*, 1985). This leads to less interception of light, less plant height and lower shoot to root ratio (Pace *et al.*, 1999). Therefore, decrease in total dry matter produced by plant. A linear decrease in stem elongation was observed as leaf water potential (LWP) was declined (Grimes and Yamada, 1982). However; no further growth was noted when LWP was as low as -2.5 MPa.

The expansion of leaves declines parallel to the decreasing water supply during a drying cycle (Radin and Mauney, 1986), while stomatal closure occurs after some threshold water deficit (Boyer, 1973; McMichael and Hesketh, 1977).

Bhatt (1987) reported that higher seed cotton yield was associated with maximum leaf number and leaf area per plant. Boll retention depends on leaf number and leaf area. Water stress reduced the leaf number, leaf area, total dry matter in comparison with irrigated condition. Water stress decreased the portioning of biomass into leaves and increased the portioning to roots. Shao *et al.* (1994) suggested that leaf number could be used as an indicator of growth stage for applying management practice.

Reddy *et al.* (1996) reported that biomass accumulation and growth rates were temperature sensitive and closely related to leaf growth. Zhang *et al.* (1999) reported that binomial curves represented the relationship between the number of expanded leaves and was higher with early sowing (on 25th May) than with late sowing (on 8th April).

2.4.3 Number of days to 50 per cent squaring

Sharma and Govila (1981) reported that higher yield in early maturing varieties are recorded as they are less damaged by bollworm. Further, they found that seed cotton yield was negatively correlated with number of days to square formation, number of days to flowering and stability of genotypes. Villarreal (1991) reported that in earliness trait early genotypes may be described as short with few nodes to first sympodial branch, early squaring, flowering and boll opening. The earliness attributes were, however, associated with reduced levels of lint recovery, fibre length and fibre strength.

Assadian (1987) reported that the number of squares was not affected by irrigation rate during flowering except with irrigation at -2.0 MPa. The number of bolls was reduced by deficit irrigation during both growth stages. Lint, seed and seed cotton yields were increased by good irrigation during flowering. Lint yield was negatively correlated with average seasonal crop water stress index.

2.4.4 Days to 50 per cent flowering

Pettiglew (2002) indicated that moisture deficit created by the dry land treatment consistently affected reproductive part development at all stages. Flowering was primarily affected late in the growing season. The plants in the irrigated plots consistently produced significantly higher number of blooms per unit ground area than did plants in dry land plots. Payton *et al.* (2004) reported that when water was withheld from flowering for 7 days, many of the bolls that were at elongation phase abscised and those that did not abscise were found to have drastically reduced size.

Ungar *et al.* (1989) reported that flowering decline from 74 per cent at L1 to 16 per cent at L4. The zero load treatment achieved the highest flowering percentage (66%) and number of fruiting positions per sympodium. the lowest flowering percentage (42%) resulted from severe and relatively late water stress. Palomo and Godoy (1994) reported that in two cultivars, Laguna 89 and Deltapine 80 had the same flowering period (77 days) but Laguna 89 had higher flowering rate, flower number and boll production.

Shaha and Dasgupta (1974) stated that seed cotton yield can be predicted from the date of the number of freshly opened flowers per day during the first few days after the start of flowering. Jambunathan (1968) stated that maturity was not significantly affected by flowering date. The early formed flowers matured into bolls in a less number of days than the later ones as these were prone to shedding.

Rabey (1982) found that yield reduction was more with stress during the early vegetative stage and lowest with stress during boll development, stress during flowering reduced the yield by 50

per cent. Singh *et al.* (1992) reported that cotton cultivars when subjected to water stress at 30, 60 and 90 DAS (Seedling, flowering and boll development stage) showed greatest reduction in biomass and seed cotton yield when water stress was imposed at 60 DAS. Lopez *et al.* (1995) reported that genotypes showing high flowering and fruiting capacity supported by a high photosynthetic rate at late in the season were the most productive under terminal drought conditions.

2.4.5 Number of days to maturity

Radin *et al.* (1989) reported that heavy fruiting, mild water stress associated with long irrigation cycles triggers deterioration of the root system that is very slow to be reversed. High frequently drip irrigation, by preventing cyclical stress, apparently minimized this deterioration during fruit filling.

Palomo and Godoy (1994) compared two cultivars and observed that boll set of Laguna was one week earlier than in Deltapine 80 boll maturation period was also 3-5 days shorter.

Reduction in maturity period under delayed sowing of the cotton crop was reported by Boquet and Walker (1980). Butter *et al.* (2007) reported that significantly less number of days was taken for physiological maturity by MRC-6307 (143 days) as compared to all other Bt cotton hybrids. Patil (1993) suggested that days to 50 per cent flowering and boll opening were the reliable method of finding out earliness in cotton, while time of appearance of fruiting nodes on first sympodial branch and mean dates of maturity were the next best method in its reliability.

2.4.6 Total dry matter production

Mosande *et al.* (1981) revealed that the seed cotton yield was positively correlated with the total dry matter per plant. Singh and Bhardwaj (1983a) opined that improvement in seed cotton yield could be achieved with varieties having high total dry matter, low shedding of squares and bolls and early setting of bolls at lower nodes positions. Halevy (1976) reported that the dry matter distribution was slow till flowering and first boll opening. Constable and Gleeson (1977) recorded maximum dry matter accumulation at LAI of about 3.0 and showed that early and highest boll growth rate was sometimes associated with the lowest LAI.

Jogev and Rymon (1988) reported that water stress decreased total dry matter production while radiation stress mainly reduced harvest index. Radiation on and near flower buds and bolls reduced abscission and increased cotton fiber weight and quality. Further it was concluded that a compromise was needed between radiation being efficiently utilized by young and active leaves while still being allowed to reach areas where buds and bolls developed. Patil (2011) reported significant decrease in total dry matter content in genotypes grown under well watered condition both in field as well as in rain out shelter compared to rainfed condition.

Kaore and Bathkal (1982) reported considerable reduction in growth and seed cotton yield with an increase in total number of soil moisture deficit weeks during the growing season. Shallow soils had higher number of stress weeks than deep soils. Reduction in dry matter was more in shallow soils. Reduction in dry matter, number of bolls and yield were almost in proportion to increase in the number of soil moisture stress weeks.

2.4.7 Relative growth rate (RGR)

Coy (1976) reported that RGR was more closely associated with vegetative growth than with lint, seed cotton yield and earliness in cotton. It observed that the RGR increased during first seven weeks of the season and then declined steadily thereafter.

Channaveeraiah (1983) assessed the performance of cotton (*G. hirsutum* L.) genotypes under rainfed condition and found that high yielding cotton genotypes (cv. Sharada) had moderate value of RGR (0.71 g/g/day). In a study with seven elite cotton (*G. hirsutum* L.) genotypes it was found that RGR showed positive correlation with LA and SLA. Upland cotton varieties and their hybrids observed 5.9 per cent greater RGR in hybrids over their parents during seedling stages

2.4.8 Net assimilation rate (NAR)

Bunce (1978) showed the importance of leaf area expansion and NAR towards dry matter production during soil water stress, in cotton and soybean. Further, the duration of stress also determined the dry matter production. Guinn *et al.* (1978) reported that per cent boll set and boll abscission were decreased with increase in number of irrigations. Loss of yield due to lower flower production was almost four times to that of an increased boll abscission in water stressed plants.

Patterson (1988) Water stress reduced plant height, leaf number, leaf area, total DM, stomatal conductance, transpiration, NAR and leaf area duration in all species, in comparison with well watered controls. Water stress decreased partitioning of plant biomass into leaves and increased partitioning into roots.

2.4.9 Leaf area index (LAI)

Landiver *et al.* (1983b) reported that maximum assimilation rate was obtained from the LAI greater than 3.0. Late maturing cultivars achieved LAI of 3.0 at earlier and maintained it for longer period than the early maturing ones. Further Puech-Swanzes *et al.* (1989) observed that the net canopy photosynthetic rate per unit ground area increased up to a LAI 3.5-4.0 in all the three cotton (*G. hirsutum* L.) genotypes studied. Landiver *et al.* (1983a) observed that the leaves of cotton (*G. hirsutum* L.) genotypes which were photosynthetically active for a period upto 70 days resulted in higher LA. The crop that intercepted higher incoming solar radiation had produced higher lint yield.

Genik *et al.* (1996) reported that water stress was imposed by replenishing a fraction of the water lost to evapotranspiration, beginning about 78 days after emergence. HQ 95 and GP 74 did not differ in LAI or in the rate of leaf area development before water stress was imposed. The rate of LAI decline and average LAI were similar between cultivars when water stress was imposed. HQ 95 produced more bolls and had higher yield under both well watered and water stressed conditions than GP 74 in each of the 2 year.

Tian Xiaoli *et al.* (2003) reported that leaf area per plant, leaf area index (LAI) of CCRI 30 were less than those of CCRI 16 (recurrent parent). Channaveeraiah (1983) observed that for selection of high yielding genotypes under rainfed condition, the cultivars having moderate duration, moderate LAI, LAD (80-85 days) and with medium size of monopodial branches are more preferred. Nagabhushana (1984) reported that high yield in rainfed cotton (*G. hirsutum* L.) cv. Sharada was associated with lower LAI, LAD and specific leaf weight (SLW) during the active process of yield formation.

Patil (2011) reported that, water stress reduced the plant height, SLW, LAI, SPAD, number of leaves, leaf area, total dry matter, RGR in genotypes under water stressed condition compared with well watered control.

2.4.10 Root traits

The cotton plant consists of a primary or tap root from which secondary and tertiary roots are emerges out (Spieth, 1933). The cotton root, whether primary or branch root, has a single layer of epidermal cells surrounding the root cortex. The endodermis, another single cell layer, surrounds the stele which contains the xylem and phloem vascular elements and a cell layer called the pericycle. The xylem elements are arranged in either a tetrarch (four distinct xylem bundles, the most common) or in a pentarch or greater bundle arrangement. This difference in arrangement is apparently genetically controlled and may result in significant genetic diversity in root branching.

As drought effects on cotton shoot growth and development, it also reduces root growth, root elongation, root length density and root distribution (Malik *et al.*, 1979). However, root elongation during drought may help plants get water from deeper soil profile and reduce the water lost by drainage when precipitation allows recovery after the drought (Ludlow and Muchow, 1990). Pace *et al.* (1999) found -that under drought stress there was increase in tap root length without any change in cotton tap root dry weight. Detrimental effects of drought on root growth were only observed after recovery where tap root as well as secondary roots dry weight was decreased (McMichael and Quisenberry, 1991; Pace *et al.*, 1999). Thus increased taproot length at the expense of thickening, in response to drought may be a common response in cotton. This response may permit cotton plants to survive under drought stress by accessing the water from deeper layer of soil profile than the soil horizons tapped during periods of adequate water supply.

The crop canopy temperature, which is often cooler than the prevailing air temperature, is a function of leaf transpiration rate but, canopy transpiration at a given leaf area is dependent on the roots to meet the evaporative demand. Thus, a significant correlation between deep root biomass and a cooler crop canopy is often observed (Blum, 1998; Garrity and Toole, 1995). In cotton, higher stomatal conductance allows greater yield for genotypes experiencing above optimal temperature under irrigated condition (Ulloa *et al.*, 2000).

Biomass accumulation in plants is always a function of total water transpired (Passioura, 1986). Thus, water mining from deeper soil profiles as associated with a deep root system is a very

important trait to sustain the water requirement for transpiration (Liu *et al.*, 2005). In their simulation experiments, Sinclair and Muchow (2001) demonstrated an increase in biomass and grain yield when root growth was better. These studies emphasise the importance of breeding to improve root systems to achieve better productivity. In cotton a good association was found between yield and root area index (Zhang *et al.*, 2006). Basal *et al.* (2005) reported a considerable genetic variation for root length, lateral root number, root fresh weight, lateral root dry weight and total root dry weight of 68 cultivated cotton race stocks during late vegetative stage.

Malik *et al.* (1979) found that as soil moisture decreased, root emergence was earlier and the initial rate of root elongation was faster. Namken *et al.* (1979) reported that the stem diameter of the cotton plant could be used as an indicator of water stress and showed that stem contraction was directly related to the degree of leaf water stress.

Khalid Iqbal *et al.* (2011) evaluated the responses of 80 genotypes/lines of *Gossypium hirsutum* at seedling stage under water stressed and non-stressed conditions in glasshouse. Plant growth was measured as longest root and shoot after 45 days. They found genotypic differences for indices of drought tolerance were statistically significant. Based upon the differences and similarities, four tolerant *i.e.*, 149F, B-557, DPL-26, BOU 1724-3 and 4 susceptible namely FH-1000, NF-801-2, CIM-446 and H-499 genotypes/lines were crossed in all possible combinations. The responses of 64 families were examined under water stress and non-stressed conditions at seedling stage. They found the genotypes B-557 and DPL-26 had the greatest tolerance index and appeared to be tolerant to water stress. In addition, BOU- 1724, 149F, VH-57, CIM-497 and BH-124 also seem to be the tolerant genotypes/lines. The genotypes/lines NF 801-2, FH- 1000, Dixi-king and H499-3 were found susceptible.

2.4.11 Stomatal conductance

Conductance is the ease with which gases can exchange between two places. Exchange occurs through stomatal pores in the epidermis. Plants control water loss by varying stomatal apertures. Under severe water stress, stomatal conductance has been shown to decrease substantially in cotton varieties. Many studies have also emphasized the association of drought resistance with the rate of excised leaf water loss, stomatal closure and abscisic acid (ABA) accumulation in the plants under water deficient conditions. The first effect of the stress may well be a loss of turgor that affects the rate of cell expansion and ultimate cell size. The result is a decrease of growth rate, stem elongation, leaf expansion and stomatal aperture.

Stomatal regulation, or adjustments that facilitate CO₂ diffusion while minimizing water loss, might enhance the drought tolerance of plants subjected to temporal or sustained water deficits this is a mechanism to adjust the water loss (Fambrini *et al.*, 1995; Fernandez and McCree, 1991; Franca *et al.*, 2000). Stomatal closure is typically detected before changes in leaf water potential during drought conditions. Stomatal conductance is very important in understanding the consequences of water stress since it is affected by several internal and external parameters such as the leaf water status, plant genotype, vapor pressure deficit, *etc.* Stomatal conductance affects several other physiological attributes which are also indicators of drought tolerance/resistance such as photosynthetic rate, vapor pressure deficit levels, *etc.*

Reduced stomatal conductance increases water use efficiency but decreases absolute rate of net photosynthesis. Stomatal closure causes a greater decrease in transpiration than photosynthesis due to additional resistance to diffusion of CO₂ relative to water vapor in the leaf (Sinclair *et al.*, 1975). Reduced stomatal conductance also causes a loss in photosynthetic N use efficiency (instantaneous use of N for photosynthetic C gain). Other studies have shown that stomata close in response to lower conductance of the soil to leaf pathway via soil drying to prevent xylem cavitation (Sparks and Black, 1999; Tyree *et al.*, 1994). Many studies have also emphasized the association of drought resistance with the rate of excised leaf water loss, stomatal closure and abscisic acid (ABA) accumulation in the plants under water deficient conditions.

Muhammad *et al.* (2011) evaluated 31 cotton genotypes/cultivars under two irrigation regimes *i.e.*, seven irrigations (Control) and two irrigations (Stress), using split plot design with four replications. Chlorophyll content, plant height, transpiration rate, stomatal conductance were significantly decreased in the cotton under water stressed condition compared to well watered condition.

2.4.12 Photosynthesis

Photosynthesis plays a major role in determining crop productivity in all species and is directly affected by water stress. Photosynthetic rates of the cotton leaves decrease as the relative water content and leaf water potential decrease (Lawlor and Cornic, 2002). The effects of water stress on photosynthesis are complex and may include a combination of stomatal closure (Sharkey and Seeman, 1990) and the inhibition of metabolic processes, including ribulose biphosphate synthesis and adenosine triphosphate synthesis.

Inadequate water availability is probably the main factor limiting photosynthesis and, consequently, plant growth and yield worldwide. At the whole plant level, the effect of stress is usually perceived as a decrease in photosynthesis and growth. This in turn is usually due to lowered diffusion rate of CO₂ in the leaves as a consequence of stomatal closure. The rate of photosynthesis is also affected by a combination of stomatal and nonstomatal limitations under conditions of moisture stress (Ephrath, 1990; Faver, 1996; Genty, 1987; Marani, 1985; Turner *et al.*, 1986). There is also a hypothesis that the non stomatal limitation could in actuality be the effect of patchy stomatal closure which causes inhomogeneous photosynthetic activity.

Photosynthetic rate could be a selection criterion for plant breeders, especially if lines with superior photosynthesis could be identified and coupled with those lines with suitable partitioning of photosynthates between reproductive and vegetative parts (Pettigrew *et al.*, 1993). The single leaf photosynthetic rate increased as the sink to source ratios increased (Quisenberry *et al.*, 1994). In cotton, several reports have indicated that water stress causes a reduction in photosynthesis rates due to a combination of stomatal and non-stomatal limitations (Leidi *et al.*, 1999).

Reduced photosynthetic C assimilation (and therefore reduced crop dry matter accumulation) is a principal effect of soil water deficit in cotton and other crops (Said and Hugh, 2005). Measurements based on the photosynthetic response to chloroplast CO₂ often confirm that the photosynthetic capacity is preserved but photosynthesis is limited by diffusive resistances in drought and salt-stressed leaves (Flexas and Merdano, 2004). Therefore reduced photosynthates in moisture deficit episodes result in reduced yields.

Some other studies have expressed yield potential with regard to an environment-related physiological trait, such as canopy temperature or water potential (Cattivelli *et al.*, 2002). Physiological traits correlated with the responses to and/or modified by drought span a wide range of vital processes. It is also significant to note that the timing and intensity of the stress may vary with time and place and plants that have been adapted to a specific type of stress may under-perform when that particular condition is different or absent (Cattivelli *et al.*, 2008). Stomatal conductance and maximal rates of photosynthesis were positively correlated with increased yields of advanced cultivars, while leaf temperatures were negatively correlated (Fischer *et al.*, 1998).

Genotypic variation for physiological attributes had been reported in cotton. Inhibition of photosynthesis and stomatal conductance due to water stress is well documented (Pettigrew, 2004; Athar and Ashraf, 2005). Although photosynthesis rates have been used to distinguish water deficit tolerant and sensitive genotypes in various species, including cotton (Levi *et al.*, 2009; Saranga *et al.*, 2004), procedures for measuring gas exchanges in photosynthetic analysis are laborious and impractical for use in a breeding program.

A few physiological parameters such as stomatal conductance, transpiration and respiration rates have been studied in relation to yield potential, some in different water regimes (Barbour *et al.*, 2000; Bray, 1993; Radin *et al.*, 1994; Ulloa *et al.*, 2000) but no single parameter has been identified as the sole trait of improving yield (Bray, 1993; Hasegawa *et al.*, 2000). Stomatal conductance response to changes in leaf water status and environment is important in regulating transpiration and photosynthesis, which in turn affect yield. There is substantial variation in the stomatal responses of higher plant species to atmospheric humidity, soil water availability and other environmental factors. This is important to agriculture, as water availability often limits production and stomatal traits could well be major determinants of water use efficiency. Lu *et al.* (1998) found a positive correlation between yield increases and increases in stomatal conductance of cotton.

Leaf photosynthesis is reduced when plants are grown under moisture deficit conditions because of a combination of stomatal and non-stomatal limitations (McMichael and Hesketh, 1982; Turner *et al.*, 1986). The effect of water deficit conditions on photosynthetic rates in cotton revealed that photosynthesis rates were reduced after only 5 days of soil drying and there was uniform displacement of the diurnal cycle of leaf water potential and corresponding decreases in transpiration

and CO₂ uptake. The studies on photosynthesis-light response curves indicated that an average two-fold reduction in photosynthesis rates occurred for solar radiation greater than 250 W/m² (Parsons *et al.*, 1979). Ennahli and Earl (2005) reported that water stress reduced leaf net photosynthetic carbon assimilation through both stomatal effects, which reduced the leaf internal CO₂ concentration (C_i) and non stomatal effects, which resulted in reduced at a given level of C_i. Physiological restrictions to photosynthesis in leaves of water stressed cotton (*Gossypium hirsutum* L.) plants revealed that combined leaf gas exchange/chlorophyll fluorescence measurements differentiate the treatments more effectively than gas exchange measurements alone. Leidi *et al.* (1993) studied cotton genotypes under drought and observed that net photosynthesis, transpiration rate and stomatal conductance decreased as water stress increased.

The threshold leaf water potential required for initiating stomatal closure became progressively more negative when cotton plants were subjected to a series of water stress cycles. The shift in the threshold water potential required for induction of stomatal closure was reported to be dependent on the number of previous stress cycles and leaf age (Ackerson, 1980). Studies on the adaptive response of cotton to various irrigation levels in terms of transpiration, stomatal role in transpiration, leaf temperature and CO₂ assimilation rate showed that stomatal area decreased significantly in response to water stress in cotton. It was concluded that cotton adapted to water stress by maintaining higher transpiration rate (Isoda and Inamullah, 2005).

2.4.13 Transpiration

The transpiration rates are higher in plants not suffering from moisture stress. Guard cells are turgid and stomata are open allowing diffusion of water vapor. Drought induced reduction in the rate of transpiration was noted in cotton by Leidi *et al.* (1993). Various studies have been conducted to show the effect of water deficit on transpiration. At low values of plant available water, the portion of the soil water holding capacity that can be absorbed by a plant, a reduction in transpiration is generally accompanied by reduction in stomatal conductance as well as decrease in photosynthesis rate, dry matter accumulation and economic yield (Turner, 1974). Farquhar and Richards (1984) concluded that water use efficiency in drought conditions showed a negative correlation with transpiration. Abscissic acid contents of shoots increased during the period of drought as water potential decreased. The increase in levels of ABA was closely associated with a decrease in rate of transpiration (Roberts and Dumbroff, 1986).

Wier *et al.* (1988) reported that high temperature increased transpiration and N loss significantly and ethylene evolution only slightly. Water stress significantly reduces transpiration.

2.4.14 Leaf temperature

Marani *et al.* (1985) suggested the changing in canopy temperature under stress is due to closure of stomata, reducing leaf activity, leaf area and increase leaf senescence.

Leaf temperature is affected to a great extent by leaf movement. The diheliotropic movement of cotton leaves increases leaf temperature. The evaporation heat of transpiration helps to keep the leaf temperature under check. Leaf temperature is affected by both the water status of the plant (Meyer and Walker, 1981) and the water status of the soil (Wang *et al.*, 1998). Studies in the past have shown that leaf temperature measurements and canopy temperature measurements are good indicators of plant tolerance/resistance to drought and that it is feasible to use such data to quantify plant water deficit (Ko and Piccinni, 2009).

Water stress increased proline accumulation. Decreasing water contents resulted in progressive increase in free proline in cotton cultivars as well as difference in the proline level between the cultivars (De Ronde *et al.*, 2000; Kar *et al.*, 2005). Increases in leaf proline contents were revealed to be positively associated with biomass recovery and negatively with reduction in yield. Tolerant genotypes accumulated more proline under water stress than the susceptible ones resulting in high biomass recovery and stability of seed cotton yield (Singh and Sahay, 1990).

Chloroplast volume under water stress decreased more rapidly in susceptible cultivars in which spongy parenchyma predominated in the leaf tissues, whereas in resistant cultivars plastid parenchyma was better developed which was thought to have an adaptive significance related to the hereditary xeromorphy of the resistant cultivars (Samiev and Marfina, 1985). Studies on cotton by Chun-yan *et al.* (2007) revealed that transpiration ability decreased while the leaf temperature increased under water stress condition. The studies further showed that although relative leaf water

content decreases with increases in water stress, but cotton has the ability in maintaining water in leaves. The stomatal density increases with an increase in water stress.

Field experiments were conducted by Bajwa and Vories (2006) with three different irrigation levels to study cotton response to water stress and the analysis of responses of canopy reflectance and temperature to water stress. The results revealed that canopy temperature was a good indicator of water stress, but it was directly related to vapor pressure deficits and both canopy and leaf temperature showed great potential to indicate water stress. Transient or prolonged drought conditions reduce the amount of water available for plant growth. In response to drought stress, physiological and biochemical changes may result in alteration of protein synthesis or degradation.

2.4.15 Water potential

In most plants, leaf water potential is reduced under drought conditions, but cotton has the ability to osmotically adjust and maintain a higher leaf turgor potential (Turner *et al.*, 1986). The bound water in living tissue is more likely to play a major role in tolerance to abiotic stresses in cotton by maintaining the structural integrity and/or cell wall extensibility of the leaves, whilst an increased amount of free water might be able to enhance solute accumulation, leading to better osmotic adjustment and tolerance to water stress and maintenance of the volumes of sub-cellular compartments for expansive leaf growth (Singh *et al.*, 2006).

Oliveira *et al.* (1979) noticed that adopted cotton plants had relatively more number of cells and stomata per unit of leaf area. Ackerson (1980) reported that adopted plants exhibited lower daily minimum leaf water potential and maintained turgor at lower leaf water potential than non-adopted cotton plants. Because of this turgor maintenance photosynthesis continued in adopted plants at lower leaf water potential.

Ackerson and Humbert (1981) observed that plants adopted to stress conditions maintained higher photosynthesis under lower leaf water potential than did control plants. Stress pre-conditioning modified cellular ultra-structure. Chloroplasts of fully turgid adopted leaves contained extremely large starch granules, seemed swollen and had less breakdown of thylakoid membrane structures. Quisenberry *et al.* (1985) used the leaf turgidity as an index to select for cotton drought tolerance. Under drought conditions the genotype T-15 had higher leaf water potential than did T-169. At 70-80 days after planting, T-15 had higher leaf conductance, photosynthetic rates and higher seed cotton yield than did T-169.

Gorham *et al.* (1998) reported that leaf chlorophyll contents increased under water deficit. Stomatal conductance was reduced by water deficit with consequent reductions in gas exchange parameters (net photosynthesis, transpiration and water use efficiency) and an increase in leaf temperature of cotton.

Nepomuceno *et al.* (1998) reported that in response to water deficits, Siokra L-23 (drought tolerant) and T-152 (moderately drought tolerant) cotton varieties showed 25 and 20 per cent reduction in leaf temperature respectively compared with un-stressed controls. At the same time temperature of these two genotypes did not differ significantly. Conversely, the decrease in the size of CS-50 (moderately susceptible) and stoneville 506 (susceptible) was not significant while their temperature decreased significantly. By maintaining a higher size during stress, the tolerant genotypes were able to maintain photosynthesis, stomata conductance and relative water content near to un-stressed control levels.

Patil (2011) reported that, water stress reduced water potential, water use efficiency, rate of photosynthesis in all the genotypes under water stressed condition compared to well watered control.

2.4.16 Specific leaf weight

The specific leaf weight indicates the thickness of the leaf and is known to have a positive correlation with photosynthetic rate (Rasulov and Asrarov, 1983).

Bharadwaj and Singh (1988) revealed a new ideotype in upland cotton (*G. hirsutum* L.) based on foliage characters such as small and thick leaves (higher SLW) with more boll number and higher boll weight. Further, the cotton (*G. hirsutum* L.) genotypes with higher leaf conductance and total chlorophyll content, especially chlorophyll 'b'. Small leaves with higher SLW had more leaf water potential values owing to lower relative water content. Further, they concluded that varieties with small thick leaves are usually drought resistant (Singh *et al.*, 1990). Lopez *et al.* (1995) showed that the specific leaf weight increased with increasing water stress under field conditions but the transpiration,

photosynthesis and leaf water potential were decreased. It has indicated that higher SLW had influence on the higher yield Landiver *et al.* (1983).

2.4.17 Proline content

Reactive oxygen species are produced during drought stress (Noctor and Foyer, 1998). There is an increase in superoxide production in drought stressed wheat and sunflower. Hydrogen peroxide also increased about three fold during drought stress (Chawdhury and Choudhuri, 1985). Many compatible solutes (*i.e.* proline, trehalose and glycine betaine) not only aid in osmotic adjustment but also protect against water deficit stress by buffering redox reactions by scavenging free radicals, preventing protein degradation, maintain membrane stability and aiding in signal transduction. Similarly, decreased osmotic potential was recorded under moisture stress (Levi *et al.*, 2009).

McMichael and Elmore (1977) reported that when pre-dawn leaf water potentials reached -1.5 MPa, leaf proline concentration increased sharply from trace to 86 m moles and to 160 m moles per g dry weight at -3.5 MPa. During the stress period, proline increased slightly from 4.6 to 6.6 g per 100 g leaf protein. Owing to the late rise in leaf proline concentration following water stress, it was concluded that proline was not a good indicator after the onset of water stress.

McMichael *et al.* (1979) observed a significant accumulation of free proline in stressed leaves (-3.5 MPa leaf water potential). There were significant genotypic differences in proline accumulation under comparable stress levels. Janagoudar *et al.* (1983) identified genotypic differences in cotton with respect to free proline accumulation drought tolerant varieties had the highest rate of proline accumulation during stress and maintained the higher level of proline even after the alleviation of stress.

Singh *et al.* (1992) recorded significantly higher leaf proline content in cotton cv. SRT- 1 when subjected to water stress at different levels. Zholkevich *et al.* (1997) revealed increase in proline content when cotton *G. hirsutum* cv. INEBR-85 and OK-Oltin were subjected to soil moisture stress. Leaves of cotton plants, *G. hirsutum* L. stressed by water deficit were analysed for level of 17 free amino acids using reversed phase higher performance liquid chromatography. Water deficit stress resulted in increased free proline levels (49.9 fold) that were correlated with diffusive resistance (second per cm) (Showler, 2002).

2.4.18 Chlorophyll content

Chlorophyll is green pigments present in chloroplasts of all green plant cells and tissues. These are essentially photosynthetic pigments capable of absorbing light energy and responsible for synthesis of carbohydrates. Chlorophyll content of the plant tissues represents the photosynthetic capacity of the plant.

Li *et al.* (1986) reported that chlorophyll content, soluble sugar content along with nitrate reductase (NR) activity and photosynthetic rate was higher in *G. barbadense*, which was followed by *G. arboreum*, *G. herbaceum* and significantly less in *G. hirsutum*. Higher chlorophyll content and photosynthetic activity recorded higher in high yielding cotton genotypes as compared to low yielding cotton genotypes (Krasichkova *et al.*, 1989).

Gadallah (1995) observed that decreasing soil matrix water potential reduced the total chlorophyll content, chlorophyll 'a' and chlorophyll 'b' in cotton. Singh and Arora (1997) found that generally chlorophyll 'b' content was observed to be more in cotton genotypes thus lowering chlorophyll a:b ratio. It may be attributed that chlorophyll 'b' has an affinity to the clear weather conditions during the growing period (Singh *et al.*, 1988).

Under different intensities of water stress, the chlorophyll content in cotton leaves in all cultivars decreased with increased water stress (Yi *et al.*, 2000).

Kar *et al.* (2001) reported that moisture deficit affected the total chlorophyll as well as proline content in cotton leaves irrespective of varieties.

2.4.19 Water use efficiency

The effect of water stress on cotton varieties studied at early reproductive stage (40 days after planting) revealed that leaf water potential (LWP) decreased under water stress. Stressed plants had higher stomatal resistance than control. More bolls were retained by un- stressed than stressed plants and this retention decreased with increase in water stress (Biswas *et al.*, 1986).

Brar (1989) reported total seed cotton yield and water use efficiency were decreased at -2.00 MPa at preflowering soil water potential at irrigation but water use efficiency increased at -1.5 MPa without affecting yield. Both yield and water use efficiency was decreased due to delayed irrigation during flowering. Patil (2011) also reported that, there was significant decrease in water use efficiency under water stressed condition compared to well watered condition in cotton genotypes.

2.4.20 Seed cotton yield

Worldwide sustainability and advancement of cotton yield are the major challenges for meeting impending threats of increasing world population in the face of diminution of arable land, depletion of water resources and environmental stresses. However, drought is one of the major yield-limiting stresses (Boyer, 1982; Ullah *et al.*, 2008).

Redulovich (1985) found that cessation of vegetative growth and the production of new squares has more reproductive dry matter under water stress than the irrigated plants early in the season. Turner (1986) reported that water deficits reduced leaf and fruiting site development, the number of floral buds and bolls retained and final yield, but the proportion of flowers that set into bolls was not affected except where substantial soil water deficits developed during early flowering. Patterson (1989) reported that water stress reduced the plant height, leaf number, leaf area, total dry weight, stomatal conductance, transpiration, net assimilation rate and leaf area duration in comparison with well watered control. Water stress decreased the partitioning into roots.

Devendra Singh *et al.* (1992) reported that cotton cultivar SRT1 was grown under rain out shelter and subjected to water stress at 30, 60 and 90 DAS (seedling, flowering and boll development stages, respectively). The greatest reductions in biomass and seed cotton yield per plant were found when water stress was imposed at 60 DAS. Kaore and Bathkal (1982) reported that reduction in dry matter, number of picked bolls and yield was almost in proportion to increase in the number of soil moisture stress during the growing season. Mc Michael and Hesketh (1982) observed that seed cotton yield was decreased from 431 g per plot in the irrigated control to 185 g/plot with no irrigation. Yield components were also reduced due to water stress.

Hoogar and Gidnavar (1997) noticed that DCH-105 recorded significantly higher leaf index and dry matter accumulation in reproductive parts and subsequently higher number of harvested boll per plant, yield per plant (g) and seed cotton yield per ha as compared to DCH- 32. Wier *et al.* (1998) reported in Mississippi that Bt cotton out yielded over the non-Bt cotton varieties by 103, 52 and 94 kg per ha in 1975, 1996 and 1997 respectively.

The heritability of yield, particularly under drought, is low which hampers the progress in improving yield and its stability under water stress conditions. Moreover, large genotype x environment interaction for yield under drought is another major reason for slow progress. Indirect selection for the secondary physiological traits exhibiting high correlation with yield may complement empirical breeding efforts to improve drought tolerance in crop plants (Cooper, 1999).

Karademir *et al.* (2011) evaluated the effect of water stress and non-stress conditions on cotton yield and fiber quality properties. By evaluating twelve cotton genotypes for yield and fiber quality properties they found significant differences among genotypes and water treatments for seed cotton yield, fiber yield, ginning percentage and all fiber quality properties except fiber uniformity.

Patil (2011) studied the effect of water stress on performance of the cotton genotypes, the study revealed that, there was significantly more yield was recorded in irrigated condition cotton genotypes both in field as well as in ROS compared to rain fed condition.

Kar *et al.* (2001) reported that yield and yield attributes decreased significantly in all the varieties in response to water stress imposed at flowering stage. The flowering stage in cotton was found to be critical to moisture stress. Significant genotypic difference for physiological attributes and seed cotton yield existed both under irrigated and water stress conditions. However, the genotypic differences were non-significant for dry stem weight and boll weight (Ahuja and Tuteja, 2001). Further, under water stress conditions, highly drought tolerant and moderately tolerant genotypes had either equal or higher values for seed index, boll number per plant, ginning out turn, mean halo length and plant height in comparison to irrigated conditions.

Vladimir and Cothren (2011) evaluated the effects of 1-Methylcyclopropene on gas exchange, plant growth and yield components of cotton under drought during the reproductive phase in cotton. Their study revealed that drought started to impact gas exchange at a moderate water stress, 5 DAT (days after 1-MCP treatment) (-1.4 MPa). The 1-MCP increased water use efficiency (WUE) in well-

watered plants at 1 DAT. Many of the yield components, plant mapping, and biomass parameters investigated were adversely affected by drought.

2.4.21 Boll weight

The technique of growth and yield analysis has been extensively used for better understanding of the impact of abiotic stresses. Under moisture stress conditions, bolls in an advanced stage of development were the better sinks and required more photosynthates as compared to younger bolls (Udayakumar *et al.*, 1971). Stress during pre and post-flowering periods resulted in stunted growth, less number of fruiting branches and flower nodes and reduction in lint yield (Morani and Levi, 1973).

Kulvir Singh (2007) reported that significantly highest and least boll weight was recorded in hybrid MRC-6304 (4.93 g) and Ankur-651 (3.31 g) respectively.

Mehta and Singh (1988) reported that boll weight is positively correlated with the number of seeds per boll ($r = 0.64$) and ginning out turn ($r = 0.49$). Singh (1988) reported that boll weight has highly significant positive association with lint weight per boll, seed weight per boll, seeds per locule.

2.4.22 Number of bolls per plant

Kadapa (1975) indicated that number of sympodia on the day of flowering is an important component of earliness and higher productivity. Further, Singh (1975) reported that moisture stress had no adverse effect on percentage of boll set. However, moisture stress during the post-flowering period decreased the yield.

Faqir *et al.* (1984) showed that 69.72 per cent of variability in cotton yield was due to variability in number of bolls per plant, which has the greatest positive correlation with yield ($r = 0.835$). Kumar and Choudhary (1986) revealed from correlation studies that seed cotton yield per plant was strongly correlated with boll number and boll weight. Similar results were also observed by Ansari *et al.* (1989) who reported that seed cotton yield was positively correlated with number of bolls per plant and plant height but not with number of monopodial branches.

Patil (2011) reported that, there was significantly more boll numbers per plant and boll weight were recorded well watered irrigated condition cotton genotypes both in field as well as in rain out shelter compared to water stressed rainfed condition.

2.4.23 Cotton fibre quality parameters

A cotton fiber is an elongated cell of the ovular epidermis that is anatomically classified as a trichome. These trichomes are epithelial cells of the cotton seed coat that can elongate up to 25-30 mm in certain species and are amongst the longest cells in the plant kingdom. There are 10,000 to 20,000 fibers per seed. There is nothing in nature that resembles the long, strong and fine fibers of modern cotton cultivars. The fibers unique structure is ideally suited for textile production as each fiber is a hollow tube a few centimeters in length that has a twisted curvature. The thickness of the secondary wall is 3-6 μm around the circumference of the approximately 20 μm diameter fiber. Thousands of these fibers together form a white, fluffy cotton boll that is harvested when mature and all the fibers from a single boll are developmental identical. The mature fiber has two clearly defined cell walls, primary and secondary cell wall. Cotton is one of the purest forms of crystalline cellulose. It is a polysaccharide polymer composed of 100-15,000 glucose molecules. Its crystalline and porous structure makes a fiber versatile, takes up dye, very absorbent and withstands repeated washing. Its most important characteristic is its "feel" which has yet to be replicated in synthetic polymers. It is 100 per cent biodegradable and doesn't require petroleum products for manufacturing, as do synthetic fibers (Ruan, 2005).

It is known that the quantity and quality of the fibre produced in cotton plant crops are directly related to water availability during the different phenological phases of development.

Drought stress leads to boll abscission if occurred during the first 14 days after anthesis (Gerik *et al.*, 1996) but after that period it generally does not cause abscission (McMichael *et al.*, 1973) but it is associated with reduction fiber quality. Fiber elongation was decreased when drought stress occurred during the fiber elongation (Spooner *et al.*, 1958; I-learn, 1976; Guinn and Mauney, 1984 while severe water stress after fiber elongation leads to fiber immaturity and low micronaire). However, minor drought stress can be beneficial due to increase in lint percentage over irrigated cotton (Longenecker and Rrie, 1968) and occasionally increased micronaire (Bilbro, 1962). Krieg

(1983) showed that the timing and severity of water deficit stress has a large effect on yield. Levi *et al.* (2009) showed 31 per cent reduction in seed cotton yield under dry land treatment.

Fibre length was affected by irrigation levels and fertilizer. Micronaire were not significantly influenced by nutrient, moisture and their interaction. Similar observations were also made by Polychronides *et al.* (1998).

Karademir *et al.* (2011) by evaluating twelve cotton genotypes for yield and fiber quality properties they found significant differences among genotypes and water treatments. There was a decrease in seed cotton yield, fiber yield, ginning percentage and all fiber quality properties except fiber uniformity.

Osborne and Banks (2006) reported that water stress event during mid-bloom caused a trend of increased micronaire as compared to the non-stressed plots. However, some researchers revealed that growing cotton under non-irrigated conditions resulted in the production of shorter and weaker fiber with reduced micronaire (Mert, 2005).

Luz *et al.* (1997) reported that water stress reduced cotton yield with greatest effect at the flowering and fruiting stages, however water stress did not affect fibre quality.

2.5 Genotypic variability studies in cotton under water stress

Ihsan ullah *et al.* (2006) evaluated 32 upland cotton (*Gossypium hirsutum* L.) for drought tolerance traits, he found large genotypic variation among genotypes for cotton productivity traits like drought susceptibility index with seed cotton yield, boll number and certain physiological attributes like net assimilation rate, stomatal conductance and transpiration rate.

Genetic variation in yield and water use efficiency has been reported for cotton subjected to water deficits (McMichael and Quisenberry, 1991). Exotic cotton strains were evaluated for plant dry matter accumulation under irrigated and limited water conditions to estimate their water use efficiency under water stress. Fifteen exotic strains and one commercial cultivar were tested under irrigated and water stressed condition. Significant variability was found among the entries for shoot dry matter accumulation, water use efficiency and shoot and root growth. It was suggested that root morphology and root growth potential were important traits in the adaptation of cotton to conditions where limited water availability is a major constraint for plant growth (Quisenberry *et al.*, 1981).

Genotypes exhibited significant difference in plant height, number of leaves, branches and other morphological characters. The studies made earlier also noticed the existence of varietal differences in plant height (Bharadwaj and Simolte, 1988).

The genotypes that maintained higher plant height at the increased moisture stress levels gave better yields compared to other genotypes (Ahuja and Tuteja, 2001 and Ansari *et al.*, 1989).

Response of shoot and root growth of cotton cultivars after a short drought and subsequent recovery period was studied by Pace *et al.* (1999). Studies were conducted under controlled conditions and 36 days after planting, plants under stressed treatment were subjected to 10 days water stress by withholding of water followed by a recovery period of 10 days. Plants under control conditions were irrigated normally. Various parameters were analysed and it was observed that all parameters were less in water stressed plants than in the control. It was observed that tap root length was greater in the stressed plants than in the control and it was concluded that tap root length after drought may be a common response in cotton and may permit cotton plants to survive drought by accessing water from deeper in the soil profile than the levels tapped during periods of adequate water supply.

Effect of moisture deficit stress on the physiology of cotton has been documented. A field study under dryland and irrigated areas with eight cotton genotypes detected genotypic variation for many of the components of photosynthetic process (Pettigrew, 2004a). Ullah *et al.* (2008) assessed genotypic variability for drought tolerance in cotton using physiological attributes with productivity traits under well watered and water stress regimes in field experiment and reported that seed cotton yield was markedly affected under water stress conditions in all cultivars studied. Substantial genotypic variations were found for physiological traits like gas exchange. Burke (2007) identified varietal differences in cotton responses to available soil water both under field and green-house conditions. It was found that varieties differed in their response for the physiological traits both under irrigated and water stress treatments.

Studies on assessing the responses of five hybrid varieties of cotton to moisture stress in the field for their relative tolerance to drought revealed that moisture deficit adversely affected the chlorophyll stability index and nitrate reductase activity. It was also reported that proline accumulation enhanced under water stress. Yield and its attributes decreased conspicuously in all the varieties in response to water stress imposed at flowering stage. Amongst the cotton hybrids, PKV Hy-4 and PKV Hy-2 were found to be relatively more drought tolerant than others on the basis of assessment of their yield performance. The flowering stage in cotton was found to be more critical to moisture stress than vegetative and ripening stages (Kar *et al.*, 2005).

Medium fibre cotton cultivars were evaluated for seed germination under water stress and it was found that there were differences in seed germination between genotypes under different water stress levels (Pereira *et al.*, 1998). Nepomuceno *et al.* (1998) studied tolerant and susceptible cotton genotypes under water deficit conditions and the genotypes were characterized for osmotic adjustment, photosynthetic rates, relative water contents and other physiological parameters. The results revealed that Australian cv. Siokra L23 and wild type T1521 partially tolerated water stress while water deficit sensitive American cv. Stoneville and Australian cv. CS50 showed sensitivity.

Based upon various morphological and physiological parameters like plant height, total leaf area, shoot, root and total plant fresh and dry weights, stomatal resistance, water potential and relative water content, cotton variety Siokra L23 was shown to be the most drought-tolerant variety based on its high stomatal resistance and water potential, it's having the smallest total leaf area and expression of drought-tolerance-related genes. The Greek cotton varieties were ranked from most to least drought tolerant (Voloudakis *et al.*, 2002). In another study, based upon the observations on the physiological parameters, cotton genotypes were tested for variability under water stress at flowering and boll development stage and high level of variability was found in almost all the characters studied (Singh *et al.*, 1996).

Differences in the photosynthetic rates of two cotton varieties *i.e.* Chirpan-603 (*Gossypium hirsutum*) and C-6037 (*Gossypium barbadense*) were examined under severe water stress conditions and differences between them were found to be mainly in lower stomatal limitation, higher carboxylating capacity and relatively higher level of the substrate limitation in C-6037 (Bojinov *et al.*, 2000).

Drought resistance and susceptible cotton genotypes were studied under field conditions. It was observed that chloroplast volume fell more under drought stress in the genotype named Tashkent 6, in which spongy parenchyma predominated in the leaf tissues compared to the other genotype named Tashkent 1, in which the palisade parenchyma was better developed. Data suggested that high development of palisade tissue was thought to have an adaptive significance related to hereditary xeromorphy of the resistant variety (Samiev and Marfina, 1985).

Mahmood (2006) evaluated eight cotton varieties (BH-118, CIM-446, FH-900, FH-901, MNH-93, MNH-552, MNH-554 and NIAB Krishma) for drought tolerance using various growth and productivity traits. These varieties were subjected to two and four water deficit cycles. The varieties showed distinct responses with respect to moisture deficit conditions. Certain growth and productivity traits provided some manifestation of drought resistance in these varieties. The MNH-93 and BH-118 appeared to be more drought tolerant for both growth and yield parameters as compared to other varieties under evaluation. MNH-552, MNH-554, CIM-446, FH-900 and NIAB-Krishma exhibited some potential to withstand drought intensities, although an affirmative relationship for growth and yield attributes cannot be established in these varieties.

Muhammad *et al.* (2011) evaluated 31 cotton genotypes/ cultivars under two irrigation regimes *i.e.*, seven irrigations (Control) and two irrigations (Stress), using split plot design with four replications. The boll numbers, boll weight, yield and chlorophyll content, plant height, transpiration rate, stomatal conductance were significantly decreased in the cotton under water stressed condition compared to well watered condition. There were high inter-varietal differences for all the parameters under control as well as drought stress. Although all the varieties for all parameters were significantly affected by drought stress however, the genotypes CRIS-9, MARVI, CRIS-134, CRIS-126, CRIS-337, CRIS-355 and CRIS-377 showed better performance for all the recorded parameters.

Genetic variability in a number of root parameters in cotton has been shown to occur across a range of environmental conditions. Quisenberry and McMichael (1996) indicated that genetic differences in rooting potential was related to plant productivity and that an increase in potential (primarily increases in root branching and distribution) could result in increases in yield of cotton under conditions of a drying soil profile. Greenhouse studies conducted using 25 cotton genotypes

ranging from exotic accessions to commercial cultivars showed significant variability in the dry weights of root systems of sixty day old plants. To obtain the dry weight the roots were removed intact from soil and subjected to oven dry. The variability was greater in the exotic accessions than in the commercial cultivars (McMichael and Quisenberry, 1993). McMichael *et al.* (1985) showed that the increased root xylem (vascular bundle) arrangements in the taproot of some of the exotic cotton accessions resulted in a significant increase in total vessel cross-sectional area and an increased number of lateral roots. This increase suggested an overall decrease in axial resistance to water flow in the root system which may be associated with characteristics of drought tolerance in plants with the increased xylem vessels. Oosterhuis and Wulfschelger (1987) supported the finding that increased water flux was associated with increased xylem cross sectional area. However, an increased number of vessel elements in the xylem of the primary root did not result in any apparent decrease in axial resistance to water flow. The increased number of lateral roots associated with increased vascular bundles resulting in increased xylem vessels may be important characteristics associated with drought tolerance in plants with the increased xylem vessels which may lead to improved yields.

Longenberger *et al* (2006) developed a design to evaluate a screening method for drought tolerance in cotton seedlings. 21 converted race stocks (CRS) and two cultivars were evaluated for seedling drought tolerance (SDT) on an individual plant basis. Genotypes were evaluated under greenhouse conditions. Seedlings were subjected to three sequential cycles of drought at 15 days after planting (DAP). Drought cycles consisted of withholding water until the moisture content of indicator 'Deltapine 491' (DP 491) plants, had an average volumetric water content of 0.07. Genotypes differed in their percent survival following three consecutive drought cycles. Drought cycles 2 and 3 did not contributed to the separation of genotypes. DP 491 was the most tolerant genotype evaluated. They observed CRS did not differ in drought tolerance with 'Acala 1517-99'. CRS M-9044-0165 was the most stable genotype across the two experiments.

2.6 PEG (polyethylene glycol) water stress studies for drought tolerance in cotton

Cotton (*Gossypium hirsutum* var. *latifolium* L.) is generally tolerant to water stress situation. However it may suffer significance growth and production reductions when exposed to such adverse conditions. Nevertheless, the response to water stress varies among cultivars and with the developmental phase of the plant. During the germination phase, the water absorbed is required for several enzymatic reactions, for solubilisation and transport of metabolites and as a reagent in the hydraulic digestion of proteins, carbohydrates and lipids from the tissue reserve of the seed towards the embryo (Woodstock, 1998; Carvalho and Nakagawa, 2000; Khajeh-Hosseini *et al.*, 2003).

Low moisture levels during germination induce protection mechanisms against drying or even prevent developmental process (Bewley and Oliver, 1992). Severe water stress, however, results in a metabolic imbalance (Blackman *et al.*, 1992) and a reduction of metabolic activities (Vertucci, 1989).

In the year 1979, first time scientists utilized PEG as drought inducer, subsequently this was used to screen drought resistant tobacco cell lines. Articles about using PEG on study of drought-resistant tomato cells, drought resistant sorghum regeneration and anti-PEG stress alfalfa cell lines were reported. Chinese researchers used cotton drought evaluation and identification by repeated drought method (Yu *et al.*, 1999). PEG was used to establish a rapid and effective cotton-drought tolerance evaluation system for selection and breeding of the drought tolerant resources.

One of the most commonly used methods to determine the tolerance of plants to abiotic stresses is the evaluation of the germination capacity of seeds under drought conditions (Larcher, 2000). To simulate water stress conditions in the laboratory, germination studies were conducted with aqueous solutions of PEG and mannitol (Costa *et al.*, 2004; Fanti and Perez, 2004). Laboratory assays simulating water stress circumstances have aided to the identification of cultivars with an elevated level of resistance to such adverse conditions in other crops, such as maize (Tonin *et al.*, 2000) and rice (Pirdashti *et al.*, 2003).

Fernandez and Mariaelena (1998) reported that water stress induced by polyethylene glycol (PEG), leads to decrease in the germination index and the morphological development of organs from young cotton plants and also reported that water absorption, retention and biomass gain were affected by water stress.

Zhang Xue-yan *et al.* (2007) evaluated eight upland cotton cultivars, two sea island cotton and three Asian cotton with varied levels of drought tolerance were studied. Cotton samples at

germination, bud-stage, cotyledon- stage and real-leaf stage were exposed to PEG stress for 12 hours. After 12 hour osmotic treatment, the survival rates were calculated, then by statistical method, curves of the mutative level of drought tolerance were obtained, proving that the 3-6 leaf stage is the key period related to cotton drought tolerance. With different PEG concentrations, the rates which 3-6-leaf seedlings revived were calculated to compare with the revival rate in real drought situation. They found that with 17 per cent PEG treatment, the rate which seedlings revived corresponded with the results in drought-shed. The results suggested that osmotic adjustment of cotton could be used to evaluate simply the drought tolerance of cotton, though the cotton after PEG-treated differed slightly in physiology with cotton after drought-treated. They concluded that this method with osmotic adjustment of PEG is simple, fast and easily operated, could be used to evaluate the drought tolerance of cotton in principle and will establish foundations for study on cotton drought tolerance molecular biology.

Carlos *et al.* (2011) evaluated the physiological quality of cotton cultivar seeds (*Gossypium hirsutum* var. *latifolium* L.) in laboratory by the simulation of water potentials with polyethyleneglycol-6000 (0.0; -0.2; -0.4; -0.6; -0.8 and -1.0 MPa), at 25°C using germitest paper as substrate. The studied variables were: germination percentage, first count of germination, germination velocity index, accelerated aging in water, electrical conductivity, humidity, vigor classification, radicle length and radicle/shoot length ratio. They found the effect of water stress on seed viability and on plantlet vigor was severe at potentials below -0.4 MPa. And the CNPA 187 8H cultivar was the least sensitive to the tested osmotic potentials, both in terms of germination and vigor. The BRS-201 cultivar was mostly affected by the viability and vigor tests under water deficit conditions. Differential viability and vigor between cultivars were observed under the water stress levels.

2.7 Molecular studies/DNA finger printing

2.7.1 DNA markers

DNA markers are simply inherited, phenotypically neutral, polymorphic, abundant and ideal for the analysis of the complex traits. Molecular markers are useful in genetics, plant breeding programmes and construction of genetic linkage maps. Marker assisted selection is one of the practical utility of markers in plant breeding. DNA markers also permit plant breeders to correctly map various interacting genes that condition complex agronomic traits. Molecular markers have been used to identify and characterize QTLs associated with several complex traits in sorghum, including plant height and maturity (Pereira *et al.*, 1994), characters associated with plant domestication (Patterson *et al.*, 1995), disease resistance (Gowda *et al.*, 1995), drought tolerance (Tuinstra *et al.*, 1996, 1997, 1998). Several types of DNA markers have been used widely (Babu *et al.*, 2004) for linkage mapping viz., RFLPs (Botstein *et al.*, 1980), RAPDs (Williams *et al.*, 1990), SSRs or microsatellites (Litt and Luty, 1989), AFLPs (Vos *et al.*, 1995), SNPs in combination with DNA chip technology (Wang *et al.*, 1998; Kanazin *et al.*, 2002) and EST-derived SSR markers (Varshney, *et al.*, 2005). Recently several derivatives of already existing markers have been in use (Rafalski and Tingley, 1999) including genetic elements such as retrovirus as markers (Long *et al.*, 1995).

2.7.2 Random Amplified Polymorphic DNA (RAPD)

Analysis of genotypic difference using molecular markers is important as it is not affected by external factors. In this technique, a single short oligonucleotide sequence is used for cyclic amplification of DNA, which exposes the polymorphism distributed throughout the genome. These amplified fragments were called as random amplified polymorphic DNAs (Williams *et al.*, 1990). This technique has been used in genome mapping and gene tagging in several crop plants (Martin *et al.*, 1991; Paran *et al.*, 1995; Reiter *et al.*, 1992). RAPD markers genetically linked to plant height (*DW2* gene) (Zhang *et al.*, 2000) and fertility restoration (*Rf1* gene) were identified in sorghum using bulked segregant analysis. RAPD markers along with RFLP were used for the identification of QTLs associated with preflowering drought tolerance in sorghum (Tuinstra *et al.*, 1996).

RAPD-PCR is an efficient and reliable tool for genetic analysis in biological system RAPD is the best assay when nucleotide sequence is not known unlike other PCR protocols which utilize two primers of defined sequence; RAPD detects nucleotide polymorphism using only one primer of an arbitrary nucleotide sequence. It has been successfully used for cultivar analysis in a number of plant species (Patil, 2005).

Iqbal *et al.* (1997) analyzed 22 varieties of *Gossypium hirsutum* and one variety of *G. arboreum* by random amplified polymorphic DNA (RAPD) markers. Out of 50 random decamer

primers, 49 primers detected polymorphism in all 23 cotton varieties, while one produced monomorphic amplification profiles. A total of 349 bands were amplified, 89.41 per cent of which were polymorphic. Cluster analysis by UPGMA showed that 17 varieties can be placed in two groups with a similarity ranging from 81.51 to 93.41%. RAPD revealed the genetic difference among the genotypes.

Rahman *et al.* (2002) conducted a study to estimate the genetic divergence among elite cotton cultivars/genotypes by DNA finger printing technology. After screening 27 cotton genotypes by different diagnostic methods such as field evaluation, whitefly-transmission studies, grafting, dot-blot hybridization and multiplex PCR using conserved primers sequences, 20 extremely resistant and moderately resistant cultivars were selected for a random amplified polymorphic DNA analysis. The genetic similarity of the exotic germplasm with the elite cultivars was in the range of 81.4 to 90.6 per cent. Similarly, the genetic relatedness among the elite cultivars was in the range of 81.6 to 94.9 per cent. The average genetic similarity among all genotypes was 89.5 per cent. They demonstrated that only cultivar VH-137 possessed a diverse genetic background.

Linou *et al.* (2002) attempted the identification and the genetic description of 28 upland cotton (*Gossypium hirsutum* L.) cultivars currently cultivated in Greece using the RAPD method. The genetic similarity of the cultivars ranged from 0.614 to 0.922, indicating a relatively narrow genetic base. Cluster analysis by the unweighted pair group method of arithmetic means (UPGMA) showed that 21 of the cultivars could be placed into 3 major groups. Punitha and Raveendran (2004) evaluated 11 coloured cotton *Gossypium hirsutum* genotypes and four white linted genotypes of different origin by random amplified polymorphic DNA (RAPD) analysis. Cluster analysis showed clear-cut separation of the coloured and white linted genotypes and thus formed three clusters.

Rana and Bhat (2005) studied the genetic diversity in 59 cotton cultivars with RAPD markers. They selected 18 RAPD primers that produced a total of 251 amplicons, which generated 97.21 per cent polymorphism. Among 56 cotton cultivars, 36 per cent genetic diversity was observed. Genetically distinct cultivars were identified that could be potentially important source of germplasm for cotton improvement. It was concluded that RAPD markers revealed sufficient genetic diversity and a high level of polymorphism. Khan *et al.* (2000) analysed 31 *Gossypium* species to evaluate genetic diversity by RAPD. A total of 579 bands were observed, with 12.9 bands per primer, of which 99.8 per cent were polymorphic. Six main clusters were observed through cluster analysis. It was observed that RAPD is the more efficient marker for construction of genetic linkage map.

Hussain *et al.* (2006) assessed 21 cotton accessions using 28 RAPD primers. The total number of amplicons detected were 323, while the number of polymorphic amplicons were 191. Thus the level of polymorphism was 59.1 per cent among the 21 accessions. Variability and relationship among eleven cotton genotypes using PCR based markers including RAPD was investigated by Hussein *et al.* (2007). The genetic similarities ranged from 63.8 per cent to 95.9 per cent for RAPD. The dendrograms clustered the 11 genotypes into two main cluster groups. The amplification profile of 11 cotton genotypes produced by 15 selected primers (PCR through RAPD) revealed a total of 112 polymorphic bands out of 177 reproducible products. This corresponds to a polymorphism level of 63.2 per cent. The results confirmed the efficiency of the molecular markers in detecting polymorphism among cotton genotypes, estimation of relatedness and identifying genotypes and species by unique fingerprints.

Patil *et al.* (2007) generated random amplified polymorphic DNA (RAPD) profiles for four cotton genotypes with 19 primers. The primers generated 123 RAPD loci, of which 97 were polymorphic. Average numbers of bands per primer were 6.47. The genetic distances were found to be 9.68 to 53.29 per cent. The genetic distances were used for cluster analysis and the dendrogram so constructed grouped the genotypes into two major clusters.

Multani and Lyon (1995) differentiated very closely related cultivars using cultivar specific RAPD marker. RAPD markers generated by 30 random decamer primers were used to fingerprint 12 released cultivars of cotton and breeding line of *G. hirsutum* and a cultivar of *G. barbadense*. Nine closely related cultivars showed 92.1-98.9 per cent similarity. Cluster analysis of genetic distances estimated between each of the cultivars revealed that phylogenetic relationship in broad agreement with lineage of cultivars. First application of RAPD's to quantify genetic diversity in a broad array of cotton genotypes was made by Tatineni *et al.* (1996). Genetic diversity of 16 near – homozygous elite cotton genotypes derived from interspecific hybridisation was investigated at DNA level using RAPD.

Genetic diversity analysis of 6 Australian species i.e., *G. sturtianum*, *G. nandewarense*, *G. robinsonii*, *G. bickii*, *G. australe* and *G. nelsonii* was made using RAPD. Among these, *G. sturtianum*, *G. nandewarense*, *G. australe* and *G. robinsonii* showed the closest affinity among the 6 species.

Cluster analysis indicated that *G. bickii* and *G. robinsonii* have a relatively distant affinity, whereas a closer affinity exists between *G. robinsonii* and *G. australe*. A chromosome classification was proposed for the 6 species based on the RAPD results, in which *G. sturtianum* and *G. nandewarensis* are 'C' genome, *G. bickii* is 'G' genome and *G. australe*, *G. nelsonii* and *G. robinsonii* are a new genome (Song *et al.*, 1999).

Khan *et al.* (2000) carried out an experiment in *Gossypium* species to evaluate genetic diversity by RAPD, using 45 random decamer primers. OPJ-17 produced the maximum number of fragments while, the minimum number of fragments was produced with primer OPA-08 and 99.8 per cent bands were polymorphic. Cluster analysis showed considerable disagreement among the D-genome (diploid new world species) and C-genome (diploid Australian species) species. Finally they concluded that interspecific genetic relationship of several species is related to their centre of origin. The results also revealed the genetic relationship of the species *G. hirsutum* to standard cultivated *G. barbadense*, *G. herbaceum* and *G. arboreum*. Cultivar Jayadhar did not cluster with any other cultivars and *G. arboreum* cultivars formed three clusters.

Abdel Ghany *et al.* (2003) studied the molecular nature of RAPD DNA fragments in the four *Gossypium barbadense* cultivars. Five RAPD DNA fragments, generated by improved RAPD-PCR technique and representing polymorphic and non-polymorphic bands were analysed at molecular level using DNA sequencing analysis. Non-polymorphic RAPD DNA fragments showed homology to previously characterized plant structural genes. Comparative nucleotide sequence analysis of two co-migrating non-polymorphic fragments revealed that these two DNA sequences are highly similar to each other, indicating the similarity of fragment size is a good predictor to middle and high repetitive DNA sequences.

Pawankumar *et al.* (2003) studied genetic diversity in a set of 30 elite cotton germplasm lines which included 20 genotypes of *G. hirsutum*, 7 of *G. arboreum*, 1 genotype each of *G. herbaceum*, *G. thurberi* and *G. klotzschianum*. For RAPD analysis they used 32 random primers and only 25 showed amplification while rest failed to amplify. A total of 108 bands amplified in 30 genotypes. They reported one primer, oligo 656 which amplified an 1100 bp *G. arboreum* specific band. Cluster analysis showed that, all the *G. hirsutum* genotypes except NPL83 group in one cluster. The *G. arboreum* genotypes grouped in the clusters and two wild species *G. thurberi* and *G. klotzschianum* from independent groups.

Mishra and Nandi (2004) reported that RAPD analysis of DNA of ten short-listed (on the basis of field performance for drought tolerance) clones of tea using 11 primers, revealed 280 PCR products of weight 131 where polymorphic bands.

MATERIAL AND METHODS

The first year (2011-12 *kharif*) research work was carried out under field condition at two locations viz. ARS Dharwad and ARS Annigeri, to assess the genetic variability of cotton genotypes for drought tolerance by biophysical and physiological traits. Simultaneously 600 cotton germplasm lines were also evaluated for their performance for physiological traits at ARS Dharwad.

In second year (2012-13), twelve selected genotypes from field experiments were evaluated in rain out shelter (ROS) to evaluate the drought tolerance by biophysical, root architecture, yield and fibre properties.

In another experiment, genotypes were evaluated for their germination and seedling vigour under different osmotic stress conditions by slanting glass plate technique with different concentrations of Polyethyleneglycol-6000 (PEG). During 2012-13 the selected twelve genotypes were studied for genetic polymorphism using RAPD markers.

The details of the materials used and techniques adopted during the course of investigation are described below.

3.1 Experimental site and soil properties (cf. Table 1.1 and 1.2)

In 2011-12 the field experiment was conducted at two locations (1) Agricultural Research Station, Dharwad Farm, UAS, Dharwad, Karnataka, India and (2) Agricultural Research Station, Annigeri Farm, UAS, Dharwad, Karnataka, India. ARS Dharwad is situated at an altitude of 678 m above mean sea level at latitude 15°26' N and longitude 76°7' East. The soil was well drained fertile medium black soil best suited for cotton cultivation with assured rainfall (Average normal rainfall is 764.6 mm).

The ARS Annigeri is more arid receiving less rainfall (average normal rainfall of 668.13 mm) as compared to ARS Dharwad (average normal rainfall of 764.6 mm).

The physico-chemical properties (established data) of the experimental sites at ARS Dharwad and ARS Annigeri are presented in Table 1.1 and Table 1.2 respectively.

3.2 Climate (cf. Table 2.1, 2.2) (cf. Fig. 1 and Fig. 2)

The meteorological data at ARS, Dharwad (Table 2.1, Fig. 1) showed that average monthly maximum and minimum temperature recorded were 30.3°C and 18.2°C respectively. During 2011, a total of 827.6 mm of rainfall has been received. During June 171.4 mm more rainfall was received which is 34 per cent more and most of sowings were done. During July there was deficit rainfall of 33%. The growth was normal up to August. Again in October there was continuous cloudy weather and more rain fall (than normal) prevailed.

At ARS Annigeri during 2011 rainfall during July, August, September, October and November was 68.1, 185.2, 34.5, 101 mm and rainy days were 8, 11, 4, 9, 0, 0, 0 and 0 days respectively. Cotton crop experienced moisture stress in the month of September, November and onwards. As total rainfall of 34.5 mm in September and there was no rainfall was received during October month onwards was coincided with critical water requirement of cotton (Table 2.2, Fig. 2).

3.3 Experimental details

3.3.1 Plant material (cf. Table 3, Fig. 4)

Thirty *Gossypium hirsutum* L. genotypes were obtained from the Principal Scientist (Cotton), ARS, Dharwad (Karnataka) and Cotton research stations located at different ecological regions of India.

All the 30 genotypes were grown in two locations under rainfed condition in *kharif* season 2011-12 (Table 3).

The 600 cotton germplasm lines were obtained from Dr. I. S. Katageri, Sr. Scientist, ARS, Dharwad farm, Dharwad, India (Appendix 1).

3.3.2 Experimental site

3.3.2.1 ARS, Dharwad: This location receives assured rainfall during crop growth period (Plate 1a).

3.3.2.2 ARS Annigeri: This location receives less rainfall and relatively arid (Plate 1b).

3.3.3 Design and layout (cf. Fig. 3 and Fig. 4)

3.3.3.1 ARS Dharwad (Assured rainfall area):

- (a) Design : RBD
 - Treatments : 30 genotypes
 - Replications : Three
- (b) Design : Augmented design
 - Treatments : 600 germplasm lines

Planting details (cf. Plate 1c)

Date of sowing : 28/06/2011
Spacing : 90 cm × 20 cm
Plot size : 5.4 × 2.7 m

3.3.3.2 ARS Annigeri (Low rainfall area)

Design : RBD
Treatments : 30 genotypes
Replications : Three

Planting details

Date of sowing : 23/06/2011
Spacing : 90 cm × 20 cm
Plot size : 5.4 × 2.7 m

The detailed plan of the layout of the experiments is given in Fig. 3 and Fig. 4.

3.3.3.3 Germplasm lines experimental material and layout details

3.3.3.3.1 Germplasm lines experimental material (cf. Appendix I)

A total of 600 genotypes (Appendix I) of *G.hirsutum* lines used in the study which includes collections (indigenous, exotic collection), released varieties and lines developed from different breeding strategies, which are available with Dr. I. S Katageri Principal Scientist, ARS Dharwad Farm are used in this study. Six checks have been used namely DS-28, ARBH-813, CPF-824, Sahana, Surabi, and MCU-5.

3.3.3.3.2 Design and layout

During germplasm evaluation, to circumvent the difficulties arising from non- replicated experiments, augmented design was used in the study. The basic idea is to include control lines for which enough material is available and repeat them several times in a standard design. Each repetition of the check lines were randomly allotted to each block and the remaining plots are assigned to test entries. Estimation of block effects and plot errors are done only with respect to checks. The estimated block effects are used to adjust the observed values of the test lines and error is used to test the significance of line differences.

3.3.3.3.3 Planting details

Seeds of 600 genotypes are treated with Imidacloprid to protect the crop from the incidence of sucking pests during early growth stage. Seeds are hand dibbled in rows of each 6m length with spacing of 90cm between rows and 20cm between plants within a row. Sowing was done in Augmented Design-II (Extended form of RBD) with 25 blocks to with six checks repeated in each block. Recommended package of practice was followed.

3.3.3.3.4 Data collection and methodology

The methods followed for recording observations (Specific leaf weight, SPAD values and gas exchange parameters) for 600 germplasm lines at 90DAS was similar to the method followed for observations at ARS Dharwad which are mentioned in section 3.5.1, 3.5.3 and 3.5.4. Here, since the

planting materials are laid out in single replications and the observations were recorded in single replication. The observations were made for the following traits, in 600 germplasm lines and six checks DS-28, ARBH-813, CPF-824, Sahana, Surabi, and MCU-5 which are allocated randomly in all the 25 blocks. The ANOVA table was obtained using Windostat version 8.5 software for different traits.

3.3.3.3.5 Screening/grouping methodology of germplasms

Based on the significance difference between the genotypes recorded (which was confirmed with ANOVA (Windostat version 8.5)) for physiological traits *viz.*, SPAD values, specific leaf weight and Gas exchange parameters (rate of photosynthesis, stomatal conductance and rate of transpiration), significant superior genotypes were identified.

Based on the highest to lowest values recorded for individual physiological traits, the germplasm lines were further divided into three groups containing 200 germplasm lines each which were named as best performer's, moderate performer's and least performer's. The best performers group genotypes having highest values of physiological trait, the least performers having least values while, moderate performers have in between these values. These performers's group varies for different physiological traits.

3.4 Cultural practices

After the harvest of the previous crop, the land was brought to fine till. Seeds of each genotype were sown by hand dibbling with spacing of 90 cm × 20 cm under rainfed condition at both locations *viz.* ARS Dharwad and at ARS Annigeri. Recommended dose of fertilizer was applied at the rate of 100:50:50 kg per ha of N:P₂O₅:K₂O. 50 per cent N was applied at the time of seedbed preparation. Plant population was maintained at four plants/m² by hand-thinning 25 days after germination. The plots were inter-cultured twice after sowing and further maintained weed free by hand weeding. The plant protection measures were taken throughout the crop growth period as per recommended schedule. The remaining 50 per cent of the N was given in two split doses at 30 DAS and 45 DAS.

3.5 Observations

Five plants from each treatment/genotype at both locations were selected randomly and tagged for recording various observations on growth and physiological observations.

3.5.1 Specific leaf weight (SLW)

The SLW or the leaf thickness was determined by taking leaf discs (1 cm² diameter) from 4th full opened leaf from the selected plants and oven dried. The results were expressed as mg/cm².

$$\text{SLW} = \text{Leaf dry weight (mg)} / \text{Leaf area (cm}^2\text{)}.$$

3.5.2 Water potential (MPa)

The measurement of water potential was made by pressure chamber method (Scholander *et al.*, 1965). A leafy shoot or single leaf was sealed in a pressure chamber with the cut surface protruding. Pressure was applied to the shoot from a tank of compressed gas unit; xylem sap appeared at the cut surface. The amount of pressure that must be applied to force water out of the leaf cell into the xylem unit it is refilled is equal to the tension originally existing in the xylem sap *i.e.* pure water will be exuded by reversed osmosis. Thus the applied pressure was equal to water potential of the cells.

3.5.3 SPAD chlorophyll meter reading (SCMR)

Leaf nitrogen status is normally manifested with the leaf chlorophyll content. A device developed by, Minolta corporation, Ramsey, NJ measures the light attenuation at 430 nm (the peak wavelength for chlorophyll a and b absorption) and that at 750 nm (near-infrared) with no transmittance. The unit less value measured by the chlorophyll meter (SPAD-502) is termed as SCMR (SPAD Chlorophyll Meter Reading) and is an estimate of chlorophyll content and hence N content. The SPAD meter (Soil Plant Analysis Development) is a simple hand held equipment, which operates with DC power (Volts) and is portable.

SCMR values were recorded at different growth stages in all treatments. The fourth fully expanded leaf from the apex was used for the SCMR determination. Several measurements were made on each leaf and averaged to make an approximate estimate of the whole leaf N status.

Table 1.1: Physical and chemical properties in the soil from experimental field at ARS, Dharwad

Particulars		Value obtained	Procedure employed
Physical properties			
I.	Particle size distribution		
	a. Coarse sand (%)	8.1	International pipette method (Piper, 1966)
	b. Fine sand (%)	9.9	-do-
	c. Silt (%)	18.2	-do-
	d. Clay (%)	63.5	-do-
II.	Field capacity (%)	36.0	Field method
III.	Wilting point (%)	15.3	Sunflower method
IV.	Bulk density (%)	1.34	Core sampler method
Chemical properties			
i.	Total nitrogen (%)	0.064	Modified micro kjeldal method (Jackson, 1967)
ii.	Available phosphorus (%)	0.0014	Olsen's method (Muhr <i>et al.</i> , 1965)
iii.	Available potassium (%)	0.0133	Flame photometer method (Muhr <i>et al.</i> , 1965)
iv.	Organic carbon (%)	0.45	Walkey and Black's wet oxidation method
v.	Soil PH	8.0	PHmeter (2.5:1) (Piper, 1966)
vi.	E.C. (m.mhos/cm)	0.33	E.C. bridge

Table 1.2: Physical and chemical properties of soil in the experimental site at ARS Annigeri

Sl. No.	Parameters	Value obtained	Method employed
I.	Physical properties		
a.	Particle size analysis		International pipette method (Piper, 1966)
	Coarse sand (%)	6.50	
	Fine sand (%)	6.62	
	Silt (%)	22.25	
	Clay (%)	64.63	
	Textural class	Clay	
b.	Bulk density (mg/m ³)	1.27	Core sample method (Dastane, 1967)
II.	Chemical properties		
a.	Available nitrogen (kg/ha)	218	Alkaline permanganate method (Subbiah and Asija, 1956)
b.	Available P ₂ O ₅ (kg/ha)	19	Olsen's method (Jackson, 1973)
c.	Available K ₂ O (kg/ha)	347	Flame photometer (Jackson, 1973)
d.	Organic carbon (g/kg)	4.9	Walkley and Black's wet oxidation method (Jackson, 1973)
e.	Soil pH (1:2.5 soil:water)	7.90	Potentiometry (Piper, 1966)
f.	Electrical conductivity (dS/m)	0.38	Conductivity bridge (Jackson, 1967)

Table 2.1: The rainfall (mm) received and temperature (⁰C) of at ARS, Dharwad (2011-12)

Months	Rainfall (mm)		Deviation		Temperature	
	Normal	2011	(mm)	(%)	Max.	Min.
January	2.1	0.0	-2.10	-100	29.2	12.6
February	2.8	15.2	12.40	442	30.8	14.0
March	7.2	0.0	-7.20	-100	35.2	18.6
April	47.7	109.6	61.91	130	34.9	20.2
May	68.8	43.2	-24.80	-36	34.7	21.3
June	127.7	171.4	43.70	34	27.5	21.3
July	132.0	88.0	-44.0	-33	26.9	20.6
August	104.3	122.4	18.10	17	26.7	20.7
September	114.4	67.0	-47.40	-41	28.1	19.9
October	121.8	204.4	82.60	68	29.9	19.5
November	32.9	6.4	-26.45	-81	29.8	15.8
December	3.8	0.0	-3.83	-100	29.5	13.7
Total	764.6	827.6	63.10	8.24	(Mean) 30.3	(Mean) 18.2

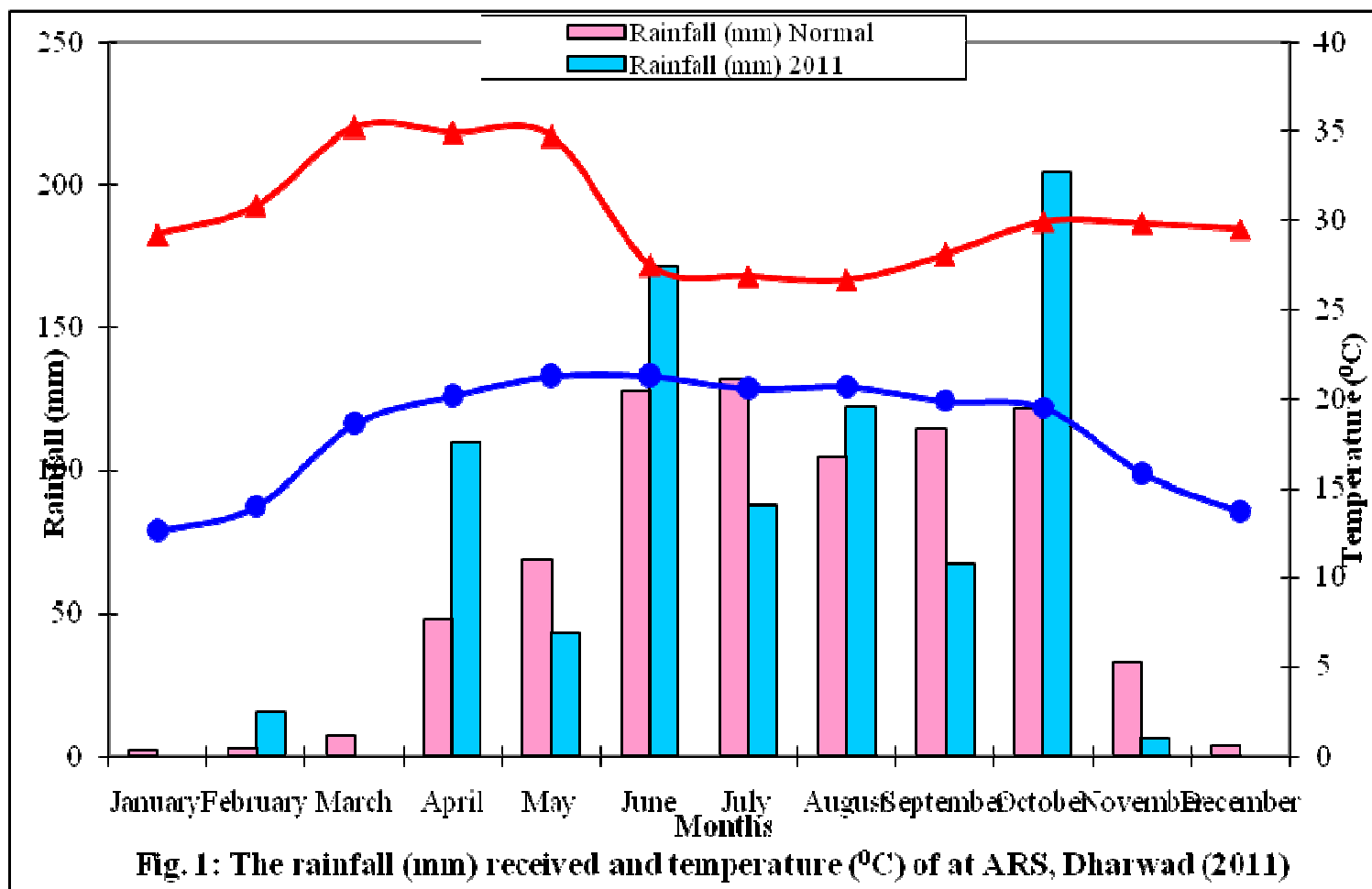


Fig.1: The rainfall (mm) received and temperature (°C) of at ARS, Dharwad (2011-12)

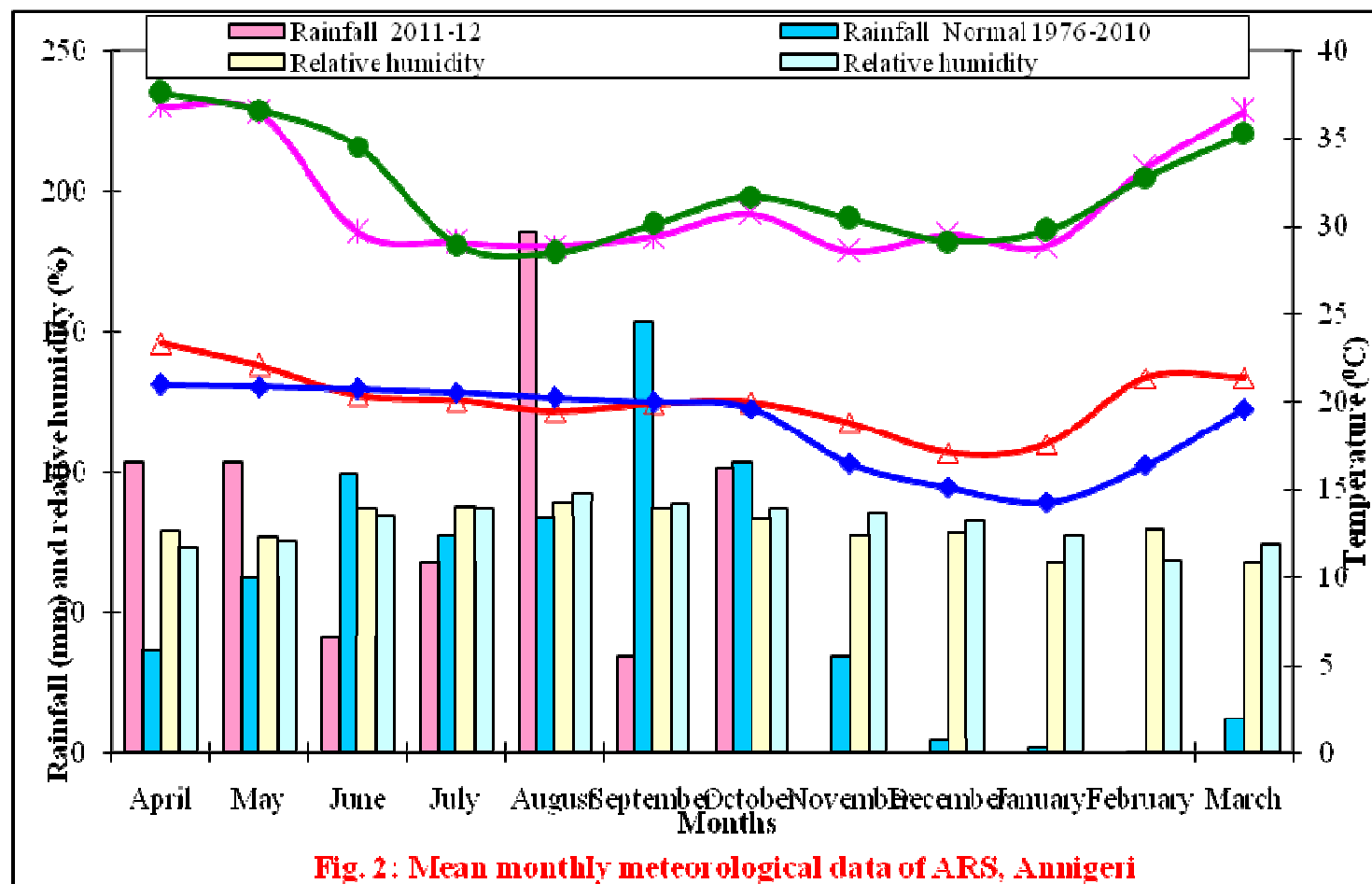


Fig.2: Mean monthly meteorological data of ARS, Annigeri

Table 3: List of *Gossypium hirsutum* genotypes used at both locations (2011-12)

Sl. No.	Genotype	Sl. No.	Genotype
1.	CPD-750	16.	RCR-4
2.	ARB-9701	17.	RAH-30
3.	Sahana	18.	RAH-101
4.	CPD-731	19.	RAS-299-1
5.	CNH-120MB	20.	L-761
6.	ARB-8908	21.	L-763
7.	GIHV-218	22.	GJHV-477
8.	CPD431	23.	F-1861
9.	GSHV-97/13	24.	LH-2076
10.	KH-138	25.	BS-279
11.	CPD-446	26.	CPD-231
12.	GSHV-01/26	27.	F-2228
13.	KH-155	28.	H-1353
14.	GJHV-358	29.	BS-30
15.	KH-134	30.	CPD-168



Plate 1a: General view of the experiment at ARS Dharwad



Plate 1b: General view of the experiment at ARS Annigeri

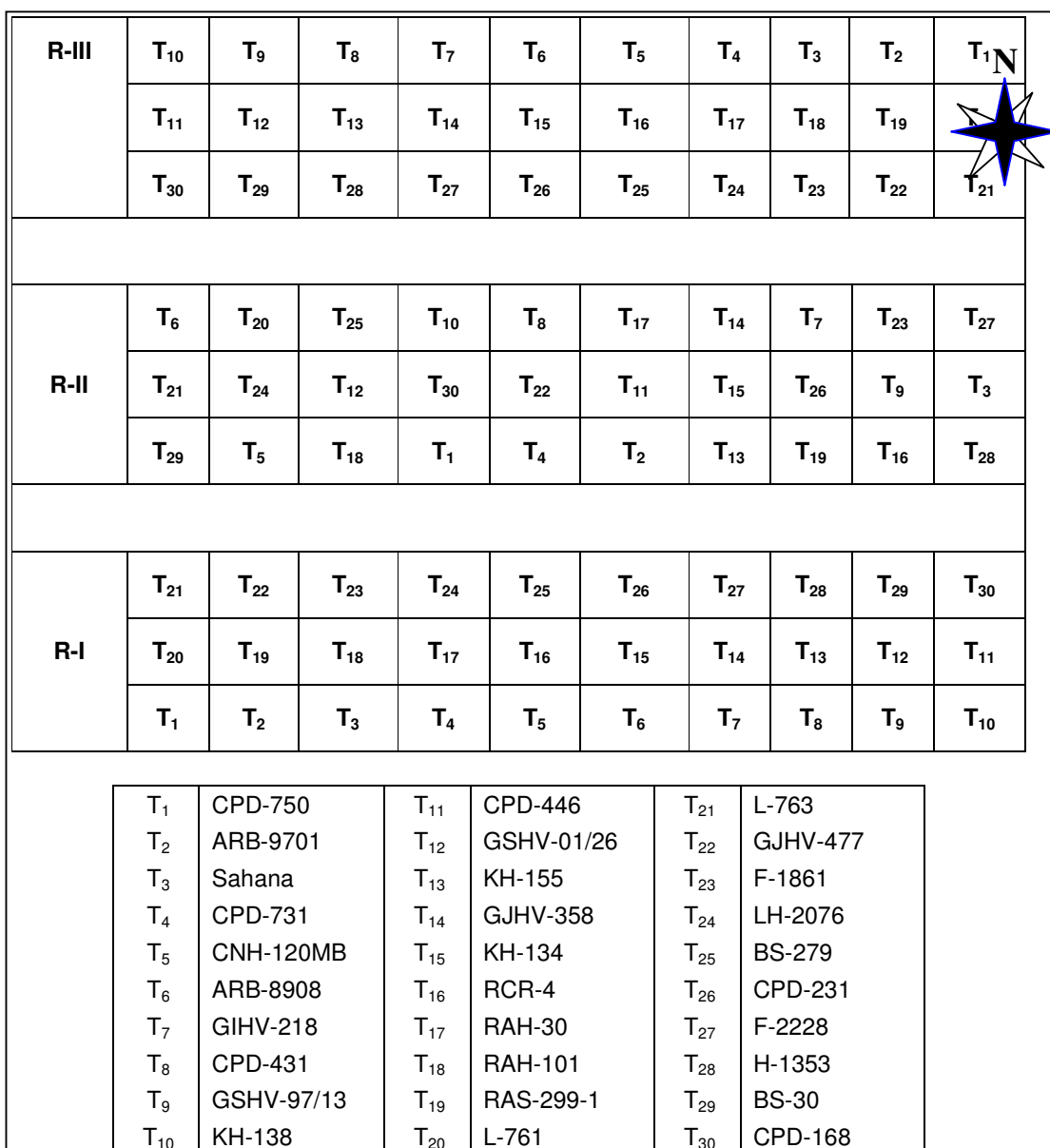


Fig. 3. Plan of layout of the experiment at ARS Dharwad and ARS Annigeri



Block 1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
1	25	49	72	96	120	144	169	193	217	C1	265	289	313	337	361	385	409	433	457	481	C1	529	553	577
2	C1	50	C1	97	121	145	170	194	218	241	266	C1	314	338	362	386	410	434	458	482	505	530	554	C1
3	26	51	73	98	122	C1	C1	195	219	242	C1	290	315	C1	363	387	C1	435	C1	483	506	C1	555	578
C1	27	52	74	C1	123	146	171	196	C1	243	267	291	C1	339	C1	388	411	C1	459	484	C2	531	556	579
4	28	53	75	99	C1	147	172	C1	220	C2	268	292	316	340	364	389	412	436	460	C1	507	532	C1	580
5	C2	54	76	100	124	148	173	197	221	244	269	293	317	341	365	C1	413	437	461	485	508	533	557	581
6	29	55	C2	101	125	C2	174	198	222	245	270	C2	318	342	366	390	414	438	462	486	509	534	558	582
7	30	56	77	102	126	149	C2	199	223	246	271	294	319	C2	367	C2	415	439	463	487	C3	535	559	C2
8	31	57	78	103	127	150	175	200	C2	247	C2	295	C2	343	368	391	416	C2	464	C2	510	536	560	583
C2	32	C1	79	C2	128	151	176	C2	224	C3	272	296	320	344	C2	392	C2	440	C2	488	511	C2	C2	584
9	C3	58	80	104	129	152	C3	201	225	248	273	C3	321	345	369	393	417	441	465	489	512	537	561	585
10	33	58	81	105	C2	153	177	202	226	249	274	297	322	346	370	C3	418	442	466	490	513	538	562	C3
11	34	C2	82	106	130	154	178	203	227	250	C3	298	C3	347	C3	394	419	C3	C3	C3	C4	539	563	586
12	C4	59	83	107	131	156	179	C3	228	251	275	299	323	C3	370	395	C5	443	467	491	514	540	564	587
13	35	60	C3	108	132	C3	180	204	C3	252	276	300	324	348	372	396	420	444	468	492	515	541	C3	588
C3	36	61	84	109	C3	157	C4	205	229	C4	277	C4	325	349	373	C4	421	445	469	493	516	C3	565	589
14	37	62	85	110	133	158	181	206	230	253	C4	301	C4	C4	374	397	422	C4	C4	494	517	542	566	C4
15	C5	63	86	C3	134	159	182	207	231	254	278	302	326	350	C4	398	C4	446	470	C4	518	543	567	590
16	38	C3	87	111	135	C4	183	208	232	255	279	303	327	351	375	399	423	447	471	495	C5	544	568	591
17	39	64	88	112	C4	160	184	C4	233	C5	280	304	328	352	376	400	424	448	472	496	519	545	C4	592
18	40	65	89	C4	136	161	185	209	234	256	281	305	329	353	C5	401	425	449	C5	497	520	546	569	C5
C4	41	C4	90	113	137	162	C5	210	C4	257	C5	306	330	C5	377	402	426	C5	473	C5	521	C4	570	593
19	C6	66	C4	114	138	163	186	211	235	258	282	C5	331	354	378	C5	427	450	474	498	522	547	571	594
20	42	67	91	115	139	C5	187	212	236	259	283	307	C5	355	379	403	C5	451	475	499	523	548	C5	595
21	43	68	92	C5	140	164	188	C5	237	C6	284	308	332	356	380	404	428	C6	476	500	C6	C5	572	596
C5	44	69	C5	116	C5	165	C6	213	C5	260	285	309	333	C6	381	405	429	452	C6	501	524	549	573	C6
22	45	C5	93	117	141	166	189	214	238	261	C6	310	C6	357	382	406	C6	453	477	502	525	550	C6	597
23	46	70	C6	118	C6	167	190	215	239	262	286	C6	334	358	C6	407	430	454	478	503	526	C6	574	598
C6	47	71	94	C6	142	C6	191	216	C6	263	287	311	335	359	383	408	431	455	479	504	527	551	575	599
24	48	C6	95	119	143	168	192	C6	240	264	288	312	336	360	384	C6	432	456	480	C6	528	552	576	600

1-600 = Germplasm lines (Note: All the germplasm lines names start with prefix GPDWD)

Check lines: C1 = DS-28, C2 = ARBH-813, C3 = CPF-824, C4 = Sahana, C5 = Surabi, C6 = MCU-5.

Fig. 4. Plan of layout of the experiment at ARS Dharwad for 600 cotton germplasm lines



Plate 1c: General view of the experiment at ARS Dharwad for 600 cotton germplasm lines

3.5.4 Gas exchange parameters using IRGA (Infrared Red Gas Analyzers)

Gas exchange traits viz. Photosynthesis/net CO₂ assimilation rate ('A'), Transpiration rate (T), stomatal conductance (g_s) and Leaf temperature (T_{leaf}) were measured from the selected plants using portable photosynthesis system LI- 6400 (LI-COR 6400, Lincoln Nebraska, USA) at 90DAS and 125DAS. The gas exchange parameters were recorded on the fully expanded leaf of fourth node from the apex. The leaf was clamped to the leaf chamber and the observations were recorded when A, g_s and C_i reached a steady value. All gas exchange parameters were recorded between 9 AM and 12 noon on bright sunny days. The leaf chamber is equipped with a peltier cooling system that can maintain the chamber temperature. The operational option provided with the system also maintains a constant chamber RH around that of the ambient air.

The following parameters were recorded, the units of which are mentioned below.

3.5.4.1 Rate of Photosynthesis : μ mole CO₂ /m²/s

3.5.4.2 Rate of Transpiration : m mole of H₂O /m²/s

3.5.4.3 Stomatal conductance : μ mole CO₂/m²/s

3.5.4.4 Leaf temperature : °C

3.5.5 Seed cotton yield (kg/ha)

Seed cotton obtained from net plot area from various pickings were considered for computation of cotton yield per hectare and expressed as kilograms per hectare.

3.6 Rain out shelter experiment

3.6.1 Experimental materials (cf. Fig. 5, Plate 3)

Based on the experimental results of 2011-12, out of thirty genotypes, ten genotypes (CPD-750, Sahana, ARB-9701, CNH-120MB, GIHV-218, BS-279, RAH-101, GJHV-477, F-2228 and KH-155) were identified as relatively drought tolerant and two were (L-761 and LH-2076) as drought susceptible. These genotypes were further evaluated in rain out shelter for drought tolerance during 2012-13 *kharif*. The detailed plan of the layout of the experiments is given in fig. 5.

Rain out shelter (ROS): Three trusses with a span of 6 m supported the structure of ROS; the trusses were made of MS pipe and inter-connected with purling at spacing of 3m. The vertical supports of each truss were attached with an extension of rod which was clamped to the ROS frame to provide an overhang on each side. This arrangement not only prevented drift of rain from sides but also help to drain the rainwater off the experimental plot effectively. The end supports were mounted on rubber wheeled castors to enable the structure to move along the two C-section channels on the plot boundary. The C-section railings were fixed on elevated reinforced concrete blocks at a height to facilitate easy movement of ROS. A galvanized iron wire is woven on all the bays of ROS over which a high-density silpauline sheet was covered. The silpauline sheet was fastened to the ROS with a nylon rope running through eyelets all-round the edge of the sheet. To prevent the ballooning of ROS during strong winds, the ROS cover was anchored firmly to the ROS frame by running nylon ropes on the top as well (Plate 2).

3.6.2 Design and layout

Design	: Split plot
Treatments	: Genotypes
Main plot	: Moisture stress levels
Sub plot	: Twelve genotypes
Replications	: Three
Date of sowing	: 01.07.2012
Spacing	: 90 cm × 20 cm

3.6.3 Moisture stress treatments (Appendix II)

The experiment consisted of three stress treatments *viz.*, control (100 per cent field capacity), moderate stress (70 per cent field capacity) and severe stress (50 per cent field capacity). To achieve different stress levels, different quantity of irrigation water was given to the microplots which were separated by two layers of polythene sheets inserted upto 1-2 m in the soil to avoid lateral movement of water from one plot to another. The water stress was imposed 30 days after the seedling establishment. Soil moisture was recorded by gravimetric method at different days (Appendix II).

Sl. No.	Moisture stress levels	Field capacity (%)
1	Control	100
2	Moderate	70
3	Severe	50

3.6.4 Observations

3.6.4.1 Growth and morphological characters

3.6.4.1.1 Plant height (cm)

The average plant height of five tagged plants was recorded at 60, 90 and 120 DAS from base of the plant to the growing tip and is expressed in centimetres.

3.6.4.1.2 Number of leaves per plant

The average number of leaves in five tagged plants was recorded at 90, 60 and 120 DAS.

3.6.4.2 Phenological characters

3.6.4.2.1 Number of days to 50 per cent squaring

The total number of days from date of sowing to the date on which the 50 per cent of the plants initiated squaring in a plot was recorded.

3.6.4.2.2 Number of days to 50 per cent flowering

The total number of days from the date of sowing to the date on which 50 per cent of the plants initiated flowering in a plot was recorded.

3.6.4.2.3 Number of days to maturity

The number of days required from sowing to the date of last picking was considered.

3.6.4.3 Morpho-physiological parameters

3.6.4.3.1 Total dry matter production

From each plot, three plants were selected randomly, cut at base and each plant was separated into different parts *viz.*, stem, leaf and reproductive parts at different growth stages. The samples were dried at 80°C till a constant weight and expressed as g plant⁻¹. From these observations the total dry matter production per plant was recorded, which was used further for computing other growth parameters. Total dry matter was recorded at 90 and 120 DAS.

3.6.4.3.2 Relative growth rate (RGR)

RGR is the increase in dry weight per unit dry weight per unit time and expressed as grams per gram per day and was calculated by the formula of Blackman (1919).

$$RGR = \frac{\log_e W_2 - \log_e W_1}{(t_2 - t_1)}$$

Where,

W_1 and W_2 = Total dry weight of plant at time t_1 and t_2 respectively.

3.6.4.3.3 Net assimilation rate (NAR)

Net assimilation rate is the rate of increase in dry weight per unit leaf area per unit time (Watson, 1952) and is expressed as grams per dm² per day. It was calculated by the formula of Radford (1967)

$$\text{NAR} = (w_2 - w_1) (\log L_2 - \log L_1) / (t_2 - t_1) (L_2 - L_1)$$

Where,

L_1 and w_1 = Leaf area and dry weight (g) of the plant respectively at time t_1

L_2 and w_2 = Leaf area and dry weight of the plant respectively at time t_2

3.6.4.3.4 Leaf Area Index (LAI)

The leaf area index was measured using LI-COR Plant canopy analyser LAI-2050 (Made in USA). Plant canopy analyser directly measures the leaf area index of the crop. The measured LAI values were later downloaded in to computer and analysed. LAI was recorded at 60, 90 and 120 DAS.

3.6.4.3.5 Specific leaf weight (SLW)

The specific leaf weight or the leaf thickness was determined by the following formula and expressed as mg/cm². SLW was recorded at 60, 90 and 120 DAS.

$$\text{SLW} = \text{Leaf dry weight (mg)} / \text{Leaf area (cm}^2\text{)}$$

3.6.4.4 Biophysical characters

Measurement of rate of photosynthesis stomatal conductance and rate of transpiration were made on the top fully expanded leaf at different growth stages by using portable photosynthesis system (LI-6400 LICOR, Nebraska, Lincoln USA). These measurements were made between 10.00 am to 12.00 noon on all the sampling dates. Measurements were recorded at 90 and 120 DAS.

The methodology and observations for measurement of biophysical parameter using Infra Red Gas Analyzer (IRGA) is same as described in section 3.5.4. Along with those parameters water use efficiency (μ mol CO₂/m mol H₂O) was recorded.

3.6.4.5 Biochemical parameters

3.6.4.5.1 SPAD chlorophyll meter reading (SCMR)

SCMR values were recorded in all cotton genotypes in all treatments under rain out shelter. The observations were recorded at different growth stages.

3.6.4.5.2 Determination of proline content (μ g/g fresh weight)

Free proline content in the leaves of cotton genotypes subjected to different drought levels were determined colorimetrically as per the method of Bates *et al.* (1973).

Procedure

A known weight (0.5 g) of fresh leaf sample was ground well in a mortar using fine sand and extracted with 10 ml of 3 per cent sulphosalicylic acid. The extract was filtered and 2 ml of the filtrate was used for proline estimation. To this 2 ml filtrate, 2 ml of acid ninhydrin reagent (2.5 g of ninhydrin was dissolved in 40 ml of 6M orthophosphoric acid and 60 ml of glacial acetic acid) and 2 ml of glacial acetic acid were added and placed in a boiling water bath for one hour. Following this, the test tubes containing the samples was transferred to ice water bath for cooling. The content of each test tube was transferred to a separating funnel and 6 ml of toluene was added, shaken thoroughly and allowed for few minutes for separation of two layers. The lower layers were discarded and the upper toluene layer containing the color was taken into a test tube. The optical density of the color complex was calculated using the formula,

$$34.11 \times \text{OD}_{520} \times V$$

$$\text{Proline } (\mu \text{ g/g dry weight}) = \frac{\text{-----}}{2 \times f}$$

$$2 \times f$$

Where,

V = Total volume of extract

f = Grams of fresh leaf

2 = Volume of extract taken

3.6.4.6 Root studies

3.6.4.6.1 Root length

The extractable roots were gently collected from the soil. Root length in all treatments was measured with measuring tape from collar region to the tip of the longest root on 80th day and was expressed in centimetres.

3.6.4.6.2 Number of roots

The extractable roots were gently collected from the soil. Number of roots (primary and secondary) was counted in all treatments at 80 DAS and was expressed in centimeters.

3.6.4.6.3 Root volume

Root volume was measured by measuring the volume of water displaced when the roots were immersed in the volumetric cylinder filled with water. Root volume was measured in all treatments at 80 DAS and was expressed in ml³.

3.6.4.7 Yield and yield components

3.6.4.7.1 Seed cotton yield (kg/ha)

Three pickings of seed cotton yield were performed at regular intervals of three weeks. Seed cotton of each plant was picked separately and put in kraft paper bags. After completion of three pickings, the total produce of each plant was cleaned and weighed using electrical balance and finally means were calculated in each replication. Seed cotton obtained from net plot area from various pickings were pooled for computation of cotton yield per hectare and expressed as kilograms per hectare.

3.6.4.7.2 Number of bolls/plant

Total number of bolls picked from the five tagged plants counted and the average was worked out.

3.6.4.7.3 Mean boll weight (g/boll)

Seed cotton obtained from 20 bolls selected randomly from the net plot covering top to bottom were weighed and mean was worked out and expressed in g/boll.

3.6.4.8 Fibre properties

3.6.4.8.1 Fibre strength (g/tex)

Fibre strength of each plant was measured by using spin lab HVI-900. This instrument provides a comprehensive profile of raw fibre and measures the most important fibre characteristics according to international trading standards.

3.6.4.8.2 Fibre length (mm)

Fibre length of each plant was measured by using spin lab HVI-900. This instrument provides a comprehensive profile of raw fiber and measures the most important fiber characteristics according to international trading standards.

3.6.4.8.3 Micronaire

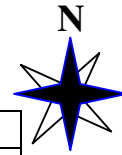
Cotton fibre micronaire was measured by using spin lab HVI-900. This instrument provides a comprehensive profile of raw fibre and measures the most important fibre characteristics according to international trading standards.

3.6.4.8.4 Ginning out turn (%)

Clean and dry samples of seed cotton of each plant were weighed and ginned with a single roller electric gin. Lint percentage was calculated, dividing lint weight by total weight of seed cotton in a sample. This character was recorded on percentage basis.

3.6.4.9 Correlation studies

The correlation between seed cotton yield versus other growth, physiological parameters and yield components of the genotypes grown at ROS has worked out.



M1	T ₁	M3	T ₈	M2	T ₁₀
	T ₃		T ₄		T ₇
	T ₅		T ₉		T ₉
	T ₇		T ₁₁		T ₆
	T ₉		T ₂		T ₁
	T ₁₁		T ₇		T ₁₁
	T ₂		T ₁₂		T ₂
	T ₄		T ₁		T ₅
	T ₆		T ₅		T ₃
	T ₈		T ₃		T ₈
	T ₁₀		T ₁₀		T ₁₂
	T ₁₂		T ₆		T ₄
M2	T ₁₀	M1	T ₁	M3	T ₈
	T ₇		T ₃		T ₄
	T ₉		T ₅		T ₉
	T ₆		T ₇		T ₁₁
	T ₁		T ₉		T ₂
	T ₁₁		T ₁₁		T ₇
	T ₂		T ₂		T ₁₂
	T ₅		T ₄		T ₁
	T ₃		T ₆		T ₅
	T ₈		T ₈		T ₃
	T ₁₂		T ₁₀		T ₁₀
	T ₄		T ₁₂		T ₆
M3	T ₈	M2	T ₁₀	M1	T ₁
	T ₄		T ₇		T ₃
	T ₉		T ₉		T ₅
	T ₁₁		T ₆		T ₇
	T ₂		T ₁		T ₉
	T ₇		T ₁₁		T ₁₁
	T ₁₂		T ₂		T ₂
	T ₁		T ₅		T ₄
	T ₅		T ₃		T ₆
	T ₃		T ₈		T ₈
	T ₁₀		T ₁₂		T ₁₀
	T ₆		T ₄		T ₁₂

M1- Control

M2- Moderate moisture stress

M3- Severe moisture stress

T₁ = CPD-750

T₂ = Sahana

T₃ = ARB-9701

T₄ = CNH-120MB

T₅ = L-761

T₆ = LH-2076

T₇ = GIHV-218

T₈ = BS-279

T₉ = RAH-101

T₁₀ = GJHV-477 T₁₁ = F-2228

T₁₂ = KH-155

Fig. 5. Plan of layout for rainout shelter experiment at ARS Dharwad



Plate2: General view of the experiment at Rain out shelter

3.7 Evaluation of cotton genotypes for drought tolerance using PEG water stress by slanting glass plate technique (2012-13)

The relative drought tolerance of 12 selected genotypes was evaluated using different osmotic stress conditions by slanting glass plate technique. Different concentrations of Poly ethylene glycol-6000 (PEG) were applied at germination stage.

To obtain information on seed quality and viability initial germination tests were performed with 200 seeds in BOD-biological oxygen demand incubator (Nanolab, India), as described in Gonela *et al.* (2004), at 25°C without photoperiod control.

The PEG solutions were prepared with osmotic potentials of 0.0 MPa, -0.05 MPa, -0.148 MPa, -0.295 MPa, -0.491 MPa, -0.735 MPa and -0.846 MPa which is equivalent to PEG concentrations of 0%, 5%, 10%, 15%, 20%, 25% and 27 per cent respectively. The concentrations of PEG required to obtain these values were determined by using the equation of Michel and Kaufmann (1973):

$$\psi_s = - (1.18 \times 10^{-2}) C - (1.18 \times 10^{-4}) C^2 + (2.67 \times 10^{-4}) CT + (8.39 \times 10^{-7}) C^2T,$$

Where ψ_s = osmotic potential (MPa)

C = concentration (g L^{-1} PEG in water)

T = temperature ($^{\circ}\text{C}$). As a control, a solution with osmotic potential $\psi_s = 0.0$ MPa was used.

3.7.1 Slanting glass plate technique methodology (cf. Plate 3)

Glass plates having 3 mm thickness with 25 cm length and 30 cm width were used. The glass plate length and breadth depends on the number of seeds used for the germination study in the laboratory. The glass plates were covered with 560 × 570 mm fine quality filter paper sheets from bottom to top. Uniform sized good quality delinted cotton seeds were selected from each of 12 different genotypes.

The delinted seeds of all the genotypes were disinfected with 0.1 per cent HgCl_2 . 10 seeds were kept on top portion of the filter paper/glass plate at 3 cm spacing. The seeds were covered with a small strip of filter paper. Suitable holding material was used to avoid the fall of seeds in slanting position. Initially little quantity of respective prepared PEG solutions was added on to the small strip of filter paper which helps in adsorption of seeds on to filter paper firmly. Glass plate was inserted in polythene cover. The plate was kept on the supporting wooden block in slanting position. Four hundred ml of corresponding concentrations (0%, 5%, 10%, 15%, 20%, 25 per cent and 27%) PEG osmotic solutions were added separately into the respective polythene cover carrying separate genotype seeds in slanting plate. The PEG solution moved upward and reached to the seeds by capillary movement through filter paper. Seedlings were allowed to grow under room temperature. Fresh PEG solutions were added in regular intervals of 3 days to maintain the level of solution. No need of providing aeration to roots, since regularly exchange of fresh PEG solutions was done.

3.7.2 Observations

3.7.2.1 Germination (%)

The seedlings which emerged from PEG solution were considered as germinated and observation was recorded on 12th and 18th DAS and expressed as percentage.

3.7.2.2 Root length (cm)

Randomly selected seedling was gently removed without damaging the seedling roots and measured from collar region to the tip of the longest root on 12th and 18th DAS and was expressed in centimeter.

3.7.2.3 Shoot length (cm)

The shoot length of above selected seedling was measured from collar region to tip of the shoot on 12th and 18th DAS and was expressed in centimeter.

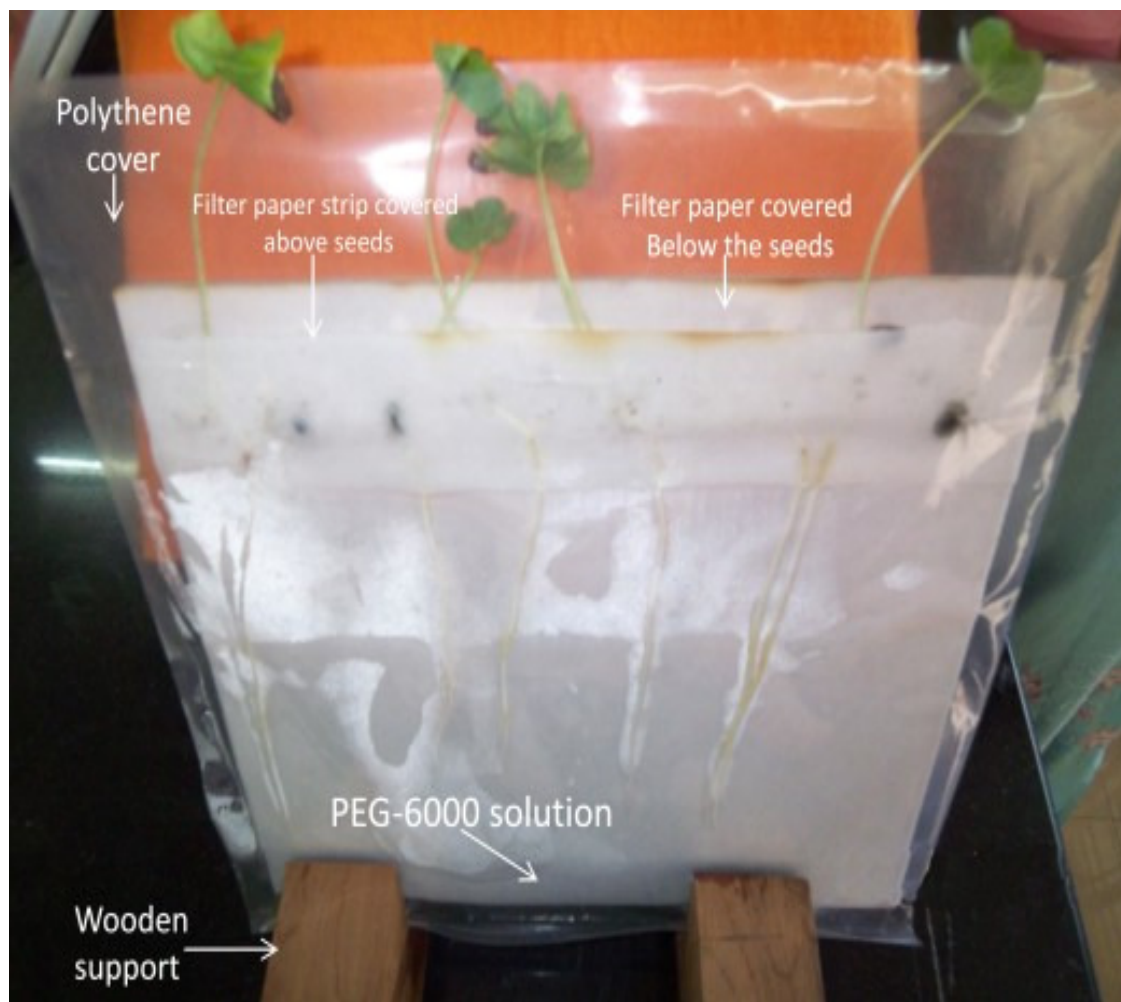


Plate.3: General view of the slanting glass plate technique experiment

3.7.2.4 Root: shoot ratio

The ratio of root length and the shoot length of each seedling selected above was calculated. Observations were recorded on 12th and 18th DAS.

3.7.2.5 Seedling vigour

Shoot and root vigour indices were calculated at 12th and 18th DAS as described by Abdul-Baki and Anderson (1973).

3.7.2.5.1 Shoot vigour index = Shoot length x germination%

3.7.2.5.2 Root length index = Root length x germination%

3.7.2.5.3 Seedling vigour index = (Root length + shoot length) x germination%

3.8 Genetic polymorphism of selected cotton genotypes using suitable molecular markers (SSR/suitable marker)

RAPD (Random Amplified Polymorphic DNA): This technique uses a polymerase chain reaction (PCR) method to amplify DNA with random primers. Using PCR, random primers of arbitrary nucleotide sequence binds to the DNA at two different sites on opposite strands of the DNA template. If the primer sites are located at a closer amplifiable distance from each other, it results in a DNA product by a thermocyclic reaction. This technique was used to detect the molecular polymorphism among 12 cotton genotypes. In the present investigation the selected 12 cotton genotypes were used for molecular polymorphism analysis using 79 RAPD markers.

3.8.1 DNA Isolation

DNA extraction from putative transformed regenerated callus by C-TAB method

For extraction of DNA from cotton plant leaves CTAB (Cetyltrimethyl Ammonium Bromide) method of DNA extraction was used as described by Doyle and Doyle (1990). Along with CTAB method commercial kit isolation method also employed to isolate DNA from cotton genotypes. The DNA was isolated separately from young leaves of all 12 genotypes.

Principle

The DNA is extracted using a suitable extraction medium and relieved of carbohydrate and other bulk impurities by adding Sodium acetate and the DNA is precipitated with isopropyl alcohol.

Materials used

1. Plant leaf sample
2. Extraction buffer:
 - 2 per cent CTAB 1.4 M NaCl
 - 20 mM EDTA, disunion (pH 8.0)
 - 100 mM Tris-HCl (pH 8.0)
 - 0.2 per cent β -mercaptoethanol added just prior to use.
3. Ethanol
4. Isopropanol
5. Chloroform: Isoamyl alcohol (24:1)
6. RNAase A (10 mg/mL)
7. TE buffer
8. 10 mM Tris-HCl
9. 1 mM EDTA

Procedure

1. Approximately 1g of fresh leaf material was weighed and placed into a mortar and a small volume of liquid nitrogen was added and ground to a fine powder using a pestle. The mortar was allowed to thaw. This thawing is necessary to prevent the precipitation of CTAB at the next stage.
2. 10 ml of extraction buffer (kept at 65°C) was added to the powdered callus material and ground to fine slurry.

The components of the extraction buffer have particular functions:

- i. CTAB is a cationic detergent which aids in the lysis of cell membranes and will form complexes with nucleic acids;
- ii. Sodium chloride aids in the formation of nucleic acid- CTAB complexes;
- iii. EDTA chelates divalent cations, particularly Ca^{2+} and Mg^{2+} and prevents the activity of metal-dependent nucleases;
- iv. β -mercaptoethanol is a reducing agent which protects DNA against quinones, disulphides, peroxidases and polyphenol oxidases.
- v. The slurry transferred to centrifuge tubes and inverted gently to mix the contents.
- vi. The tubes incubated at 65°C for 60 minutes and occasionally mixed gently.

Following incubation, the tubes were allowed to cool to ambient temperature.

- The sample at this stage is treated gently so that the DNA is not sheared.
- The solution is left to cool, otherwise vapour builds up and the mixture explodes.
- At this stage the cell membranes breakdown and form a soluble CTAB-nucleic acid complex.
- Chloroform-isoamyl alcohol (24:1, 10 ml) was added and mixed by inversion to form an emulsion.
- After mixing thoroughly the samples were spun at 3000 rpm for 20 minutes at room temperature.
- The top aqueous solution transferred to a new centrifuge tube using a wide bore tip. The purpose of this stage is to remove proteins and carbohydrates.
- If the aqueous phase is not clear, chloroform: amyl alcohol mix is added again and the mix is centrifuged at 3000 rpm for 20 minutes.
- The aqueous phase was taken and 2/3 rd volume of isopropanol was added. The mixture was left at room temperature. After 10-15 minutes whitish strands visible.
- The tubes were centrifuged at 3000 rpm for 10 minutes.
- The supernatant poured off and pellet washed with cold 70 per cent ethanol. Pellet dried under vacuum.
- Pellet was dissolved in 500 μ l TE overnight at 4 to 6°C and transferred to 1.5 ml eppendorf tubes.
- RNAase (3 μ l) added and incubated in 37 °C water bath for approximately one hour.
- Equal volume of phenol: chloroform (24:1) was added to each eppendorf tube and spin at 5,000 rpm for 15 minutes. The upper layer was collected in a new tube.
- Two volumes of absolute ethanol was added; mixed and left overnight in freezer (-80°C).
- The mixture was centrifuged at 5,000 rpm for 20 minutes. The pellet was washed with 70 per cent ethanol.
- The pellet was dried under vacuum and 200 μ l of sterile water was added. The nucleic acid solution was stored at – 40°C until use.

3.8.2 DNA quantity and quality estimation

The concentration of DNA was quantified spectrophotometrically and also by gel electrophoresis using 0.8 per cent agarose with known concentrations of DNA.

The spectrophotometric analysis was done by taking 5µl of DNA sample and it was diluted to 3000µl with TE. The spectrophotometer readings were recorded at 260/280 nm using TE as a blank. A good DNA preparation generally exhibits the following spectral properties. $A_{260}/A_{280} > 1.80$

DNA concentration was calculated using OD values at 260 nm using the following formula.

$$\text{Concentration of DNA } (\mu\text{l/ml}) = \text{OD at 260 nm} \times 50$$

To test the quality of DNA, samples were run on 0.8 per cent agarose gel in 1X TAE buffer and stained with ethidium bromide. DNA was evaluated by comparing it with a standard undigested DNA sample. If RNA was found in higher concentration, the sample was treated with RNase enzyme.

3.8.3 RAPD Primers

In this technique, a single short oligonucleotide sequence primers were used for cyclic amplification of DNA, which exposes the polymorphism distributed throughout the genome. These amplified fragments were called as random amplified polymorphic DNAs (Williams *et al.*, 1990).

The required random amplified polymorphic DNAs molecular markers (primers) were obtained from Dr. I. S. Katageri, Sr. Scientist, ARS, Dharwad, Karnataka, India. The details of the randomprimers (Name, sequence information and T_m value) used for the study is presented in Table 4.

3.8.4 Amplification reaction mixture

Amplification reaction mixture was prepared in 0.5 ml thin walled PCR tubes containing following components in a total volume of 20 µl.

Sl. No.	Components	Quantity (µl/reaction)
1	Template DNA	2.0
2	dNTPs mix (2.5mM each)	1.0
3	Primer (5PM)	1.0
4	MgCl ₂ (25mM)	1.0
5	10x assay buffer	2.5
6	Taq DNA polymerase	0.34
7	Sterile distilled water	12.16

Except DNA template, the master mix was distributed to PCR tubes (20 µl tube) and later 2 µl of template DNA from the respective genotypes was added making up the final volume to 20 µl.

3.8.5 The Thermo profile of PCR

The PCR amplification for RAPD analysis was performed, the amplification conditions were as follows:

Sl. No.	Steps	Temperature (°C)	Duration (min)	Number of cycles
1	Initial denaturation	94	5	1
2	Final denaturation	94	1	
3	Annealing	36	1.2	40
4	Extension	72	2	
5	Final extension	72	10	1

After the completion of PCR, the products were stored at 4°C until the gel electrophoresis was done.

Table 4. List of random primers used for RAPD with their sequence and T_m.

Sl. No.	Name	Sequence (5'-3')	T _m
1	OPI 1	ACCTGGACAC	33.4
2	OPI 2	GGAGGAGAGG	33.4
3	OPI 3	CAGAAGCCCA	34.1
4	OPI 4	CCGCCTAGTC	35.8
5	OPI 5	TGTTCCACGG	34.9
6	OPI 6	AAGGCGGCAG	41.1
7	OPI 7	CAGCGACAAG	33.5
8	OPI 8	TTTGCCCGGT	38.6
9	OPI 9	TGGAGAGCAG	33.1
10	OPI 10	ACAACGCGAG	36.7
11	OPI 11	ACATGCCGTG	36.4
12	OPI 12	AGAGGGCACA	36.0
13	OPI 13	CTGGGGCTGA	38.4
14	OPI 14	TGACGGCGGT	43.2
15	OPI 15	TCATCCGAGG	32.7
16	OPI 16	TCTCCGCCCT	40.7
17	OPI 17	GGTGGTGATG	31.8
18	OPI 18	TGCCCAGCCT	42.3
19	OPI 19	AATGCGGGAG	35.1
20	OPI 20	AAAGTGCGGG	36.2
21	OPN 4	GACCGACCCA	38.6
22	OPN 5	ACTGAACGCC	35.7
23	OPN 7	CAGCCCAGAG	36.0
24	OPN 8	ACCTCAGCTC	33.1
25	OPN 9	TGCCGGCTTG	41.7
26	OPN13	AGCGTCACTC	34.7
27	OPN16	AAGCGACCTG	35.1
28	OPN19	GTCCGTACTG	31.1
29	OPE2	GGTGCGGGAA	40.4
30	OPE3	CCAGATGCAC	32.6
31	OPE4	GTGACATGCC	33.2
32	OPE13	CCCGATTCTGG	37.0
33	OPL04	GA CTGCACAC	33.3
34	OPL05	ACGCAGGCAC	41.7
35	OPL07	AGGCGGGAAC	39.8
36	OPL09	TGCCAGAGTC	34.2
37	OPL10	TGGGAGATGG	32.2
38	OPL13	ACCGCCTGCT	43.2
39	OPL14	GTGACAGGCT	34.3
40	OPL18	ACCACCCACC	38.7
41	OPAP 01	AACTGGCCCC	39.4
42	OPL 19	TCTGCCAGTG	34.3

Contd.....

Sl. No.	Name	Sequence (5'-3')	T _m
43	OLIGO 612	GCCTGGTGCC	43.2
44	OLIGO623	ATCAGAACGC	30.7
45	OLIGO 626	ACCAGCACGC	41.7
46	OLIGO 640	TTGCATCCGC	37.1
47	OLIGO 644	CCACAAGCGC	39.8
48	OLIGO 647	TGAACATCGC	31.3
49	OLIGO 652	AGTATGTCGC	29.6
50	OLIGO 656	TGAACAAGGC	30.6
51	OLIGO 662	ACCCCCAGGC	43.9
52	OLIGO 667	TCAGTGAGGC	33.7
53	OLIGO 676	ATATGTCGGC	29.5
54	OLIGO 677	AACACAGGGC	35.3
55	OLIGO 678	TAGGGTCGGC	38.1
56	OLIGO 685	ACCACTGGGC	39.5
57	OLIGO 686	GAGACTGGGC	36.0
58	OLIGO 688	GAGGCTGGGC	42.0
59	UBC 431	CTGCGGGTCA	39.9
60	UBC 757	GGAAGGGAGG	34.4
61	OPP07	GTCCATGCCA	34.2
62	BNL 2634	CCCAGCTGCTTATTGGTTTC	55.1
63	BNL 3563	AATGGGCAAGAAAAGGGAAC	54.8
64	BNL 3090	TTGCTCCTGATTTTCCAGCT	55.8
65	BNL 2895	TACCATCTCACGGATCCACA	56.3
66	BNL 3441	CGTCATAAACCGTGCTTGTG	55.4
67	BNL 2895	CGATTTTACTGCTTCAGACTTG	53.2
68	BNL 3792	CATATTCCAGTCAAACCAAACG	53.5
69	BNL 3599	TTTAGCCCCAGTAACATGC	53.5
70	BNL2572	GTCCTATTACTAAAATTGTTAATTTAG	53.0
71	BNL 3090	GAAATCATTGGAAGAACATATACTAC	53.1
72	BNL 3563	AAGCATAAACTTGACACAAGC	55.5
73	BNL 3792	TTCGAGATCCCCTGTTCTGA	56.2
74	BNL 2572	CGATGTTAAATCAATCAAGGTC	51.0
75	BNL 3441	GGCCACTTTAAGGCTGTCAC	57.2
76	BNL 3599	ACTGCAAGCTCTGCCCTAAA	58.0
77	BNL 2634	AACAACATTGAAAGTCGGGG	54.6
78	A1A13	CAGGCCCTTCCAGCACCAC	63.6
79	A9B7	GGTGACGCAGGGGTAACGCC	63.5

3.8.6 Separation of amplified products by agarose gel electrophoresis

Agarose Gel Electrophoresis

Agarose gel (4%) electrophoresis was used to resolve the different molecular configuration of a DNA molecule as well as to separate DNA fragments of different lengths. The distance migrated by the marker is used to calculate the molecular weight of the plasmid DNA. DNA was visualized by using the intercalating dye. The relative concentration of the DNA sample was estimated by visual comparison with the ethidium bromide-stained DNA standard.

Materials

1. TAE 50X (per liter 48.4 g of Trizma base, 11.42 ml of glacial acetic acid, 20 ml of 0.5M EDTA at pH 8.0).
2. 1X loading buffer: 0.25 per cent bromophenol blue, 40 per cent sucrose.
3. 4 per cent agarose gel (horizontal).
4. Gel frames and well formers.
5. DNA molecular size markers (100 bp ladder).
6. Ethidium bromide (10 mg/ml).
7. UV (356 nm wavelength) transilluminator box.

Protocol (Sambrook *et al.*, 1989)

1. DNA samples were prepared in a volume that will not overflow the gel wells by addition of appropriate amount of loading buffer.
2. The samples were loaded into the wells and care was taken to connect the leads so that the DNA will migrate from anode (negative lead) to cathode (positive lead).
3. The electrophoresis apparatus was connected to the power supply. The electrophoresis was carried out at 50V.
4. When the bromophenol blue dye had migrated to three-fourths of the gel, electrophoresis was stopped.
5. The gel was moved carefully to the UV trans illuminator and the distance of each DNA band was measured.

The amplified products along with 2 μ l of loading dye (Bromo phenol blue) were separated on 4 per cent agarose gel at 80 volts using 1X TAE buffer of pH 8.0 containing ethidium bromide (0.5 μ l/10 ml of gel). 100 bp standard ladder marker was used in gel. The gels were viewed under UV-trans illuminator and photographed for documentation.

3.8.7 Similarity matrices and dendrogram

Similarity matrices are matrices whose elements are the relative distance between points located on a certain manifold. Dendrogram is a 'treelike' diagram that summaries the process of clustering.

A dendrogram was constructed using NTSYSpc programme. On the basis of this analysis, the populations were clustered into groups. Similarity matrices and dendrograms were constructed based on diversity coefficients generated for individual primers and also for pooled data by using UPGMA method susing NTSYSpc, a computer programme for distance/similarity estimation.

NTSYSpc programme: It can be used to discover pattern and structure in multivariate data. For example, one may wish to discover that a sample of data points suggests that the samples may have come from two or more distinct populations or to estimate a phylogenetic tree using the neighbor-joining or UPGMA methods for constructing dendrograms. Of equal interest is the discovery that the variations in some subsets of variables are highly inter-correlated (clustered).

Features include in NTSYSpc are listed below

- Similarity and dissimilarity: correlation, distance, 34 association coefficients and 11 genetic distance coefficients.

- Clustering: UPGMA and other hierarchical SAHN methods (allows for ties). Neighbor-joining method (including the new unweighted version). Several types of consensus trees.
- Graph theoretic methods: minimum-length spanning trees. Graphs (unrooted trees) from the neighbor-joining method.
- Ordination: principal components and principal coordinates analysis, correspondence analysis, metric and non-metric multidimensional scaling analysis, singular-value decompositions, projections onto axes and Burnaby's method. Canonical variates analysis. Programs for multiple factor analysis, common principal components analysis, partial least-squares, multiple correlation and canonical correlations are also included.
- Multivariate tests: canonical variates analysis, tests for homogeneity of covariance matrices, tests for number of dimensions, generalized multivariate multiple regression analysis. There are also provisions for bootstrap, jackknife and simulation experiments.
- Geometric morphometrics: includes specialized modules for Procrustes analysis to superimpose landmark configurations, plotting the results of a Procrustes analysis, Fourier analysis (including 2D and 3D elliptic) of outline shapes, plotting outlines and Fourier coefficients and computation of 2D and 3D partial warp scores and estimates of the uniform component
- Other: includes comparison of matrices by cophenetic correlation, Mantel test, 3-way Mantel test, data standardization and matrix transformations (simple functions, deletion and now matrix transpose). Matrices can be split or combined.

3.8.8 Per cent polymorphism

The presence of several distinct forms of a gene or phenotypic trait within a population with frequencies greater than 1 per cent. Percent polymorphism was calculated by using formula:

$$\text{Per cent polymorphism} = \frac{\text{Total number of Polymorphic bands}}{\text{Total number of bands}} \times 100$$

3.9 Statistical analysis and the interpretation of data

The data collected from the experiment at different growth stages and at harvest was subjected to statistical analysis as prescribed by Gomez and Gomez (1984). The level of significance used for 'F' and 't' test was $P = 0.05$. The year-wise data was highlighted in Results and Discussion chapters. Critical difference values were calculated whenever 'F' test was found significant. In case of non-significant effects, value of standard error of means alone was presented in Tables. The mean value of main plot, sub plot and interaction were separately subjected to Duncan' multiple range test (DMRT) using the corresponding error mean sum of squares and degrees of freedom values.

EXPERIMENTAL RESULTS

Results obtained from the different experiments are presented in this chapter with the following headings.

4.1 Assessment of genetic variability of cotton genotypes for drought tolerance by biophysical and physiological analysis

4.1.1 Field experiment at ARS Dharwad and ARS Annigeri

A field experiment was conducted at ARS, Dharwad and ARS Annigeri, using 30 genotypes. In both locations the genotypes were evaluated for drought tolerance for biophysical and physiological traits and the results were as follows.

4.1.1.1 Specific leaf weight (SLW) (cf. Table 5)

In general, SLW increased as the growth of the crop advanced at both locations. The SLW values were higher at ARS Dharwad compared to ARS Annigeri at all the crop growth stages.

The mean SLW values of the cotton genotypes grown at ARS Dharwad was 8.5 mg/cm², 8.8 mg/cm², 9.9 mg/cm² at 60 DAS, 90 DAS and 125 DAS respectively. Whereas at ARS Annigeri the mean SLW recorded were 7.7 mg/cm², 8.4 mg/cm², 8.9 mg/cm² respectively.

4.1.1.1.1 At ARS Dharwad

The results indicated that significant differences among the genotypes for SLW recorded at all the crop stages *i.e.*, 60 DAS, 90 DAS and 125 DAS.

At 60 DAS, the genotype GIHV-218 (9.7 mg/cm²) recorded significantly higher SLW over other genotypes and was on par with CNH-120MB (9.6 mg/cm²), GJHV-477 (9.6 mg/cm²), CPD-750 (9.5 mg/cm²), GJHV-358 (9.5 mg/cm²), GSHV-97/13 (9.4 mg/cm²), CPD-168 (9.3 mg/cm²) and Sahana (9.3 mg/cm²). While, L-763 (7.1 mg/cm²) showed least SLW and was on par with RAH-30 (7.2 mg/cm²), L-761 (7.2 mg/cm²), CPD-431 (7.3 mg/cm²), LH-2076 (7.4 mg/cm²), RAS-299-1 (7.5 mg/cm²) and H-1353 (7.5 mg/cm²).

At 90 DAS, the genotypes GIHV-218 (10.4 mg/cm²) and GJHV-477 (10.3 mg/cm²) recorded significantly higher SLW over other genotypes, however, these were on par with CNH-120MB (10.2 mg/cm²), CPD-750 (10.1 mg/cm²), GJHV-358 (10.1 mg/cm²) and GSHV-97/13 (9.9 mg/cm²); followed by CPD-750 (10.1 mg/cm²) and Sahana (9.6 mg/cm²). While, L-761 (7.4 mg/cm²) and L-763 (7.4 mg/cm²) showed least SLW over all the genotypes and on par with CPD-431 (7.5 mg/cm²), RAH-30 (7.5 mg/cm²), LH-2076 (7.7 mg/cm²), RAS-299-1 (7.8 mg/cm²) and H-1353 (7.9 mg/cm²).

At 125 DAS, the genotypes GIHV-218 (11.5 mg/cm²), GJHV-477 (11.4 mg/cm²) and CNH-120MB (11.3 mg/cm²) recorded significantly higher SLW over other genotypes, however, on par with CPD-750 (11.2 mg/cm²) and GJHV-358 (11.2 mg/cm²); followed by CPD-168 (10.9 mg/cm²), GSHV-97/13 (10.9 mg/cm²) and Sahana (10.7 mg/cm²). While, L-763 (8.5 mg/cm²), RAH-30 (8.6 mg/cm²) and L-761 (8.6 mg/cm²) showed least SLW and was on par with RAS-299-1 (8.7 mg/cm²), CPD-431 (8.7 mg/cm²), LH-2076 (8.7 mg/cm²) and H-1353 (8.8 mg/cm²).

4.1.1.1.2 At ARS Annigeri

The results indicated that significant differences among the genotypes for SLW recorded at all the stages *i.e.*, 60 DAS, 90 DAS and 125 DAS.

At 60 DAS, the genotypes GIHV-218 (8.5 mg/cm²) and CPD-750 (8.5 mg/cm²) recorded significantly higher SLW over other genotypes, however, these were on par with ARB-9701 (8.4 mg/cm²), Sahana (8.4 mg/cm²), BS-30 (8.4 mg/cm²), BS-279 (8.3 mg/cm²), ARB-8908 (8.2 mg/cm²), GJHV-477 (8.2 mg/cm²) and CNH-120MB (8.1 mg/cm²); followed by GSHV-97/13 (8 mg/cm²) and F-2228 (7.9 mg/cm²). While, L-761 (6.9 mg/cm²) showed least SLW over all other the genotypes and was on par with CPD-168 (7 mg/cm²), L-763 (7 mg/cm²), RAH-30 (7.1 mg/cm²), LH-2076 (7.1 mg/cm²), RAS-299-1 (7.2 mg/cm²), KH-138 (7.2 mg/cm²), F-1861 (7.2 mg/cm²), KH-134 (7.3 mg/cm²) and CPD-446 (7.3 mg/cm²).

At 90 DAS the genotypes CPD-750 (9.7 mg/cm²) and GIHV-218 (9.6 mg/cm²) recorded significantly higher SLW over other genotypes and were on par with Sahana (9.5 mg/cm²) and ARB-9701 (9.4 mg/cm²); followed by BS-279 (9.2 mg/cm²), BS-30 (9.2 mg/cm²), ARB-8908 (9.0 mg/cm²)

and GJHV-477 (7.6 mg/cm²). While L-761 (7.3 mg/cm²) and L-763 (7.3 mg/cm²) showed least SLW and was on par with CPD-168 (7.4 mg/cm²), RAH-30 (7.5 mg/cm²), F-1861 (7.6 mg/cm²) and LH-2076 (7.6 mg/cm²).

At 125 DAS, the genotype CPD-750 (10.2 mg/cm²) recorded significantly higher SLW over other genotypes and was on par with GIHV-218 (10.1 mg/cm²), Sahana (10.0 mg/cm²) and ARB-9701 (9.8 mg/cm²); followed by BS-279 (9.7 mg/cm²), BS-30 (9.7 mg/cm²), ARB-8908 (9.6 mg/cm²), CNH-120MB (9.4 mg/cm²) and GJHV-477 (9.4 mg/cm²). While, L-761 (7.6 mg/cm²) and L-763 (7.7 mg/cm²) showed least SLW and was on par with CPD-168 (7.9 mg/cm²) and RAH-30 (8.0 mg/cm²).

4.1.1.2 SPAD values (Chlorophyll content) (cf. Table 6)

In both locations the SPAD values decreased at 120 DAS. Higher SPAD values recorded in ARS, Dharwad location compared to ARS Annigeri at all the crop growth stages.

The mean SPAD values of the cotton genotypes grown at ARS Dharwad was 35.5, 39.75 and 33.5 at 60 DAS, 90 DAS and 125 DAS respectively. Whereas in ARS Annigeri it was 29.6, 35.1 and 28.1 at 60 DAS, 90 DAS and 125 DAS respectively.

4.1.1.2.1 At ARS Dharwad

The results indicated that significant difference among the cotton genotypes for SPAD values at all the crop stages *i.e.*, 60 DAS, 90 DAS and 125 DAS.

At 60 DAS, the cotton genotypes GIHV-218 (38.0) and CNH-120MB (37.9) recorded significantly higher SPAD value over other genotypes and were on par with BS-30 (37.5); followed by KH-155 (37.2), ARB-9701 (37.1) and CPD-168 (36.9). While, L-761 (31.3) showed least SPAD value among the genotypes followed by KH-138 (32) and H-1353 (32.6).

At 90 DAS, there was significant difference among cotton genotypes for SPAD values was observed. The genotypes GIHV-218 (42.7) showed significantly higher SPAD values over other genotypes and was on par with however and was on par with CNH-120MB (42.6), BS-30 (42.1), KH-155 (41.7), ARB-9701 (41.5), CPD-168 (41.3), GSHV-01/26 (41.2) and Sahana (41.1); followed by GJHV-477 (41.0). While, L-761 (35.8) showed significantly less SPAD value and was on par with KH-138 (36.2), H-1353 (36.3), LH-2076 (36.9) and F-2228 (37.1).

At 125 DAS, the genotypes GIHV-218 (37.2) and CNH-120MB (37.1) showed significantly higher SPAD values over other genotypes, and were on par with BS-30 (37.0), KH-155 (36.9), ARB-9701 (36.8), CPD-168 (36.7), GSHV-01/26 (36.4), Sahana (36.1), GJHV-477 (35.8), CPD-231 (35.4), CPD-446 (34.9), RAH-101 (34.7), ARB-8908 (34.3), RAH-30 (34.2) and CPD-750 (34.0). While, L-761 (29.3) showed significantly less SPAD values and was on par with H-1353 (29.4), LH-2076 (29.6), F-2228 (29.8), KH-134 (30.1), KH-138 (30.5), BS-279 (30.9), F-1861 (31.1), GSHV-97/13 (31.3), L-763 (31.5) and CPD731 (31.9).

4.1.1.2.2 At ARS Annigeri

The results indicated that significant difference among the genotypes for SPAD values at all the crop stages *i.e.*, 60 DAS, 90 DAS and 125 DAS.

At 60 DAS the genotypes GIHV-218 (34.4) recorded significantly higher SPAD value over other genotypes, and was on par with BS-279 (34.1), CNH-120MB (34.1), KH-155 (34.0), ARB-9701 (34.0), CPD-750 (32.6), Sahana (32.4), GSHV-01/26 (32.2), RAH-101 (32.1), GJHV-477 (32.0), CPD-231 (31.8), BS-30 (31.3), ARB-8908 (31.3) and RAH-30 (31.2). While, LH-2076 (24.0) showed least SPAD value among the genotypes, followed by L-761 (24.4) this was on par with H-1353 (25.0), KH-138 (25.4), F-1861 (25.7), KH-134 (25.8), F-2228 (26.2), L-763 (26.3), CPD-446 (26.6), GSHV-97/13 (27.2) and RAS-299-1 (27.3).

At 90 DAS, there was significant difference among genotypes for SPAD values observed. The genotype CNH-120MB (40.7) showed significantly higher SPAD values over other genotypes, however, this was on par with BS-279 (40.6), KH-155 (39.7), ARB-9701 (39.0), CPD-750 (38.6), Sahana (38.2) and GSHV-01/26 (38.1). While, LH-2076 (27.3) showed significantly less SPAD values and was on par with L-761 (29.2) and H-1353 (29.9).

At 125 DAS, there was significant difference among genotypes for SPAD values observed. The genotype GIHV-218 (36.1) showed significantly higher SPAD values over other genotypes, however, this was on par with CNH-120MB (35.3) followed by BS-279 (33.2), KH-155 (32.3), ARB-9701 (31.6), CPD-750 (31.2), Sahana (31.1), GSHV-01/26 (30.7) and RAH-101 (30.3). While, LH-2076 (20.4) showed significantly less SPAD values and was on par with L-761 (22.4) and H-1353 (23.1).

Table 5. Genotypic differences in cotton for specific leaf weight (mg/cm²) in ARS Dharwad and ARS Annigeri at different growth stages

Sl. No	Genotypes	60 DAS		90 DAS		125 DAS	
		Dharwad	Annigeri	Dharwad	Annigeri	Dharwad	Annigeri
1	GSHV-97/13	9.4 a-c	8.0 b-e	9.9 a-d	8.8 d-f	10.9 bc	9.3 e-g
2	CPD-446	8.3 hi	7.3 h-k	8.5 i-l	7.9 i-k	9.5 h-j	8.3 i-l
3	KH-155	9.2 b-e	7.8 d-g	9.3 e-g	8.7 d-f	10.4 de	9.2 fg
4	RAH-101	9.2 b-e	7.6 e-h	9.4 d-f	8.7 d-f	10.5 de	9.3 e-g
5	Sahana	9.3 a-d	8.4 ab	9.6 c-e	9.5 ab	10.7 cd	10.0 a-c
6	F-1861	8.2 hi	7.2 h-k	8.3 j-m	7.6 k-m	9.4 i-k	8.2 j-l
7	RAS-299-1	7.5 k-m	7.2 h-k	7.8 m-p	7.7 j-l	8.7 no	8.3 i-l
8	BS-30	7.6 kl	8.4 ab	8.2 k-n	9.2 bc	9.0 l-n	9.7 b-e
9	RCR-4	8.5 gh	7.4 g-j	8.7 h-k	8.0 h-j	9.8 gh	8.6 h-j
10	L-761	7.2 lm	6.9 k	7.4 p	7.3 m	8.6 o	7.6 m
11	GJHV-358	9.5 ab	7.4 g-j	10.1 a-c	8.3 gh	11.2 ab	8.7 hi
12	CPD-731	7.7 jk	7.8 d-g	8.3 j-m	8.7 d-f	9.1 k-m	9.2 fg
13	F-2228	8.9 d-f	7.9 c-f	9.0 f-i	8.7 d-f	10.0 fg	9.3 e-g
14	GSHV-01/26	8.0 ij	7.6 e-h	8.3 j-m	8.6 e-g	9.2 j-l	9.2 fg
15	CPD-750	9.5 ab	8.5 a	10.1 a-c	9.7 a	11.2 ab	10.2 a
16	CPD-431	7.3 k-m	7.5 f-i	7.5 op	8.6 e-g	8.7 no	9.2 fg
17	CPD-168	9.3 a-d	7.0 jk	9.7 b-e	7.4 lm	10.9 bc	7.9 lm
18	ARB-8908	9.2 b-e	8.2 a-d	9.5 d-f	9.0 cd	10.6 c-e	9.6 c-f
19	H-1353	7.5 k-m	7.4 g-j	7.9 m-p	8.1 hi	8.8 m-o	8.7 hi
20	LH-2076	7.4 k-m	7.1 i-k	7.7 n-p	7.6 k-m	8.7 no	8.2 j-l
21	KH-138	7.6 kl	7.2 h-k	8.0 l-o	7.7 j-l	9.0 l-n	8.2 j-l
22	CNH-120MB	9.6 ab	8.1 a-d	10.2 ab	8.8 d-f	11.3 a	9.4 d-g
23	RAH-30	7.2 lm	7.1 i-k	7.5 op	7.5 lm	8.6 o	8.0 k-m
24	GIHV-218	9.7 a	8.5 a	10.4 a	9.6 a	11.5 a	10.1 ab
25	L-763	7.1 m	7.0 jk	7.4 p	7.3 m	8.5 o	7.7 m
26	BS-279	9.0 c-e	8.3 a-c	9.2 e-h	9.2 bc	10.3 ef	9.7 b-e
27	KH-134	8.8 e-g	7.3 h-k	8.8 g-j	8.0 h-j	9.9 g	8.4 i-k
28	CPD-231	8.4 h	7.5 f-i	8.7 h-k	8.5 fg	9.7 g-i	9.0 gh
29	GJHV-477	9.6 ab	8.2 a-d	10.3 a	8.9 c-e	11.4 a	9.4 d-g
30	ARB-9701	8.6 f-h	8.4 ab	8.7 h-k	9.4 ab	9.9 g	9.8 a-d
Mean		8.5	7.7	8.8	8.4	9.9	8.9
SEm $\pm$		0.13	0.14	0.18	0.11	0.12	0.14

DAS= Days after sowing

Table 6. Genotypic differences in cotton for SPAD values at ARS Dharwad and ARS Annigeri at different growth stages

Sl. No.	Genotypes	60 DAS		90 DAS		125 DAS	
		Dharwad	Annigeri	Dharwad	Annigeri	Dharwad	Annigeri
1	GSHV-97/13	34.7 m-o	27.2 ef	39.0 i-l	32.7 i-n	31.3 g-m	26.0 k-o
2	CPD-446	36.4 e-i	26.6 ef	40.8 c-h	32.4 i-n	34.9 a-f	25.6 k-o
3	KH-155	37.2 bc	34.0 a-c	41.7 a-d	39.7 a-c	36.9 ab	32.3 cd
4	RAH-101	36.3 e-i	32.1 a-c	40.8 c-h	37.7 b-g	34.7 a-f	30.3 c-h
5	Sahana	36.7 c-g	32.4 a-c	41.1 a-f	38.2 a-e	36.1 a-d	31.1 c-f
6	F-1861	34.5 no	25.7 ef	38.9 jkl	31.1 l-o	31.1 h-m	24.4 m-p
7	RAS-299-1	35.3 k-m	27.3 ef	39.4 g-k	33.0 i-m	32.5 e-l	26.2 j-n
8	BS-30	37.5 ab	31.3 a-c	42.1 abc	36.7 d-h	37.0 ab	29.3 d-j
9	RCR-4	35.8 i-k	30.9 bc	40.1 d-j	35.2 f-i	33.8 b-i	28.4 f-k
10	L-761	31.3 u	24.4 ef	35.8 o	29.2 op	29.3 m	22.4 pq
11	GJHV-358	35.5 j-l	30.6 cd	39.8 e-k	34.6 h-k	33.4 c-j	27.8 g-l
12	CPD-731	35.0 l-n	27.5 e	39.3 h-k	33.6 i-l	31.9 f-m	26.8 i-n
13	F-2228	33.4 qr	26.2 ef	37.1 m-o	32.0 k-o	29.8 lm	25.2 l-p
14	GSHV-01/26	36.8 c-f	32.2 a-c	41.2 a-f	38.1 a-f	36.4 a-c	30.7 c-g
15	CPD-750	35.9 h-k	32.6 a-c	40.2 d-j	38.6 a-d	34.0 a-i	31.2 c-f
16	CPD-431	35.4 kl	27.8 de	39.6 f-k	34.2 h-k	33.2 d-k	27.4 h-m
17	CPD-168	36.9 b-e	30.6 cd	41.3 a-e	35.0 g-j	36.7 ab	28.2 f-l
18	ARB-8908	36.2 f-i	31.3 a-c	40.6 c-i	35.4 e-i	34.3 a-g	28.6 e-k
19	H-1353	32.6 s	25.0 ef	36.3 no	29.9 n-p	29.4 lm	23.1 o-q
20	LH-2076	33.0 rs	24.0 f	36.9 m-o	27.3 p	29.6 lm	20.4 q
21	KH-138	32.0 t	25.4 ef	36.2 no	30.6 m-o	30.5 j-m	23.9 n-p
22	CNH120MB	37.9 a	34.1 ab	42.6 ab	40.7 a	37.1 a	35.3 ab
23	RAH-30	36.1 g-j	31.2 a-c	40.4 d-j	35.3 e-i	34.2 a-h	28.5 e-k
24	GIHV-218	38.0 a	34.4 a	42.7 a	43.5 h-k	37.2 a	36.1 a
25	L-763	34.9 l-n	26.3 ef	39.3 h-k	32.2 j-n	31.5 g-m	25.5 k-o
26	BS-279	34.2 op	34.1 ab	38.4 k-m	40.6 ab	30.9 i-m	33.2 bc
27	KH-134	33.8 pq	25.8 ef	37.6 l-n	31.8 k-o	30.1 k-m	25.1 l-p
28	CPD-231	36.5 d-h	31.8 a-c	40.9 c-h	36.8 c-h	35.4 a-e	29.3 d-j
29	GJHV-477	36.7 c-g	32.0 a-c	41.0 b-g	37.0 c-h	35.8 a-d	29.4 d-i
30	ARB-9701	37.1 b-d	34.0 a-c	41.5 a-d	39.0 a-d	36.8 ab	31.6
Mean		35.5	29.6	39.75	35.1	33.5	28.1
SEm $\pm$		0.21	1.01	0.49	0.89	0.942	0.93

DOS = Days after sowing

4.1.1.3 Water potential (-MPa) (cf. Table 7)

In both locations in general the water potential status was decreased as the age crop growth up to 125 DAS. It has observed that at ARS, Dharwad location cotton genotypes maintained higher water potential status compared to ARS Annigeri at all the crop growth stages.

The mean leaf water potential values of the genotypes grown at ARS Dharwad was -0.97 MPa, -1.33 MPa, -2.05 MPa at 60 DAS, 90 DAS and 125 DAS respectively. Whereas in Annigeri it was -1.17 MPa, -1.46 MPa and -2.44 MPa at 60 DAS, 90 DAS and 125 DAS respectively.

4.1.1.3.1 At ARS Dharwad

The results indicated that significant difference among the genotypes for water potential values at different stages *i.e.*, 60 DAS, 90 DAS and 125 DAS.

At 60 DAS, the genotype GIHV-218 (-0.78 MPa) was maintained significantly higher water potential status over other genotypes; however, this was on par with CNH-120MB (-0.79 MPa), BS-30 (-0.80 MPa), KH-155 (-0.81 MPa) and ARB-9701 (-0.82 MPa). Followed by CPD-168 (-0.83 MPa), GSHV-01/26 (-0.85 MPa), Sahana (-0.87 MPa) and GJHV-477 (-0.89 MPa). While, L-761 (-1.18 MPa) was maintained lower water potential status and was on par with H-1353 (-1.14 MPa); followed by LH-2076 (-1.13 MPa), F-2228 (-1.12 MPa) and KH-134 (-1.10 MPa).

At 90 DAS, the genotype GIHV-218 (-1.10 MPa) was maintained significantly higher water potential status over other genotypes and was on par with CNH-120MB (-1.11 MPa), BS-30 (-1.13 MPa), KH-155 (-1.14 MPa) and ARB-9701 (-1.15 MPa) followed by CPD-168 (-1.17 MPa), GSHV-01/26 (-1.18 MPa). While, L-761 (-1.57 MPa) was maintained significantly lower water potential status and was on par with H-1353 (-1.55 MPa), LH-2076 (-1.54 MPa) and F-2228 (-1.53 MPa).

At 125 DAS, the genotype GIHV-218 (-1.80 MPa) was maintained significantly higher water potential status over other genotypes; however, this was on par with CNH-120MB (-1.80 MPa), BS-30 (-1.83 MPa), KH-155 (-1.84 MPa), ARB-9701 (-1.86 MPa), CPD-168 (-1.87 MPa) and GSHV-01/26 (-1.88 MPa). While, L-761 (-2.30 MPa) was maintained significantly lower water potential status and was on par with H-1353 (-2.28 MPa), LH-2076 (-2.27 MPa) and F-2228 (-2.24 MPa).

4.1.1.3.2 At ARS Annigeri

The results indicated that significant difference among the genotypes for water potential values at different stages *i.e.*, 60 DAS, 90 DAS and 125 DAS.

At 60 DAS, the genotypes GIHV-218 (-0.84 MPa), CNH-120MB (-0.87 MPa), KH-155 (-0.87 MPa), BS-279 (-0.87 MPa) and ARB-9701 (-0.89 MPa) was maintained significantly higher water potential status over other genotypes, followed by CPD-750 (-0.96 MPa) and Sahana (-0.97 MPa). While, LH-2076 (-1.45 MPa), L-761 (-1.44 MPa), H-1353 (-1.42 MPa), KH-138 (-1.42 MPa) and F-1861 (-1.42 MPa) maintained significantly lower water potential status among the genotypes followed by KH-134 (1.40 MPa).

At 90 DAS, the genotype GIHV-218 (-1.15 MPa) was maintained significantly higher water potential status over other genotypes; however, this was on par CNH-120MB (-1.17 MPa), BS-279 (-1.18 MPa), KH-155 (-1.19 MPa) and ARB-9701 (-1.20 MPa) followed by CPD-750 (-1.23 MPa), Sahana (-1.28 MPa), GSHV-01/26 (-1.32 MPa) and RAH-101 (-1.35 MPa). While, LH-2076 (-1.75 MPa), L-761 (-1.74 MPa), H-1353 (-1.73 MPa) and KH-138 (-1.72 MPa) maintained significantly lower water potential status among the genotypes followed by F-1861 (-1.69 MPa) and KH-134 (-1.68 MPa).

At 125 DAS the genotypes GIHV-218 (-1.84 MPa) maintained significantly higher water potential status over other genotypes, followed by CNH-120MB (-1.93 MPa), however, this was on par with BS-279 (-1.98 MPa) and KH-155 (-1.99 MPa) followed by ARB-9701 (-2.04 MPa). While, LH-2076 (-2.94 MPa), L-761 (-2.93 MPa), H-1353 (-2.92 MPa), KH-138 (-2.92 MPa) and F-1861 (-2.90 MPa) maintained significantly lower water potential status among the genotypes followed by KH-134 (-2.82 MPa).

4.1.1.4 Bio physical character

4.1.1.4.1 Rate of Photosynthesis ($\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) (cf. Table 8)

In both locations in general the rate of photosynthesis was significantly differed among the genotypes.

The mean photosynthesis rate of the genotypes grown at ARS Dharwad was higher ($31.4\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) compared to mean of photosynthesis rate of the genotypes grown at ARS Annigeri ($25.5\mu\text{ mol CO}_2/\text{m}^2/\text{s}$).

At ARS Dharwad: At 90 DAS there was significant difference recorded among cotton genotypes for rate of photosynthesis. Among the genotypes, GIHV-218 ($34.6\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) and CNH-120MB ($34.5\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) recorded highest photosynthesis rate, however, which were on par with BS-30 ($34.2\mu\text{ mol CO}_2/\text{m}^2/\text{s}$), KH-155 ($34.1\mu\text{ mol CO}_2/\text{m}^2/\text{s}$), ARB-9701 ($34.0\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) and CPD-

168 (33.6 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$). While the lowest photosynthesis rate recorded in L-761 (28.0 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), however, this was on par with H-1353 (28.2 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), LH-2076 (28.3 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), F-2228 (28.6) and KH-134 (29.2 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$).

At ARS Annigeri: There was significant difference among cotton genotypes for rate of photosynthesis recorded at 90 DAS. Among the cotton genotypes GIHV-218 (29.4 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) recorded significantly highest photosynthesis rate over other genotypes followed by BS-279 (28.3 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) and CNH-120MB (28.3 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) however, these were on par with KH-155 (27.8 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$). While the least photosynthesis rate recorded in LH-2076 (19.2 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) followed by L-761 (20.1 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), H-1353 (23.0 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), KH-138 (23.3 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), F-1861 (23.4 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) and KH-134 (23.6 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$).

4.1.1.4.2 Stomatal Conductance ($\mu\text{mol CO}_2/\text{m}^2/\text{s}$) (cf. Table 8)

In both locations in general the stomatal conductance was significantly differed among the genotypes. It has observed that at ARS, Dharwad location the cotton genotypes recorded higher stomatal conductance compared to ARS, ARS Annigeri.

The mean stomatal conductance of the cotton genotypes grown at ARS Dharwad was higher (0.30 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) compared to ARS Annigeri (0.23 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$).

At ARS Dharwad: At 90 DAS, among the cotton genotypes GIHV-218 (0.42 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) recorded highest stomatal conductance over other genotypes, followed by CNH-120MB (0.41 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) however, this was on par with BS-30 (0.41 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), KH-155 (0.4 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), ARB-9701 (0.38 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), CPD-168 (0.38 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) and 14 (0.37 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$). Whereas the lowest stomatal conductance was recorded in the genotypes L-761 (0.20 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) and H-1353 (0.21 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) however which were on par with LH-2076 (0.22 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), KH-134 (0.23 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), F-2228 (0.23 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), KH-138 (0.24 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), BS-279 (0.24 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), GSHV-97/13 (0.25 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) and L-763 (0.25 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$).

At ARS Annigeri: At 90 DAS, there was significant difference among cotton genotypes for stomatal conductance. Among the genotypes GIHV-218 (0.32 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) recorded significantly highest stomatal conductance over other genotypes and was on par with BS-279 (0.31 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), CNH-120MB (0.31 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), KH-155 (0.30 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) and ARB-9701 (0.29 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$); followed by CPD-750 (0.28 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$). Whereas the least stomatal conductance was recorded in LH-2076 (0.16 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), H-1353 (0.16 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) and L-761 (0.16 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) however, these were on par with KH-134 (0.17 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), F-2228 (0.17 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), CPD-446 (0.18 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), KH-138 (0.18 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), L-763 (0.18 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$), F-1861 (0.19 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$) and GSHV-97/13 (0.19 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$).

4.1.1.4.3 Rate of transpiration ($\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$) (cf. Table 9)

In both locations in general the rate of transpiration was significantly different among the genotypes. The mean rate of transpiration of the cotton genotypes grown at ARS Dharwad was higher (4.4 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$) compared to genotypes grown at ARS Annigeri (2.9 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$).

At ARS Dharwad: At 90 DAS, there was significant difference among the genotypes for rate of transpiration. Among the genotypes GIHV-218 (5.5 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$) recorded highest rate of transpiration however, this was on par with CNH-120MB (5.4 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), KH-155 (5.3 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), BS-30 (5.3 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), ARB-9701 (5.2 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), CPD-168 (5.2 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), GSHV-01/26 (5.2 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), Sahana (5.1 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$) and GJHV-477 (5.0 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$). Whereas the lowest rate of transpiration was recorded in L-761 (3.3 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$) over other genotypes however, this was on par with H-1353 (3.4 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), L-761 (3.3 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), F-2228 (3.5 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), KH-134 (3.6 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), KH-138 (3.7 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$) and BS-279 (3.8 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$).

At ARS Annigeri: At 90 DAS, there was significant difference among genotypes for rate of transpiration. Among the cotton genotypes GIHV-218 (3.8 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$) recorded significantly highest rate of transpiration, however, this was on par with BS-279 (3.7 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$) and CNH-120MB (3.7 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$) followed by KH-155 (3.5 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), ARB-9701 (3.4 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), CPD-750 (3.4 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), Sahana (3.3 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$), GJHV-477 (3.3 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$) and GSHV-01/26 (3.3 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$). Whereas, the least rate of transpiration was recorded in L-761 (2.0 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$) and was on par with H-1353 (2.1 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$) and LH-2076 (2.2 $\text{mmol H}_2\text{O}/\text{m}^2/\text{s}$).

Table 7. Genotypic differences in cotton for water potential (MPa) in Dharwad and Annigeri locations at different growth stages

Sl. No	Genotypes	60 DAS		90 DAS		125 DAS	
		Dharwad	Annigeri	Dharwad	Annigeri	Dharwad	Annigeri
1	GSHV-97/13	1.05 e-g	1.28 c-e	1.42 de	1.58 d-f	2.16 c-h	2.68 de
2	CPD-446	0.90 n-p	1.28 c-e	1.27 jk	1.59 d-f	1.99 l-n	2.71 cd
3	KH-155	0.81 s-u	0.87 l	1.14 no	1.19 rs	1.84 pq	1.99 no
4	RAH-101	0.91 m-p	1.05 j	1.28 i-k	1.35 no	2.01 k-m	2.15 kl
5	SAHANA	0.87 p-r	0.97 k	1.20 lm	1.28 pq	1.90 op	2.11 k-m
6	F-1861	1.06 d-f	1.42 a	1.45 cd	1.69 ab	2.17 c-g	2.90 a
7	RAS-299-1	1.01 g-j	1.27 de	1.38 e-g	1.56 e-g	2.13 e-h	2.65 de
8	BS-30	0.80 tu	1.12 i	1.13 no	1.41 k-n	1.83 pq	2.29 ij
9	RCR-4	0.97 j-l	1.16 g-i	1.34 gh	1.47 i-k	2.08 g-k	2.41 h
10	L-761	1.18 a	1.44 a	1.57 a	1.74 a	2.30 a	2.93 a
11	GJHV-358	0.99 i-k	1.20 fg	1.35 f-h	1.49 hi	2.11 f-j	2.54 fg
12	CPD-731	1.03 f-i	1.23 ef	1.40 d-f	1.54 f-h	2.14 d-h	2.61 ef
13	F-2228	1.12 bc	1.34 bc	1.53 ab	1.64 b-d	2.24 a-c	2.80 b
14	GSHV-01/26	0.85 q-s	1.04 j	1.18 mn	1.32 op	1.88 o-q	2.12 kl
15	CPD-750	0.95 k-m	0.96 k	1.33 g-i	1.23 qr	2.07 h-l	2.09 lm
16	CPD-431	1.00 h-j	1.22 e-g	1.37 e-g	1.51 g-i	2.12 e-i	2.56 fg
17	CPD-168	0.83 r-t	1.19 f-h	1.17 mn	1.48 h-j	1.87 o-q	2.51 g
18	ARB-8908	0.93 l-o	1.13 hi	1.30 h-j	1.42 j-m	2.03 j-m	2.35 hi
19	H-1353	1.14 ab	1.42 a	1.55 ab	1.73 a	2.28 ab	2.92 a
20	LH-2076	1.13 bc	1.45 a	1.54 ab	1.75 a	2.27 ab	2.94 a
21	KH-138	1.09 c-e	1.42 a	1.48 c	1.72 a	2.21 b-e	2.92 a
22	CNH-120MB	0.79 tu	0.87 l	1.11 o	1.17 rs	1.80 q	1.93 o
23	RAH-30	0.94 l-n	1.16 g-i	1.31 h-j	1.45 i-l	2.04 i-l	2.38 h
24	GIHV-218	0.78 u	0.84 l	1.10 o	1.15 s	1.80 q	1.84 p
25	L-763	1.04 f-h	1.33 cd	1.42 de	1.62 c-e	2.15 c-h	2.76 bc
26	BS-279	1.07 d-f	0.87 l	1.47 c	1.18 rs	2.20 b-f	1.98 no
27	KH-134	1.10 b-d	1.40 ab	1.50 bc	1.68 a-c	2.23 a-d	2.82 b
28	CPD-231	0.90 n-p	1.10 ij	1.24 kl	1.39 l-n	1.95 m-o	2.27 j
29	GJHV-477	0.89 o-q	1.05 j	1.23 kl	1.36 m-o	1.91 n-p	2.18 k
30	ARB-9701	0.82 s-u	0.89 l	1.15 m-o	1.20 rs	1.86 pq	2.04 mn
Mean		0.97	1.17	1.33	1.46	2.05	2.45
SEm $\pm$		0.015	0.022	0.017	0.022	0.028	0.025

DAS=Days after sowing

Table 8. Genotypic differences in cotton for rate of photosynthesis (μ mol $\text{CO}_2/\text{m}^2/\text{s}$), stomatal conductance (μ mol $\text{CO}_2/\text{m}^2/\text{s}$) in ARS Dharwad and ARS Annigeri at 90 DAS

Sl. No.	Genotypes	Rate of photosynthesis		Stomatal conductance	
		Dharwad	Annigeri	Dharwad	Annigeri
1	GSHV-97/13	30.2 i-k	25.2 lm	0.25 i-k	0.19 k-n
2	CPD-446	32.2 d-f	25.1 m	0.33 d-g	0.18 l-n
3	KH-155	34.1 ab	27.8 bc	0.40 a-c	0.30 a-c
4	RAH-101	32.0 d-g	26.8 d-g	0.32 e-g	0.26 d-g
5	Sahana	33.0 b-d	27.1 c-f	0.36 b-f	0.27 c-f
6	F-1861	30.0 i-k	23.4 no	0.25 i-k	0.19 k-n
7	RAS-299-1	30.9 f-j	25.3 k-m	0.26 h-k	0.20 j-m
8	BS-30	34.2 ab	26.4 e-i	0.41 ab	0.25 e-h
9	RCR-4	31.3 e-i	26.0 g-l	0.30 f-i	0.22 h-k
10	L-761	28.0 n	20.1 p	0.20 k	0.16 n
11	GJHV-358	31.2 e-i	25.7 i-m	0.28 g-j	0.21 i-l
12	CPD-731	30.8 g-j	25.4 k-m	0.25 i-k	0.20 j-m
13	F-2228	28.6 l-n	23.9 n	0.23 jk	0.17 mn
14	GSHV-01/26	33.1 b-d	27.0 d-f	0.37 a-e	0.27 c-f
15	CPD-750	31.6 e-h	27.2 c-e	0.31 f-h	0.28 b-e
16	CPD-431	31.1 f-i	25.5 j-m	0.28 g-j	0.21 i-l
17	CPD-168	33.6 a-c	25.9 h-m	0.38 a-d	0.22 h-k
18	ARB-8908	31.6 e-h	26.3 f-j	0.32 e-g	0.24 f-i
19	H-1353	28.2 mn	23.0 o	0.21 k	0.16 n
20	LH-2076	28.3 mn	19.2 q	0.22 jk	0.16 n
21	KH-138	29.4 k-m	23.3 no	0.24 i-k	0.18 l-n
22	CNH120MB	34.5 a	28.3 b	0.41 ab	0.31 ab
23	RAH-30	31.6 e-h	26.1 g-k	0.31 f-h	0.23 g-j
24	GIHV-218	34.6 a	29.4 a	0.42 a	0.32 a
25	L-763	30.5 h-k	24.0 n	0.25 i-k	0.18 l-n
26	BS-279	29.7 j-l	28.3 b	0.24 i-k	0.31 ab
27	KH-134	29.2 k-n	23.6 no	0.23 jk	0.17 mn
28	CPD-231	32.5 c-e	26.5 e-i	0.33 d-g	0.26 d-g
29	GJHV-477	32.9 b-d	26.7 d-h	0.35 c-f	0.26 d-g
30	ARB-9701	34.0 ab	27.4 cd	0.38 a-d	0.29 a-d
Mean		31.4	25.5	0.30	0.23
SEm $\pm$		0.41	0.25	0.02	0.01

DOS= Days after sowing

Table 9. Genotypic differences in cotton for rate of transpiration (mmol H₂O/m²/s), leaf temperature (°C) in ARS Dharwad and ARS Annigeri at 90 DAS

Sl. No.	Genotypes	Rate of transpiration		Leaf temperature	
		Dharwad	Annigeri	Dharwad	Annigeri
1	GSHV-97/13	3.9 j-m	2.6 j-l	30.1 a-e	31.3
2	CPD-446	4.8 c-g	2.5 k-m	29.1 g-k	31.3
3	KH-155	5.3 a-c	3.5 bc	28.6 jk	30.5
4	RAH-101	4.7 d-h	3.2 d-f	29.2 f-j	30.7
5	Sahana	5.1 a-e	3.3 c-e	29.0 h-k	30.6
6	F-1861	3.9 j-m	2.6 j-l	30.2 a-d	31.6
7	RAS-299-1	4.2 h-k	2.8 h-j	29.7 c-g	31.2
8	BS-30	5.3 a-c	3.1 e-g	28.6 jk	30.9
9	RCR-4	4.3 g-j	2.9 g-i	29.5 e-i	31.0
10	L-761	3.3 n	2.0 p	30.7 a	31.8
11	GJHV-358	4.2 h-k	2.8 h-j	29.6 d-h	31.0
12	CPD-731	4.0 i-l	2.7 i-k	29.8 b-f	31.2
13	F-2228	3.5 l-n	2.3 m-o	30.4 ab	31.5
14	GSHV-01/26	5.2 a-d	3.3 c-e	29.0 h-k	30.7
15	CPD-750	4.5 f-i	3.4 cd	29.5 e-i	30.6
16	CPD-431	4.2 h-k	2.8 h-j	29.7 c-g	31.1
17	CPD-168	5.2 a-d	2.9 g-i	28.9 h-k	31.0
18	ARB-8908	4.6 e-h	3.1 e-g	29.3 f-i	30.9
19	H-1353	3.4 mn	2.1 op	30.6 a	31.7
20	LH-2076	3.5 l-n	2.2 n-p	30.6 a	31.9
21	KH-138	3.7 k-n	2.5 k-m	30.4 ab	31.7
22	CNH120MB	5.4 ab	3.7 ab	28.5 k	30.4
23	RAH-30	4.5 f-i	3.0 f-h	29.4 f-i	30.9
24	GIHV-218	5.5 a	3.8 a	28.5 k	30.3
25	L-763	3.9 j-m	2.7 i-k	30.1 a-e	31.4
26	BS-279	3.8 j-n	3.7 ab	30.3 a-c	30.4
27	KH-134	3.6 l-n	2.4 l-n	30.4 ab	31.5
28	CPD-231	4.9 b-f	3.2 d-f	29.1 g-k	30.8
29	GJHV-477	5.0 a-f	3.3 c-e	29.0 h-k	30.8
30	ARB-9701	5.2 a-d	3.4 cd	28.8 i-k	30.5
Mean		4.4	2.9	29.6	31.0
SEm $\pm$		0.16	0.08	0.21	3.92

DOS= Days after sowing

4.1.1.4.4 Leaf temperature ($^{\circ}\text{C}$) (cf. Table 9)

At ARS Dharwad the leaf temperature was significantly differed among the genotypes but it was non-significant at ARS Annigeri. The mean leaf temperature of the cotton genotypes grown at ARS Dharwad was lower (29.6°C) compared to ARS Annigeri (31.0°C).

At ARS Dharwad: At 90 DAS, there was significant difference among cotton genotypes for leaf temperature observed. Among the cotton genotypes GIHV-218 (28.5°C) and CNH-120MB (28.5°C) maintained least leaf temperature and were on par with KH-155 (28.6°C), BS-30 (28.6°C), ARB-9701 (28.8°C), CPD-168 (28.9°C), GSHV-01/26 (29.0°C), Sahana (29.0°C), GJHV-477 (29.0°C), CPD-231 (29.1°C) and CPD-446 (29.1°C). Whereas L-761 (30.7°C), H-1353 (30.6°C) and LH-2076 (30.6°C) maintained significantly highest leaf temperature among all other genotypes, and was on par with F-2228 (30.4°C), KH-138 (30.4°C), KH-134 (30.4°C), BS-279 (30.3°C), F-1861 (30.2°C), GSHV-97/13 (30.1°C) and L-763 (30.1°C).

At ARS Annigeri: At 90 DAS, there was no significant difference among genotypes for leaf temperature. Among the genotypes GIHV-218 (30.3°C) maintained lowest leaf temperature followed by BS-279 (30.4°C), CNH-120MB (30.4°C), ARB-9701 (30.5°C), KH-155 (30.5°C), Sahana (30.6°C), CPD-750 (30.6°C), GSHV-01/26 (30.7°C) and RAH-101 (30.7°C). While LH-2076 (31.9°C) maintained highest leaf temperature followed by L-761 (31.8°C), H-1353 (31.7°C), KH-138 (31.7°C), F-1861 (31.6°C), F-2228 (31.5°C) and KH-134 (31.5°C).

4.1.1.5 Seed cotton yield (kg/ha) (cf. Table 10)

In both locations in general the seed cotton yield was significantly differed among the genotypes. The mean seed cotton yield of the genotypes grown at ARS Dharwad was higher (2155 kg/ha) compared to ARS Annigeri (1616 kg/ha).

At ARS Dharwad: Among the genotypes GIHV-218 (2566 kg/ha) and CNH-120MB (2541 kg/ha) recorded significantly highest seed cotton yield, however, these were on par with BS-30 (2488 kg/ha), KH-155 (2468 kg/ha), ARB-9701 (2459 kg/ha), CPD-168 (2432 kg/ha), BS-279 (2412 kg/ha), Sahana (2399 kg/ha), GJHV-477 (2387 kg/ha), CPD-231 (2358 kg/ha), CPD-446 (2343 kg/ha) and RAH-101 (2311 kg/ha). While L-761 (1500 kg/ha), H-1353 (1502 kg/ha), LH-2076 (1512 kg/ha) and F-2228 (1521 kg/ha) had recorded least and was on par with KH-134 (1554 kg/ha), KH-138 (1599 kg/ha), GSHV-01/26 (1700 kg/ha) and F-1861 (1748 kg/ha).

At ARS Annigeri: There was significant difference among genotypes for seed cotton yield. Among the genotypes GIHV-218 (2180 kg/ha), CNH-120MB (2172 kg/ha) and BS-279 (2164 kg/ha) recorded highest seed cotton yield, however, which, were on par with KH-155 (2128 kg/ha) and ARB-9701 (2093 kg/ha), followed by CPD-750 (2029 kg/ha). While LH-2076 had recorded lowest (1171 kg/ha) and was on par with L-761 (1187 kg/ha), H-1353 (1198 kg/ha), KH-138 (1213 kg/ha), F-1861 (1239 kg/ha) and KH-134 (1288 kg/ha).

4.1.2 Field experiment at ARS Dharwad to evaluate 600 cotton germplasm lines for drought tolerance

The results of the experiment conducted to evaluate the 600 *Gossypium hirsutum* germplasm lines for drought tolerance is presented in this section.

In 2011-12 *kharif* season, a field experiment was conducted at ARS, Dharwad, using 600 *Gossypium hirsutum* germplasm lines. These lines were evaluated for drought tolerance for biophysical and physiological traits.

4.1.2.1 ANOVA for 600 germplasm lines (Statistical analysis) (cf. Table 11.1)

The analysis of variance obtained by statistical analysis using Windostat version 8.5 software indicated the presence of significantly higher difference among the germplasm lines for all the characters studied viz., SPAD values, specific leaf weight and gas exchange parameters in the experiment consisting of 600 *G. hirsutum* germplasm lines Table 11.1. The results of the statistical analysis are as follows.

The ANOVA for augmented analysis for the physiological traits revealed that, there was highly significant genotypic difference observed for all the physiological traits viz., SLW, SPAD values at 90DAS, SPAD values at 120DAS, rate of photosynthesis, stomatal conductance and rate of transpiration. There was also highly significant difference was observed for the interaction between checks and varieties.

The CD value for comparing the any two entries across the block for the traits SLW, SPAD values at 90DAS, SPAD values at 120DAS, rate of photosynthesis, stomatal conductance and rate of transpiration were 0.147, 1.699, 0.134, 0.148, 0.013 and 0.149 respectively.

The CD value for comparison between checks and varieties for the traits SLW, SPAD values at 90DAS, SPAD values at 120DAS, rate of photosynthesis, stomatal conductance and rate of transpiration were 0.106, 1.225, 0.097, 0.107, 0.01 and 0.107 respectively.

(i) Specific leaf weight: Among the germplasm lines GPDWD597, GPDWD 613, GPDWD 606, GPDWD 622, GPDWD 608, GPDWD 591, GPDWD 619, GPDWD 621, GPDWD 612, GPDWD 603, GPDWD 617, GPDWD 589, GPDWD 501, GPDWD 520, GPDWD 554, GPDWD 484, GPDWD 585, GPDWD 561, GPDWD 607, GPDWD 592, GPDWD 596, GPDWD 610, GPDWD 614, GPDWD 611, GPDWD 601 and GPDWD 620 having significantly higher SLW and statistically on par for with each other. The SLW values were ranged from 10.8-8.8 mg/cm² with a mean of 9.8 mg/cm².

(ii) SPAD AT 90DAS : Among the germplasm lines GPDWD 607, GPDWD 592, GPDWD 596, GPDWD 610, GPDWD 614, GPDWD 611, GPDWD 601, GPDWD 620, GPDWD 616, GPDWD 598, GPDWD 624, GPDWD 593, GPDWD 604, GPDWD 618, GPDWD 599, GPDWD 590, GPDWD 602, GPDWD 623, GPDWD 615, GPDWD 605, GPDWD 609, GPDWD 600, GPDWD 594, GPDWD 595, GPDWD 597, GPDWD 613, GPDWD 606, GPDWD 622, GPDWD 608, GPDWD 591, GPDWD 619, GPDWD 621, GPDWD 612, GPDWD 603, GPDWD 617, GPDWD 589, GPDWD 501, GPDWD 520, GPDWD 554, GPDWD 484, GPDWD 585, GPDWD 561, GPDWD 479, GPDWD 560, GPDWD 477, GPDWD 505, GPDWD 410, GPDWD 489, GPDWD 570, GPDWD 532, GPDWD 411, GPDWD 562, GPDWD 391, GPDWD 362, GPDWD 580, GPDWD 374, GPDWD 557, GPDWD 574, GPDWD 567, GPDWD 513, GPDWD 559, GPDWD 588, GPDWD 476, GPDWD 506, GPDWD 538, GPDWD 436, GPDWD 544, GPDWD 552, GPDWD 555, GPDWD 573, GPDWD 512 and GPDWD 419 having significantly higher SPAD values and were statistically on par each other. The SPAD values were ranged from 45.1-35.5 with a mean of 39.4.

(iii) SPAD at110DAS: Among the germplasm lines GPDWD 607, GPDWD 592, GPDWD 596, GPDWD 610, GPDWD 614, GPDWD 611, GPDWD 601, GPDWD 620, GPDWD 616 and GPDWD 598 having significantly higher SPAD values and statistically on par with each other. The SPAD values were ranged from 50.1-41.6 with a mean of 46.0.

(iv) Rate of photosynthesis: Among the germplasm lines GPDWD 607, GPDWD 592, GPDWD 596, GPDWD 610, GPDWD 614, GPDWD 611, GPDWD 601, GPDWD 620, GPDWD 616, GPDWD 598, GPDWD 624, GPDWD 593, GPDWD 602, GPDWD 623, GPDWD 615 having significantly higher photosynthesis rate and statistically on par each other. The rate of photosynthesis values ranged from 33.4-27.6 μ mol CO₂/ m²/s with a mean of 30.6 μ mol CO₂/ m²/s.

(v) Stomatal conductance: Among the germplasm lines GPDWD 607, GPDWD 592, GPDWD 596, GPDWD 610, GPDWD 614, GPDWD 611, GPDWD 601, GPDWD 620, GPDWD 616, GPDWD 598, GPDWD 624, GPDWD 593, GPDWD 602, GPDWD 623, GPDWD 615, GPDWD 605, GPDWD 609, GPDWD 600, GPDWD 604, GPDWD 618, GPDWD 599, GPDWD 590, GPDWD 594, GPDWD 595, GPDWD 597, GPDWD 613, GPDWD 606, GPDWD 622, GPDWD 608 having significantly higher conductance and statistically on par each other. The stomatal conductance values ranged from 0.45-0.26 μ mol CO₂/m²/s with a mean of 0.35 μ mol CO₂/m²/s.

(vi) Rate of transpiration: Among the germplasm lines GPDWD 620, GPDWD 616, GPDWD 598, GPDWD 600, GPDWD 604, GPDWD 618, GPDWD 599, GPDWD 590, GPDWD 594, GPDWD 607, GPDWD 592, GPDWD 596, GPDWD 610, GPDWD 614, GPDWD 611, GPDWD 601, GPDWD 595, GPDWD 597, GPDWD 613, GPDWD 606, GPDWD 622, GPDWD 608, GPDWD 591, GPDWD 624, GPDWD 593, GPDWD 602, GPDWD 623, GPDWD 615, GPDWD 605, GPDWD 609, GPDWD 501, GPDWD 520, GPDWD 554, GPDWD 484, GPDWD 585, GPDWD 561 having significantly higher transpiration rate and statistically on par each other. The rate of transpiration values ranged from 6.3-3.7 m mol H₂O/ m²/s with a mean of 5.12 m mol H₂O/ m²/s.

4.1.2.1 Grouping of the germplasm lines

Based on the highest to lowest values recocorded for individual traits these germ plasm lines were further divided in to three group's containing 200 germplasm lines each which were named as best performer's, moderate performer's and least performer's. The best performers genotypes group having highest values of above mentioned physiological traits and least least performers having least

values while, moderate performers have in between these values. These performers's group varies for different physiological traits.

4.1.2.1.1 SPAD values (cf. Table 11.2)

In general the SPAD values were increased with the age crop growth up to 110 DAS.

At 90 DAS the mean SPAD values among the 600 cotton germplasm lines were ranged from 43.1 to 36.3. Among 600 germplasm lines, the best performer's 200 germplasm lines recorded highest SPAD values ranged from 45.1 to 40.4 and the mean was 43.1.

In moderate performer's 200 germplasm lines, SPAD values were ranged from 40.3 to 37.5 and the mean was 38.8. Whereas in least performer's 200 germplasm lines, it ranged from 37.4 to 35.5 and the mean was 36.3.

At 110 DAS the mean SPAD values of the 600 cotton germplasm lines were ranged from 50.1 to 41.6. Among 600 germplasm lines, the best performer's 200 germplasm lines recorded highest SPAD values ranged from 50.1 to 47.5 and the mean was 48.9.

In moderate performer's 200 germplasm lines, SPAD values were ranged from 47.4 to 44.6 and the mean was 45.9. Whereas in least performer's 200 germplasm lines, SPAD values were ranged from 44.4 to 41.6 and the mean was 43.2.

4.1.2.1.2 Specific leaf weight (SLW) (mg/cm^2) (cf. Table 11.3)

At 90 DAS the mean SLW (mg/cm^2) of the 600 cotton germplasm lines were ranged from 10.8 mg/cm^2 to 8.8 mg/cm^2 . Among 600 germplasm lines, the best performer's 200 germplasm lines recorded highest SLW ranged from 10.8 mg/cm^2 to 10.2 mg/cm^2 and the mean was 10.5 mg/cm^2 .

In moderate performer's 200 germplasm lines, SLW were ranged from 10.1 mg/cm^2 to 9.5 mg/cm^2 and the mean SLW was 9.8 mg/cm^2 . Whereas in least performer's 200 germplasm lines, SLW was ranged from 9.4 mg/cm^2 to 8.8 mg/cm^2 and the mean was 9.1 mg/cm^2 .

4.1.2.1.3 Rate of photosynthesis ($\mu\text{mol CO}_2/\text{m}^2/\text{s}$) (cf. Table 11.4)

At 90 DAS the mean rate of photosynthesis ($\mu\text{mol CO}_2/\text{m}^2/\text{s}$) of the 600 cotton germplasm lines was ranged from 33.4 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ to 27.6 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$.

Among 600 germplasm lines, the best performer's 200 germplasm lines recorded highest rate of photosynthesis ranged from 33.4 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ to 31.6 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ and the mean was 32.6 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$.

In moderate performer's 200 germplasm lines, rate of photosynthesis ranged from 31.4 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ to 29.6 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ and the mean was 30.5 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$. Whereas in least performer's 200 germplasm lines, rate of photosynthesis were ranged from 29.4 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ to 27.6 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ and the mean was 28.6 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$.

4.1.2.1.4 Stomatal Conductance ($\mu\text{mol CO}_2/\text{m}^2/\text{s}$) (cf. Table 11.4)

At 90 DAS the mean stomatal conductance ($\mu\text{mol CO}_2/\text{m}^2/\text{s}$) of the 600 cotton germplasm lines were ranged from 0.45 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ to 0.26 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$.

Among 600 germplasm lines, the best performer's 200 germplasm lines recorded highest stomatal conductance ranged from 0.45 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ to 0.38 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ and the mean was 0.41 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$.

In moderate performer's 200 germplasm lines, stomatal conductance were ranged from 0.37 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ to 0.32 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ and the mean was 0.35 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$. Whereas in least performer's 200 germplasm lines, it ranged from 0.31 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ to 0.26 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ and the mean was 0.29 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$.

4.1.2.1.5 Rate of transpiration ($\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$) (cf. Table 11.5 and 11.6)

At 90 DAS the mean rate of transpiration of the 600 cotton germplasm lines ranged from 6.3 $\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$ to 3.7 $\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$.

Among 600 germplasm lines, the best performer's 200 germplasm lines recorded highest rate of transpiration ranged from 6.3 $\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$ to 5.7 $\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$ and the mean was 6.05 $\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$.

In moderate performer's 200 germplasm lines, rate of transpiration were ranged from 5.6 $\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$ to 4.8 $\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$ and the mean was 5.25 $\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$. Whereas in least performer's 200 germplasm lines, it ranged from 4.7 $\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$ to 3.7 $\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$ and the mean was 4.23 $\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$.

Performance of the germplasm lines for different physiological traits at ARS Dharwad is presented in the pooled table Table 11.6.

Table 10. Genotypic differences in cotton genotypes for seed cotton yield (kg/ha) at Dharwad and Annigeri locations

Sl. No.	Genotypes	Seed cotton yield (kg/ha)	
		Dharwad	Annigeri
1	GSHV-97/13	1770 j-l	1384 j-l
2	CPD-446	2343 c-e	1343 k-m
3	KH-155	2468 a	2128 ab
4	RAH-101	2311 d-f	1805 d
5	Sahana	2399 cd	1952 c
6	F-1861	1748 j-m	1239 m-p
7	RAS-299-1	1971 h-j	1437 i-k
8	BS-30	2488 a	1714 d-f
9	RCR-4	2110 f-h	1547 g-i
10	L-761	1500 n	1187 op
11	GJHV-358	2060 g-i	1492 h-j
12	CPD-731	1913 h-k	1451 i-k
13	F-2228	1521 mn	1311 l-o
14	GSHV-01/26	1700 c	1920 c
15	CPD-750	2137 f-h	2029 bc
16	CPD-431	1999 g-i	1483 h-j
17	CPD-168	2432 bc	1471 ij
18	ARB-8908	2229 e-g	1645 e-g
19	H-1353	1502 n	1198 op
20	LH-2076	1512 n	1171 p
21	KH-138	1599 l-n	1213 n-p
22	CNH-120MB	2541 a	2172 a
23	RAH-30	2213 e-g	1601 f-h
24	GIHV-218	2566 a	2180 a
25	L-763	1862 i-k	1337 k-n
26	BS-279	2412 k-n	2164 a
27	KH-134	1554 l-n	1288 l-p
28	CPD-231	2358 cd	1734 de
29	GJHV-477	2387 cd	1778 d
30	ARB-9701	2459 ab	2093 ab
Mean		2155	1616
SEm $\pm$		72.25	39.91

Table 11.1. ANOVA for augmented RBD for physiological traits for germplasm lines

Augmented R.B.D. ANOVA (Summary)							
	DF	SLW (mg/cm ²) at 90 DAS	SPAD at 90 DAS	SPAD at 110 DAS	Rate of photosynthesis (μ mol CO ₂ / m ² /s) at 90 DAS	Rate of stomatal conductance (μ mol CO ₂ /m ² /s) at 90DAS	Rate of transpiration (m mol H ₂ O/ m ² /s) at 90 DAS
Block (eliminating Check+Var.)	24	0.001	0.002	0.001	0.002	0.001	0.001
Entries (ignoring Blocks)	605	0.544 ***	14.175 ***	8.733 ***	4.439 ***	0.005 ***	0.867 ***
Checks	5	0.036 ***	4.787 ***	2.141 ***	0.174 ***	0.000 ***	0.022 ***
Varieties	599	0.358 ***	8.535 ***	5.944 ***	2.914 ***	0.003 ***	0.632 ***
Checks vs. Varieties	1	114.700***	3439.838***	1712.491***	939.121***	1.197 ***	145.729***
ERROR	120	0.002	0.315	0.002	0.002	0.001	0.002
Ci - Cj	1	0.027	0.315	0.025	0.027	0.002	0.028
BiVi - BiVj	1	0.136	1.573	0.124	0.137	0.012	0.138
BiVi - BjVj	1	0.147	1.699	0.134	0.148	0.013	0.149
Ci - Vi	1	0.106	1.225	0.097	0.107	0.01	0.107
Overall mean		9.8	39.4	46.0	30.6	0.35	5.12
Overall range		10.8-8.8	45.1-35.5	50.1-41.6	33.4-27.6	0.45-0.26	6.3-3.7

Table 11.2. Genotypic differences in cotton genotypes for SPAD values at ARS Dharwad for 600 germplasm lines at different growth stages

Sl. No.	Best performers				Moderate performers				Least performers			
	90 DAS		110 DAS		90 DAS		110 DAS		90 DAS		110 DAS	
	GN	SPAD value	GN	SPAD value	GN	SPAD value	GN	SPAD value	GN	SPAD value	GN	SPAD value
1	607	45.1	618	50.1	409	40.3	461	47.4	503	37.4	313	44.4
2	592	45.1	599	50.1	541	40.3	462	47.4	445	37.3	448	44.4
3	596	45.1	590	50.1	492	40.3	493	47.4	87	37.3	194	44.4
4	610	45.1	602	50.1	440	40.3	214	47.4	275	37.3	218	44.4
5	614	45.0	623	50.1	441	40.3	350	47.4	173	37.3	82	44.4
6	611	45.0	615	50.0	553	40.3	434	47.4	45	37.3	311	44.4
7	601	45.0	605	50.0	153	40.3	517	47.4	384	37.2	172	44.4
8	620	45.0	609	50.0	432	40.2	388	47.4	39	37.2	240	44.4
9	616	45.0	600	50.0	276	40.2	469	47.4	77	37.1	442	44.4
10	598	45.0	594	50.0	253	40.2	156	47.4	204	37.1	3	44.4
11	624	45.0	595	49.9	369	40.2	578	47.4	219	37.1	125	44.4
12	593	44.9	597	49.9	414	40.2	435	47.4	212	37.1	111	44.4
13	604	44.9	613	49.9	246	40.2	490	47.4	85	37.0	428	44.3
14	618	44.9	606	49.9	423	40.2	328	47.4	47	37.0	201	44.3
15	599	44.9	607	49.9	317	40.2	449	47.4	221	37.0	470	44.3
16	590	44.9	592	49.9	209	40.2	569	47.3	228	37.0	534	44.3
17	602	44.9	596	49.9	349	40.2	321	47.3	22	36.8	232	44.3
18	623	44.9	610	49.9	519	40.1	401	47.3	21	36.8	266	44.3
19	615	44.9	614	49.8	348	40.1	330	47.3	458	36.8	403	44.3
20	605	44.8	611	49.8	308	40.1	400	47.3	215	36.8	186	44.3
21	609	44.8	601	49.8	341	40.1	511	47.0	456	36.7	245	44.3
22	600	44.8	620	49.8	510	40.1	453	47.0	267	36.7	264	44.3
23	594	44.8	616	49.8	518	40.1	42	47.0	252	36.7	415	44.3
24	595	44.8	598	49.8	359	40.1	331	46.9	418	36.7	161	44.3
25	597	44.8	624	49.8	213	40.1	233	46.9	1	36.7	242	44.3
26	613	44.8	593	49.8	326	40.1	365	46.8	29	36.7	366	44.3
27	606	44.8	604	49.8	405	40.1	486	46.8	285	36.7	327	44.3
28	622	44.5	621	49.8	333	40.1	504	46.8	303	36.7	37	44.2
29	608	44.5	419	49.7	177	40.1	360	46.8	23	36.7	280	44.2
30	591	44.5	421	49.7	353	40.1	254	46.7	248	36.7	57	44.2
31	619	44.2	568	49.7	376	40.1	474	46.7	103	36.7	103	44.2
32	621	44.3	371	49.7	385	40.1	488	46.7	146	36.6	148	44.2
33	612	44.3	586	49.7	427	40.0	556	46.7	36	36.6	188	44.2
34	603	44.3	498	49.7	288	40.0	433	46.7	370	36.6	79	44.2
35	617	44.3	547	49.7	310	40.0	346	46.7	17	36.6	167	44.2
36	589	44.3	525	49.7	539	40.0	226	46.7	452	36.6	217	44.2
37	501	44.3	545	49.7	281	40.0	314	46.7	34	36.6	20	44.2
38	520	44.3	487	49.7	344	40.0	516	46.6	84	36.6	28	44.2
39	554	44.3	399	49.7	543	40.0	312	46.6	96	36.6	141	44.2
40	484	44.2	582	49.7	527	39.9	378	46.6	144	36.6	25	44.2
41	585	44.2	514	49.7	437	39.9	443	46.6	124	36.6	351	44.2
42	561	44.2	337	49.7	237	39.8	135	46.6	182	36.6	352	44.2
43	479	44.2	619	49.7	255	39.8	168	46.6	193	36.6	19	44.2
44	560	44.2	479	49.7	298	39.8	238	46.6	273	36.6	120	44.1
45	477	44.2	560	49.7	556	39.8	301	46.6	412	36.6	224	44.1
46	505	44.2	477	49.7	394	39.7	426	46.5	24	36.6	24	44.1
47	410	44.2	505	49.7	203	39.7	222	46.5	205	36.6	205	44.1
48	489	44.1	410	49.7	416	39.7	385	46.5	402	36.6	402	44.1

Contd....

Sl. No.	Best performers				Moderate performers				Least performers			
	90 DAS		110 DAS		90 DAS		110 DAS		90 DAS		110 DAS	
	GN	SPAD value	GN	SPAD value	GN	SPAD value	GN	SPAD value	GN	SPAD value	GN	SPAD value
49	570	44.1	489	49.6	152	39.7	281	46.5	27	36.6	27	44.1
50	532	44.1	570	49.6	397	39.7	344	46.5	44	36.5	44	44.1
51	411	44.1	532	49.6	457	39.7	457	46.5	9	36.5	73	44.1
52	562	44.0	411	49.6	256	39.7	256	46.4	148	36.5	431	44.1
53	391	44.0	562	49.6	306	39.7	306	46.4	188	36.5	86	44.0
54	362	44.0	391	49.6	523	39.7	523	46.4	79	36.5	112	44.0
55	580	44.0	362	49.6	192	39.7	192	46.4	167	36.5	78	44.0
56	374	44.0	580	49.6	296	39.7	296	46.4	217	36.5	93	43.9
57	557	44.0	374	49.6	413	39.7	413	46.4	20	36.5	97	43.9
58	574	43.8	557	49.6	335	39.7	335	46.4	28	36.5	15	43.8
59	567	43.8	574	49.6	278	39.6	278	46.4	141	36.5	91	43.8
60	513	43.8	567	49.6	450	39.6	450	46.4	25	36.5	33	43.8
61	559	43.8	513	49.6	338	39.6	338	46.4	351	36.5	81	43.7
62	588	43.7	559	49.6	536	39.5	536	46.3	73	36.4	107	43.7
63	476	43.7	588	49.6	223	39.5	223	46.3	431	36.4	272	43.7
64	506	43.7	476	49.6	387	39.5	387	46.3	86	36.4	32	43.7
65	538	43.7	506	49.5	318	39.5	318	46.3	112	36.4	143	43.7
66	436	43.6	538	49.5	363	39.4	363	46.3	78	36.4	268	43.7
67	544	43.6	436	49.5	373	39.4	373	46.3	93	36.4	35	43.7
68	552	43.6	544	49.5	316	39.4	316	46.3	97	36.4	293	43.7
69	555	43.5	552	49.5	393	39.4	393	46.3	15	36.4	290	43.7
70	573	43.5	555	49.5	447	39.3	447	46.3	91	36.4	297	43.6
71	512	43.5	573	49.5	312	39.3	455	46.3	33	36.4	63	43.6
72	419	43.5	512	49.5	378	39.3	575	46.2	81	36.4	99	43.6
73	421	43.4	612	49.5	443	39.2	265	46.2	107	36.4	162	43.6
74	568	43.4	603	49.5	135	39.2	394	46.2	272	36.4	165	43.6
75	371	43.4	617	49.5	168	39.2	203	46.2	32	36.4	9	43.5
76	586	43.4	589	49.5	238	39.1	416	46.2	143	36.4	146	43.5
77	498	43.4	501	49.5	301	39.1	583	46.2	268	36.4	36	43.5
78	524	43.4	520	49.5	426	39.0	483	46.2	35	36.4	370	43.5
79	526	43.3	554	49.5	222	39.0	176	46.0	293	36.3	17	43.5
80	572	43.3	484	49.2	336	38.9	332	46.0	290	36.3	452	43.5
81	262	43.3	585	49.2	455	38.8	152	46.0	297	36.3	34	43.4
82	471	43.3	561	49.2	575	38.8	397	45.9	63	36.3	84	43.4
83	579	43.3	622	49.2	265	38.8	405	45.9	99	36.3	96	43.4
84	180	43.3	608	49.2	433	38.8	333	45.9	162	36.3	144	43.4
85	475	43.3	591	49.2	346	38.8	177	45.8	165	36.3	124	43.4
86	547	43.3	375	49.2	226	38.8	353	45.8	352	36.3	182	43.4
87	525	43.3	531	49.2	314	38.8	376	45.8	19	36.3	193	43.4
88	545	43.3	576	49.2	516	38.8	336	45.8	120	36.3	273	43.4
89	487	43.3	406	49.2	546	38.8	546	45.8	224	36.3	412	43.4
90	399	43.3	478	49.2	300	38.8	300	45.7	225	36.3	225	43.4
91	582	43.3	356	49.2	345	38.8	345	45.7	211	36.3	211	43.3
92	514	43.3	364	49.2	181	38.8	181	45.7	322	36.3	322	43.3
93	337	43.3	473	49.2	150	38.7	150	45.7	56	36.3	56	43.3
94	375	43.3	389	49.2	396	38.7	396	45.7	110	36.3	110	43.3
95	531	43.3	540	49.2	241	38.7	241	45.7	169	36.3	169	43.3
96	576	43.3	558	49.2	309	38.7	309	45.7	8	36.3	8	43.3
97	406	43.3	550	49.2	368	38.7	368	45.7	119	36.3	109	43.3
98	478	43.3	524	49.2	195	38.6	195	45.7	65	36.3	65	43.2
99	356	43.3	526	49.2	289	38.6	289	45.7	136	36.3	136	43.2
100	364	43.3	572	49.2	339	38.6	339	45.7	2	36.3	2	43.2

Contd....

Sl. No.	Best performers				Moderate performers				Least performers			
	90 DAS		110 DAS		90 DAS		110 DAS		90 DAS		110 DAS	
	GN	SPAD value	GN	SPAD value	GN	SPAD value	GN	SPAD value	GN	SPAD value	GN	SPAD value
101	473	43.3	262	49.2	230	38.6	230	45.6	49	36.3	49	43.2
102	389	43.2	471	49.0	138	38.6	138	45.6	52	36.3	52	43.2
103	540	43.2	579	49.0	132	38.6	132	45.6	395	36.3	395	43.2
104	558	43.2	180	49.0	277	38.5	277	45.6	104	36.3	104	43.2
105	550	43.2	475	49.0	187	38.5	187	45.6	422	36.2	422	43.1
106	565	43.2	565	49.0	354	38.5	354	45.6	130	36.2	130	43.1
107	530	43.2	530	48.9	323	38.5	323	45.6	439	36.2	439	43.1
108	584	43.2	584	48.9	258	38.5	258	45.6	250	36.2	250	43.1
109	466	43.2	466	48.9	286	38.5	286	45.6	377	36.2	377	43.1
110	587	43.1	587	48.8	242	38.4	535	45.6	48	36.2	48	43.1
111	522	43.1	522	48.8	366	38.4	139	45.6	101	36.2	101	43.1
112	537	43.1	537	48.8	428	38.4	430	45.6	357	36.2	357	43.0
113	495	43.1	495	48.8	201	38.4	247	45.6	108	36.2	108	43.0
114	521	43.1	521	48.8	470	38.4	355	45.6	31	36.2	31	43.0
115	361	43.1	380	48.8	534	38.4	251	45.6	89	36.2	89	43.0
116	497	43.1	325	48.8	232	38.3	429	45.6	106	36.2	106	43.0
117	454	43.0	367	48.8	266	38.3	121	45.4	67	36.2	67	43.0
118	529	43.0	564	48.6	403	38.3	468	45.4	207	36.2	207	43.0
119	425	43.0	509	48.6	41	38.3	236	45.4	10	36.2	145	43.0
120	486	43.0	420	48.6	460	38.3	496	45.4	58	36.2	128	42.9
121	504	43.0	482	48.5	140	38.3	38	45.4	50	36.2	305	42.9
122	360	43.0	408	48.5	160	38.2	324	45.4	191	36.2	46	42.9
123	254	42.9	446	48.5	535	38.2	320	45.4	94	36.2	66	42.9
124	474	42.9	551	48.5	139	38.2	185	45.4	202	36.2	249	42.9
125	488	42.9	392	48.5	430	38.2	244	45.4	279	36.2	7	42.9
126	435	42.8	175	48.5	247	38.2	83	45.4	117	36.2	51	42.9
127	490	42.8	407	48.5	355	38.2	53	45.4	190	36.2	149	42.9
128	328	42.8	451	48.5	251	38.2	123	45.4	54	36.2	542	42.9
129	449	42.8	491	48.5	429	38.2	234	45.4	174	36.2	271	42.8
130	569	42.7	563	48.5	257	38.2	269	45.4	189	36.1	302	42.8
131	581	42.7	581	48.3	270	38.1	60	45.4	59	36.1	163	42.8
132	502	42.6	502	48.3	329	38.1	261	45.4	80	36.1	4	42.8
133	424	42.6	424	48.3	304	38.1	41	45.4	13	36.1	100	42.8
134	507	42.6	507	48.2	464	38.1	460	45.3	114	36.1	438	42.8
135	548	42.5	548	48.2	415	38.1	140	45.3	145	36.1	40	42.8
136	463	42.5	566	48.1	161	38.1	160	45.3	128	36.1	260	42.8
137	528	42.5	342	48.1	299	38.1	299	45.3	70	36.1	5	42.8
138	381	42.4	404	48.0	508	38.1	508	45.3	282	36.1	184	42.8
139	515	42.4	472	48.0	216	38.1	216	45.3	95	36.1	76	42.7
140	577	42.2	494	48.0	235	38.1	235	45.3	229	36.1	122	42.7
141	380	42.2	379	47.9	239	38.1	239	45.3	198	36.1	113	42.7
142	325	42.2	480	47.9	485	38.1	485	45.3	26	36.1	343	42.7
143	367	42.2	467	47.9	340	38.1	340	45.3	62	36.1	444	42.7
144	564	42.1	499	47.9	183	38.1	183	45.3	292	36.1	88	42.7
145	509	42.1	500	47.9	481	38.1	481	45.3	6	36.1	71	42.7
146	420	42.0	533	47.9	200	38.0	200	45.1	40	36.1	12	42.6
147	482	42.0	459	47.9	220	38.0	220	45.1	260	36.1	75	42.6
148	408	42.0	319	47.8	196	38.0	196	45.1	5	36.1	243	42.6
149	446	42.0	386	47.8	284	38.0	284	45.1	184	36.1	263	42.6
150	551	41.9	390	47.8	11	38.0	11	45.1	76	36.1	98	42.6
151	392	41.9	571	47.8	291	38.0	291	45.1	122	36.1	294	42.6
152	175	41.9	383	47.8	206	38.0	206	45.1	113	36.1	74	42.6

Contd....

Sl. No.	Best performers				Moderate performers				Least performers			
	90 DAS		110 DAS		90 DAS		110 DAS		90 DAS		110 DAS	
	GN	SPAD value	GN	SPAD value	GN	SPAD value	GN	SPAD value	GN	SPAD value	GN	SPAD value
153	407	41.8	334	47.8	358	38.0	358	45.0	343	36.1	109	42.6
154	566	41.7	382	47.8	347	37.9	347	45.0	444	36.1	259	42.5
155	342	41.7	463	47.8	208	37.9	208	45.0	88	36.1	117	42.5
156	404	41.7	528	47.7	549	37.9	549	45.0	71	36.1	190	42.4
157	472	41.7	381	47.7	43	37.9	43	45.0	12	36.1	54	42.4
158	494	41.7	515	47.7	126	37.9	126	45.0	75	36.0	174	42.4
159	379	41.7	577	47.7	30	37.9	30	45.0	243	36.0	189	42.4
160	480	41.6	361	47.7	60	37.8	16	45.0	263	36.0	59	42.4
161	467	41.6	497	47.7	261	37.8	158	45.0	98	36.0	80	42.4
162	499	41.6	454	47.7	186	37.8	257	45.0	294	36.0	13	42.4
163	500	41.5	529	47.6	245	37.8	270	45.0	74	36.0	114	42.4
164	533	41.5	425	47.6	264	37.8	329	45.0	109	36.0	10	42.4
165	459	41.4	510	47.6	14	37.8	304	45.0	259	36.0	58	42.4
166	319	41.3	518	47.6	307	37.6	464	45.0	4	36.0	50	42.3
167	386	41.3	359	47.6	313	37.6	456	44.9	100	36.0	191	42.3
168	390	41.3	213	47.6	448	37.6	267	44.9	438	36.0	94	42.3
169	571	41.2	326	47.6	194	37.6	252	44.9	90	36.0	202	42.3
170	383	41.2	543	47.6	218	37.6	418	44.9	61	36.0	279	42.3
171	334	41.2	527	47.6	16	37.6	1	44.9	69	36.0	70	42.3
172	382	41.1	437	47.6	158	37.6	29	44.9	92	36.0	282	42.3
173	462	41.1	237	47.6	121	37.6	285	44.9	64	36.0	95	42.3
174	493	41.1	255	47.6	468	37.6	303	44.9	116	36.0	229	42.3
175	214	41.1	298	47.6	236	37.6	228	44.9	115	36.0	198	42.2
176	350	41.0	209	47.6	496	37.6	22	44.9	147	36.0	26	42.2
177	434	41.0	349	47.6	38	37.6	21	44.9	315	36.0	62	42.2
178	517	41.0	409	47.6	324	37.6	458	44.8	102	35.9	292	42.2
179	388	40.9	541	47.6	320	37.6	287	44.8	105	35.9	6	42.2
180	469	40.9	492	47.6	185	37.6	274	44.8	72	35.9	90	42.2
181	156	40.8	440	47.6	244	37.5	503	44.8	295	35.9	61	42.2
182	578	40.8	441	47.6	83	37.5	173	44.8	68	35.9	69	42.0
183	451	40.8	553	47.6	53	37.5	45	44.8	127	35.9	92	42.0
184	491	40.8	276	47.5	123	37.5	384	44.8	283	35.9	64	42.0
185	563	40.7	253	47.5	234	37.5	39	44.8	118	35.9	116	42.0
186	321	40.7	369	47.5	269	37.5	77	44.8	142	35.8	115	41.9
187	401	40.6	414	47.5	82	37.5	204	44.8	18	35.8	147	41.9
188	330	40.6	246	47.5	311	37.5	219	44.8	417	35.8	315	41.9
189	400	40.5	423	47.5	172	37.5	212	44.8	197	35.8	102	41.9
190	511	40.5	317	47.5	240	37.5	23	44.8	305	35.8	105	41.9
191	453	40.4	153	47.5	442	37.5	248	44.7	46	35.8	72	41.8
192	42	40.4	432	47.5	3	37.5	85	44.7	66	35.6	295	41.8
193	331	40.4	519	47.5	125	37.5	47	44.7	249	35.6	68	41.8
194	233	40.4	348	47.5	111	37.5	221	44.7	7	35.6	127	41.8
195	365	40.4	308	47.5	327	37.5	445	44.6	51	35.6	283	41.7
196	461	40.4	341	47.5	37	37.5	87	44.6	149	35.5	118	41.7
197	583	39.7	427	46.5	280	37.5	275	44.6	542	35.5	142	41.7
198	483	39.7	288	46.5	57	37.5	215	44.6	271	35.5	18	41.6
199	176	39.7	310	46.5	287	37.4	14	44.4	302	35.5	417	41.6
200	332	39.7	539	46.5	274	37.4	307	44.4	163	35.5	197	41.6
Mean		43.1		48.9		38.8		45.9		36.3		43.2

Note: (i) GN= Germplasm name, Note: (ii) All the germplasm lines names start with prefix 'GPDWD'
DAS=Days after sowing

Table 11.3. Genotypic differences in cotton genotypes for specific leaf weight (mg/cm²) at ARS Dharwad for 600 germplasm lines at 90 DAS

Sl. No.	Specific leaf weight (mg/cm ²)					
	GN	Best performers	GN	Moderate performers	GN	Least performers
1	597	10.8	383	10.1	123	9.4
2	613	10.8	334	10.1	234	9.4
3	606	10.8	382	10.1	269	9.4
4	622	10.8	462	10.1	257	9.4
5	608	10.8	493	10.1	270	9.4
6	591	10.8	214	10.1	329	9.4
7	619	10.8	350	10.1	304	9.4
8	621	10.8	578	10.1	464	9.4
9	612	10.8	451	10.1	415	9.4
10	603	10.8	491	10.1	161	9.4
11	617	10.8	563	10.1	299	9.4
12	589	10.8	321	10.1	508	9.4
13	501	10.8	401	10.1	216	9.4
14	520	10.8	330	10.1	235	9.4
15	554	10.8	400	10.1	82	9.4
16	484	10.8	511	10.1	311	9.4
17	585	10.8	453	10.1	172	9.4
18	561	10.8	42	10.1	240	9.4
19	607	10.8	331	10.1	442	9.4
20	592	10.8	233	10.1	3	9.4
21	596	10.8	365	10.1	125	9.4
22	610	10.8	461	10.1	258	9.4
23	614	10.8	342	10.1	286	9.4
24	611	10.8	404	10.1	242	9.4
25	601	10.8	472	10.1	366	9.4
26	620	10.8	494	10.1	428	9.4
27	616	10.7	379	10.0	368	9.4
28	598	10.7	480	10.0	195	9.4
29	602	10.7	467	10.0	289	9.4
30	623	10.7	499	10.0	339	9.4
31	615	10.7	500	10.0	230	9.3
32	605	10.7	533	10.0	138	9.3
33	609	10.7	459	10.0	239	9.3
34	600	10.7	434	10.0	485	9.3
35	594	10.7	517	10.0	340	9.3
36	595	10.7	388	10.0	183	9.3
37	624	10.7	469	10.0	481	9.3
38	593	10.7	156	10.0	200	9.3
39	604	10.7	423	10.0	220	9.3
40	618	10.7	317	10.0	196	9.3
41	599	10.7	209	10.0	284	9.3
42	590	10.7	349	10.0	11	9.3
43	544	10.7	519	10.0	212	9.3
44	552	10.7	348	10.0	85	9.3
45	555	10.6	393	10.0	47	9.3
46	573	10.6	447	10.0	221	9.3
47	512	10.6	312	9.9	228	9.3
48	419	10.6	378	9.9	22	9.3
49	421	10.6	443	9.9	33	9.3
50	568	10.6	135	9.9	81	9.3

Contd.....

Sl. No.	Specific leaf weight (mg/cm ²)					
	GN	Best performers	GN	Moderate performers	GN	Least performers
51	371	10.6	168	9.9	32	9.2
52	586	10.6	238	9.9	143	9.2
53	498	10.6	301	9.9	268	9.2
54	524	10.6	426	9.9	35	9.2
55	526	10.6	222	9.9	293	9.2
56	572	10.6	336	9.9	290	9.2
57	262	10.6	455	9.9	297	9.2
58	471	10.6	575	9.9	63	9.2
59	579	10.6	265	9.9	99	9.2
60	180	10.6	433	9.9	162	9.2
61	475	10.6	346	9.9	165	9.2
62	547	10.6	226	9.9	352	9.2
63	525	10.6	314	9.9	19	9.2
64	545	10.6	516	9.9	120	9.2
65	487	10.6	546	9.9	224	9.2
66	399	10.6	300	9.9	225	9.2
67	582	10.6	345	9.9	211	9.2
68	514	10.6	181	9.9	322	9.2
69	337	10.5	150	9.9	56	9.2
70	375	10.5	396	9.9	110	9.2
71	479	10.5	241	9.8	169	9.2
72	560	10.5	309	9.8	8	9.2
73	477	10.5	583	9.8	119	9.1
74	505	10.5	483	9.8	65	9.1
75	410	10.5	176	9.8	205	9.1
76	489	10.5	332	9.8	402	9.1
77	570	10.5	152	9.8	27	9.1
78	532	10.5	397	9.8	44	9.1
79	411	10.5	457	9.8	9	9.1
80	562	10.5	256	9.8	148	9.1
81	391	10.5	306	9.8	188	9.1
82	362	10.5	523	9.8	79	9.1
83	580	10.5	192	9.8	167	9.1
84	374	10.5	296	9.8	217	9.1
85	557	10.5	413	9.8	20	9.1
86	574	10.5	335	9.8	28	9.1
87	567	10.5	278	9.8	141	9.1
88	513	10.5	450	9.8	25	9.1
89	559	10.5	338	9.8	351	9.1
90	588	10.5	536	9.8	73	9.1
91	476	10.5	223	9.8	431	9.1
92	506	10.5	387	9.8	86	9.1
93	538	10.5	318	9.8	112	9.1
94	436	10.5	363	9.8	78	9.1
95	522	10.5	373	9.8	93	9.1
96	537	10.4	316	9.8	97	9.1
97	495	10.4	201	9.8	15	9.1
98	521	10.4	470	9.7	91	9.1
99	361	10.4	534	9.7	89	9.1
100	497	10.4	232	9.7	106	9.0
101	454	10.4	266	9.7	67	9.0
102	529	10.4	403	9.7	207	9.0
103	425	10.4	41	9.7	10	9.0

Contd.....

Sl. No.	Specific leaf weight (mg/cm ²)					
	GN	Best performers	GN	Moderate performers	GN	Least performers
104	486	10.4	460	9.7	58	9.0
105	504	10.4	140	9.7	50	9.0
106	360	10.4	160	9.7	191	9.0
107	254	10.4	535	9.7	94	9.0
108	474	10.4	139	9.7	202	9.0
109	488	10.4	430	9.7	279	9.0
110	435	10.4	247	9.7	117	9.0
111	490	10.4	355	9.7	190	9.0
112	473	10.4	251	9.7	54	9.0
113	389	10.4	429	9.7	174	9.0
114	540	10.4	132	9.7	189	9.0
115	558	10.4	277	9.7	59	9.0
116	550	10.4	187	9.7	422	9.0
117	177	10.4	354	9.7	130	9.0
118	353	10.4	323	9.7	439	9.0
119	376	10.4	111	9.7	250	9.0
120	385	10.4	327	9.7	377	9.0
121	427	10.4	37	9.7	149	9.0
122	288	10.3	280	9.7	542	9.0
123	310	10.3	57	9.7	271	9.0
124	539	10.3	43	9.6	302	9.0
125	281	10.3	126	9.6	163	9.0
126	344	10.3	30	9.6	243	8.9
127	543	10.3	60	9.6	263	8.9
128	527	10.3	261	9.6	98	8.9
129	437	10.3	186	9.6	294	8.9
130	237	10.3	245	9.6	74	8.9
131	255	10.3	264	9.6	109	8.9
132	298	10.3	14	9.6	259	8.9
133	556	10.3	307	9.6	4	8.9
134	394	10.3	313	9.6	100	8.9
135	203	10.3	448	9.6	438	8.9
136	416	10.3	194	9.6	90	8.9
137	409	10.3	218	9.6	61	8.9
138	541	10.3	16	9.6	69	8.9
139	551	10.3	158	9.6	92	8.9
140	392	10.3	291	9.6	64	8.9
141	175	10.3	206	9.6	116	8.9
142	407	10.3	358	9.6	343	8.9
143	566	10.3	347	9.6	444	8.9
144	492	10.3	208	9.6	88	8.9
145	440	10.3	549	9.6	71	8.9
146	441	10.3	121	9.6	12	8.9
147	553	10.3	468	9.6	75	8.9
148	153	10.3	236	9.6	115	8.9
149	432	10.3	496	9.6	147	8.9
150	276	10.3	38	9.6	315	8.9
151	253	10.3	324	9.6	102	8.9
152	369	10.3	320	9.6	105	8.9
153	414	10.3	185	9.6	72	8.9
154	308	10.3	244	9.6	295	8.9
155	341	10.3	83	9.6	68	8.9
156	510	10.3	53	9.6	127	8.9

Contd.....

Sl. No.	Specific leaf weight (mg/cm ²)					
	GN	Best performers	GN	Moderate performers	GN	Least performers
157	171	10.3	285	9.6	283	8.9
158	328	10.3	303	9.6	118	8.9
159	449	10.3	23	9.6	142	8.9
160	569	10.3	248	9.6	18	8.9
161	581	10.3	103	9.6	417	8.9
162	502	10.3	146	9.6	80	8.9
163	424	10.3	36	9.6	13	8.9
164	507	10.3	370	9.6	114	8.9
165	548	10.3	17	9.6	145	8.9
166	463	10.3	452	9.6	128	8.9
167	528	10.3	34	9.6	70	8.9
168	381	10.3	84	9.6	282	8.9
169	518	10.3	96	9.6	95	8.9
170	359	10.3	144	9.6	229	8.9
171	213	10.3	124	9.6	198	8.9
172	326	10.3	182	9.6	26	8.9
173	405	10.3	193	9.6	197	8.9
174	333	10.3	273	9.6	305	8.9
175	246	10.3	412	9.6	46	8.9
176	565	10.3	24	9.6	66	8.9
177	530	10.3	287	9.6	249	8.9
178	584	10.3	274	9.6	7	8.9
179	466	10.3	503	9.6	51	8.9
180	587	10.3	445	9.6	48	8.9
181	531	10.3	87	9.6	101	8.9
182	576	10.3	275	9.6	357	8.9
183	406	10.3	173	9.6	108	8.9
184	478	10.3	45	9.6	31	8.9
185	356	10.3	384	9.6	136	8.9
186	364	10.3	39	9.6	2	8.9
187	515	10.3	77	9.6	49	8.9
188	577	10.2	204	9.6	52	8.9
189	380	10.2	21	9.6	395	8.9
190	325	10.2	458	9.5	104	8.9
191	367	10.2	215	9.5	62	8.9
192	564	10.2	456	9.5	292	8.8
193	509	10.2	267	9.5	6	8.8
194	420	10.2	252	9.5	40	8.8
195	482	10.2	418	9.5	260	8.8
196	408	10.2	1	9.5	5	8.8
197	319	10.1	29	9.5	184	8.8
198	386	10.1	219	9.5	76	8.8
199	390	10.1	107	9.2	122	8.8
200	571	10.1	272	9.2	113	8.8
	Mean	10.5		9.8		9.1

Note: (i) GN= Germplasm name

Note: (ii) All the germplasm lines names start with prefix 'GPDWD'.

Table 11.4 Genotypic differences in cotton genotypes for Rate of photosynthesis (μ mol CO₂/m²/s) and stomatal conductance (μ mol CO₂/m²/s) at ARS Dharwad for 600 germplasm lines at 90 DAS

Sl. No.	Best performers		Moderate performers		Least performers		Best performers		Moderate performers		Least performers	
	GN	Photosynthesis rate	GN	Photosynthesis rate	GN	Photosynthesis rate	GN	Stomatal conductance	GN	Stomatal conductance	GN	Stomatal conductance
1	607	33.4	441	31.4	503	29.4	611	0.45	308	0.37	384	0.31
2	592	33.4	553	31.4	445	29.4	601	0.45	341	0.37	39	0.31
3	596	33.4	153	31.4	87	29.4	620	0.45	510	0.37	77	0.31
4	610	33.4	432	31.4	275	29.4	616	0.45	518	0.37	204	0.31
5	614	33.4	276	31.4	173	29.4	598	0.45	359	0.37	219	0.31
6	611	33.4	253	31.4	45	29.4	624	0.45	213	0.37	212	0.31
7	601	33.4	369	31.4	384	29.4	593	0.45	326	0.37	21	0.31
8	620	33.4	414	31.3	39	29.4	607	0.45	317	0.37	458	0.31
9	616	33.4	246	31.3	77	29.4	592	0.45	209	0.37	215	0.31
10	598	33.4	423	31.3	204	29.3	596	0.45	349	0.37	456	0.31
11	624	33.4	308	31.3	219	29.3	610	0.45	519	0.37	287	0.31
12	593	33.4	341	31.3	212	29.3	614	0.45	348	0.37	274	0.31
13	602	33.4	510	31.3	21	29.3	602	0.45	405	0.37	503	0.31
14	623	33.4	518	31.3	458	29.3	623	0.45	333	0.37	445	0.31
15	615	33.4	359	31.3	215	29.3	615	0.45	409	0.37	87	0.31
16	605	33.3	213	31.3	456	29.3	605	0.45	541	0.37	275	0.31
17	609	33.3	326	31.3	267	29.3	609	0.45	492	0.37	285	0.31
18	600	33.3	317	31.3	252	29.3	613	0.45	440	0.37	303	0.31
19	604	33.3	209	31.3	418	29.3	606	0.45	441	0.37	23	0.31
20	618	33.3	349	31.3	85	29.2	622	0.45	553	0.37	248	0.31
21	599	33.3	519	31.3	47	29.2	608	0.45	153	0.37	103	0.31
22	590	33.3	348	31.2	221	29.2	591	0.45	432	0.37	146	0.31
23	594	33.3	405	31.2	228	29.2	619	0.45	276	0.37	36	0.31
24	595	33.3	333	31.2	22	29.2	617	0.45	253	0.37	370	0.31
25	597	33.3	177	31.2	1	29.2	589	0.45	373	0.37	17	0.31
26	613	33.3	353	31.2	29	29.2	501	0.45	316	0.37	452	0.31
27	606	33.3	376	31.2	285	29.2	520	0.45	393	0.37	34	0.31
28	622	33.3	385	31.2	303	29.2	554	0.45	447	0.37	84	0.31
29	608	33.3	427	31.2	23	29.2	484	0.44	312	0.37	96	0.31
30	591	33.2	288	31.2	248	29.2	585	0.44	378	0.37	144	0.31
31	619	33.2	310	31.2	103	29.2	561	0.44	443	0.36	124	0.31
32	621	33.2	539	31.2	146	29.1	479	0.44	135	0.36	182	0.31
33	612	33.2	281	31.2	36	29.1	374	0.44	168	0.36	267	0.31
34	603	33.2	344	31.1	370	29.1	557	0.44	238	0.36	252	0.30
35	617	33.2	543	31.1	17	29.1	574	0.44	301	0.36	418	0.30
36	589	33.2	527	31.1	452	29.1	567	0.44	426	0.36	85	0.30
37	501	33.2	437	31.1	34	29.1	513	0.44	222	0.36	47	0.30
38	520	33.1	237	31.1	84	29.1	559	0.44	483	0.36	221	0.30
39	554	33.1	255	31.1	96	29.1	588	0.44	176	0.36	228	0.30
40	484	33.1	298	31.1	144	29.1	600	0.44	332	0.36	22	0.30
41	585	33.1	556	31.1	124	29.1	604	0.44	152	0.36	1	0.30
42	561	33.1	394	31.1	182	29.1	618	0.44	397	0.36	29	0.30
43	479	33.1	203	31.1	193	29.1	599	0.44	457	0.36	290	0.30
44	374	33.1	416	31.1	273	29.1	590	0.44	256	0.36	297	0.30
45	557	33.1	583	31.0	412	29.1	594	0.44	306	0.36	402	0.30
46	574	33.1	335	31.0	24	29.1	595	0.44	523	0.36	27	0.30
47	567	33.1	278	31.0	205	29.1	597	0.44	192	0.36	44	0.30
48	513	33.1	450	31.0	25	29.0	621	0.44	296	0.36	9	0.30

Contd....

Sl. No.	Best performers		Moderate performers		Least performers		Best performers		Moderate performers		Least performers	
	GN	Photosynthesis rate	GN	Photosynthesis rate	GN	Photosynthesis rate	GN	Stomatal conductance	GN	Stomatal conductance	GN	Stomatal conductance
49	559	33.1	338	31.0	351	29.0	612	0.44	413	0.36	148	0.30
50	588	33.1	536	31.0	73	29.0	603	0.44	516	0.36	188	0.30
51	476	33.1	223	31.0	431	29.0	477	0.43	527	0.36	79	0.30
52	506	33.0	387	31.0	86	29.0	505	0.43	437	0.36	167	0.30
53	538	33.0	318	31.0	112	29.0	410	0.43	237	0.36	217	0.30
54	436	33.0	363	30.9	78	29.0	489	0.43	255	0.35	20	0.30
55	544	33.0	373	30.9	93	29.0	570	0.43	298	0.35	28	0.30
56	552	33.0	316	30.9	97	29.0	532	0.43	556	0.35	141	0.30
57	555	33.0	393	30.9	15	29.0	411	0.43	394	0.35	225	0.30
58	573	33.0	447	30.9	91	29.0	562	0.43	203	0.35	112	0.30
59	512	33.0	312	30.9	33	29.0	391	0.43	416	0.35	78	0.30
60	419	33.0	378	30.9	81	29.0	362	0.42	546	0.35	93	0.30
61	421	32.9	443	30.9	107	29.0	580	0.42	300	0.35	97	0.30
62	568	32.9	135	30.9	272	29.0	547	0.42	345	0.35	15	0.30
63	371	32.9	168	30.9	32	28.9	525	0.42	181	0.35	91	0.30
64	586	32.9	238	30.9	143	28.9	545	0.42	150	0.35	33	0.30
65	498	32.9	301	30.9	268	28.9	487	0.42	396	0.35	24	0.30
66	560	32.9	426	30.8	35	28.9	552	0.42	241	0.35	205	0.30
67	477	32.9	222	30.8	293	28.9	555	0.42	309	0.35	25	0.29
68	505	32.8	483	30.8	290	28.9	573	0.42	368	0.35	351	0.29
69	410	32.8	176	30.8	297	28.9	512	0.42	177	0.35	73	0.29
70	489	32.7	332	30.8	402	28.9	419	0.42	353	0.35	431	0.29
71	570	32.7	152	30.8	27	28.9	421	0.41	376	0.35	86	0.29
72	532	32.6	397	30.8	44	28.9	568	0.41	385	0.35	81	0.29
73	411	32.6	457	30.8	9	28.9	371	0.41	427	0.35	107	0.29
74	562	32.6	256	30.7	148	28.9	586	0.41	288	0.35	272	0.29
75	391	32.6	306	30.7	188	28.9	498	0.41	310	0.35	32	0.29
76	362	32.6	523	30.7	79	28.8	560	0.41	539	0.35	143	0.29
77	580	32.6	192	30.7	167	28.8	476	0.41	281	0.35	268	0.29
78	547	32.6	296	30.7	217	28.8	506	0.41	344	0.35	35	0.29
79	525	32.6	413	30.7	20	28.8	538	0.41	543	0.35	293	0.29
80	545	32.6	516	30.6	28	28.8	436	0.41	583	0.35	193	0.29
81	487	32.6	546	30.6	141	28.8	544	0.41	335	0.35	273	0.29
82	399	32.6	300	30.6	225	28.8	540	0.41	278	0.35	412	0.29
83	582	32.6	345	30.6	211	28.8	558	0.41	450	0.35	224	0.29
84	514	32.6	181	30.6	322	28.7	550	0.41	338	0.35	422	0.29
85	337	32.6	150	30.6	56	28.7	565	0.41	536	0.34	130	0.29
86	375	32.6	396	30.6	110	28.7	530	0.41	223	0.34	439	0.29
87	531	32.6	241	30.5	169	28.7	584	0.41	387	0.34	250	0.29
88	576	32.5	309	30.5	8	28.7	466	0.41	318	0.34	377	0.29
89	406	32.5	368	30.5	119	28.7	587	0.41	363	0.34	48	0.29
90	478	32.5	195	30.5	65	28.6	522	0.41	195	0.34	101	0.29
91	356	32.5	289	30.5	136	28.6	537	0.41	289	0.34	357	0.29
92	364	32.5	339	30.5	2	28.6	495	0.41	339	0.34	108	0.29
93	524	32.5	230	30.5	49	28.6	399	0.41	230	0.34	31	0.29
94	526	32.5	138	30.5	52	28.6	582	0.40	138	0.34	89	0.29
95	572	32.5	336	30.5	395	28.6	514	0.40	336	0.34	118	0.29
96	262	32.5	455	30.5	104	28.6	337	0.40	455	0.34	65	0.29
97	471	32.5	575	30.4	63	28.6	375	0.40	575	0.34	136	0.29
98	579	32.5	265	30.4	99	28.6	531	0.40	265	0.34	2	0.29
99	180	32.5	433	30.4	162	28.6	576	0.40	433	0.34	49	0.29
100	475	32.5	346	30.4	165	28.5	406	0.40	346	0.34	52	0.29
101	473	32.5	226	30.4	352	28.5	478	0.40	226	0.34	211	0.29

Contd....

Sl. No.	Best performers		Moderate performers		Least performers		Best performers		Moderate performers		Least performers	
	GN	Photosynthesis rate	GN	Photosynthesis rate	GN	Photosynthesis rate	GN	Stomatal conductance	GN	Stomatal conductance	GN	Stomatal conductance
102	389	32.4	314	30.4	19	28.5	356	0.40	314	0.34	322	0.29
103	540	32.4	132	30.4	120	28.5	364	0.40	132	0.34	56	0.29
104	558	32.4	277	30.3	224	28.5	524	0.40	277	0.34	110	0.29
105	550	32.4	187	30.3	422	28.5	526	0.40	187	0.34	169	0.29
106	565	32.4	354	30.3	130	28.4	572	0.40	354	0.34	8	0.29
107	530	32.4	323	30.3	439	28.4	262	0.40	323	0.34	99	0.29
108	584	32.4	258	30.3	250	28.4	471	0.40	258	0.34	162	0.29
109	466	32.4	286	30.3	377	28.4	579	0.40	286	0.34	165	0.29
110	587	32.4	242	30.3	48	28.4	180	0.40	242	0.34	352	0.29
111	522	32.4	366	30.3	101	28.4	475	0.40	366	0.34	19	0.29
112	537	32.4	428	30.3	357	28.4	473	0.40	428	0.34	120	0.29
113	495	32.4	201	30.3	108	28.4	389	0.40	201	0.34	395	0.29
114	521	32.4	470	30.2	31	28.4	435	0.40	470	0.34	104	0.29
115	361	32.4	534	30.2	89	28.4	490	0.39	534	0.34	63	0.29
116	497	32.4	232	30.2	106	28.4	328	0.39	232	0.34	61	0.29
117	454	32.4	266	30.2	67	28.4	449	0.39	266	0.34	69	0.29
118	529	32.3	403	30.2	207	28.4	569	0.39	347	0.34	92	0.29
119	425	32.3	41	30.2	10	28.4	581	0.39	82	0.34	292	0.29
120	486	32.3	460	30.2	58	28.4	502	0.39	311	0.34	6	0.29
121	504	32.3	140	30.2	50	28.4	424	0.39	172	0.34	40	0.29
122	360	32.3	160	30.2	191	28.3	507	0.39	240	0.34	260	0.29
123	467	32.3	535	30.2	94	28.3	548	0.39	430	0.34	5	0.29
124	499	32.3	139	30.2	202	28.3	463	0.39	247	0.34	184	0.29
125	500	32.3	245	30.1	279	28.3	528	0.39	355	0.34	76	0.29
126	533	32.3	264	30.1	117	28.3	381	0.39	251	0.34	122	0.29
127	459	32.3	14	30.1	259	28.3	515	0.39	429	0.34	113	0.28
128	319	32.3	307	30.1	4	28.3	407	0.39	257	0.34	106	0.28
129	386	32.3	313	30.1	100	28.3	566	0.39	270	0.34	67	0.28
130	390	32.3	448	30.1	438	28.3	342	0.39	329	0.34	207	0.28
131	577	32.3	194	30.1	90	28.3	521	0.39	307	0.34	10	0.28
132	380	32.3	218	30.1	61	28.3	361	0.39	313	0.34	58	0.28
133	325	32.3	485	30.1	69	28.3	497	0.39	448	0.34	50	0.28
134	367	32.3	340	30.1	92	28.3	454	0.39	194	0.34	191	0.28
135	564	32.3	183	30.1	292	28.2	529	0.39	218	0.34	94	0.28
136	509	32.2	481	30.1	6	28.2	425	0.39	485	0.34	202	0.28
137	420	32.2	200	30.0	40	28.2	486	0.39	340	0.34	343	0.28
138	482	32.2	220	30.0	260	28.2	504	0.39	183	0.33	444	0.28
139	408	32.2	196	30.0	5	28.2	360	0.39	481	0.33	88	0.28
140	446	32.2	284	30.0	184	28.2	467	0.39	200	0.33	71	0.28
141	551	32.2	11	30.0	76	28.2	499	0.39	220	0.33	197	0.28
142	392	32.2	291	30.0	122	28.2	500	0.39	196	0.33	305	0.28
143	175	32.2	206	30.0	113	28.2	533	0.39	284	0.33	46	0.28
144	563	32.2	358	30.0	343	28.2	459	0.39	11	0.33	66	0.28
145	321	32.2	347	30.0	444	28.2	319	0.39	291	0.33	190	0.28
146	401	32.2	82	30.0	88	28.2	386	0.39	206	0.33	54	0.28
147	330	32.1	311	30.0	71	28.2	390	0.39	358	0.33	174	0.28
148	254	32.1	172	30.0	197	28.2	577	0.39	403	0.33	279	0.28
149	474	32.1	240	30.0	305	28.2	380	0.39	41	0.33	117	0.28
150	488	32.1	430	29.9	46	28.1	325	0.39	460	0.33	259	0.28
151	435	32.0	247	29.9	66	28.1	367	0.38	140	0.33	4	0.28
152	490	32.0	355	29.9	190	28.1	564	0.38	160	0.33	100	0.28
153	328	32.0	251	29.9	54	28.1	509	0.38	535	0.33	438	0.28
154	449	32.0	429	29.9	174	28.1	420	0.38	139	0.33	90	0.28

Contd....

Sl. No.	Best performers		Moderate performers		Least performers		Best performers		Moderate performers		Least performers	
	GN	Photosynthesis rate	GN	Photosynthesis rate	GN	Photosynthesis rate	GN	Stomatal conductance	GN	Stomatal conductance	GN	Stomatal conductance
155	569	32.0	257	29.9	189	28.1	482	0.38	245	0.33	116	0.28
156	581	32.0	270	29.9	59	28.1	408	0.38	264	0.33	115	0.28
157	502	32.0	329	29.9	80	28.1	446	0.38	14	0.33	147	0.28
158	424	32.0	304	29.9	13	28.1	551	0.38	236	0.33	315	0.28
159	507	32.0	464	29.9	114	28.1	392	0.38	496	0.33	102	0.28
160	548	32.0	415	29.9	145	28.1	175	0.38	38	0.33	105	0.28
161	463	32.0	161	29.9	128	28.1	563	0.38	324	0.33	72	0.28
162	528	32.0	299	29.8	70	28.1	321	0.38	320	0.33	295	0.28
163	381	32.0	508	29.8	282	28.1	401	0.38	185	0.33	68	0.28
164	515	32.0	216	29.8	95	28.1	330	0.38	244	0.33	127	0.28
165	407	31.9	235	29.8	229	28.0	254	0.38	83	0.33	283	0.28
166	566	31.9	239	29.8	198	28.0	474	0.38	53	0.33	118	0.28
167	342	31.9	208	29.8	26	28.0	488	0.38	123	0.33	142	0.28
168	404	31.9	549	29.8	62	28.0	383	0.38	234	0.33	18	0.28
169	472	31.9	43	29.8	12	28.0	334	0.38	269	0.33	417	0.28
170	494	31.9	126	29.8	75	28.0	382	0.38	43	0.33	12	0.28
171	379	31.9	30	29.8	243	28.0	462	0.38	126	0.33	75	0.28
172	480	31.9	60	29.8	263	28.0	493	0.38	30	0.33	243	0.28
173	400	31.8	261	29.8	98	28.0	214	0.38	60	0.33	263	0.26
174	511	31.8	186	29.7	294	28.0	350	0.38	261	0.33	98	0.26
175	453	31.8	442	29.7	74	28.0	434	0.38	186	0.33	294	0.26
176	42	31.8	3	29.7	109	28.0	517	0.38	442	0.33	74	0.26
177	331	31.8	125	29.7	249	28.0	388	0.38	111	0.33	109	0.26
178	233	31.8	111	29.7	7	27.9	469	0.38	327	0.33	249	0.26
179	365	31.8	327	29.7	51	27.9	156	0.38	37	0.33	189	0.26
180	461	31.8	37	29.7	149	27.9	578	0.38	280	0.33	59	0.26
181	571	31.7	280	29.7	542	27.9	451	0.38	299	0.33	80	0.26
182	383	31.7	57	29.7	271	27.9	491	0.38	508	0.33	13	0.26
183	334	31.7	16	29.7	302	27.9	404	0.38	216	0.33	114	0.26
184	382	31.7	158	29.7	163	27.8	472	0.38	235	0.33	145	0.26
185	462	31.7	121	29.6	64	27.8	494	0.38	239	0.33	128	0.26
186	493	31.7	468	29.6	116	27.8	379	0.38	208	0.32	70	0.26
187	214	31.6	236	29.6	115	27.8	480	0.38	549	0.32	282	0.26
188	350	31.6	496	29.6	147	27.8	400	0.38	304	0.32	95	0.26
189	434	31.6	38	29.6	315	27.8	233	0.38	464	0.32	229	0.26
190	517	31.6	324	29.6	102	27.7	365	0.38	415	0.32	198	0.26
191	388	31.6	320	29.6	105	27.7	461	0.38	161	0.32	26	0.26
192	469	31.6	185	29.6	72	27.7	571	0.38	57	0.32	62	0.26
193	156	31.6	244	29.6	295	27.7	511	0.38	16	0.32	7	0.26
194	578	31.6	83	29.6	68	27.6	453	0.38	158	0.32	51	0.26
195	451	31.6	53	29.6	127	27.6	42	0.38	121	0.32	149	0.26
196	491	31.6	123	29.6	283	27.6	331	0.38	468	0.32	542	0.26
197	409	31.4	234	29.6	118	27.6	369	0.37	3	0.32	271	0.26
198	541	31.4	269	29.6	142	27.6	414	0.37	125	0.32	302	0.26
199	492	31.4	287	29.4	18	27.6	246	0.37	173	0.31	163	0.26
200	440	31.4	274	29.4	417	27.6	423	0.37	45	0.31	64	0.26
	Mean	32.6		30.5		28.6		0.41		0.35		0.29

Note (i) GN= Germplasm name,

Note (ii): All the germplasm lines names start with prefix 'GPDWD'

DAS=Days after sowing

Table 11.5. Genotypic differences in cotton genotypes for rate of transpiration (m mol H₂O/m²/s) at ARS Dharwad for 600 germplasm lines at 90 DAS

Sl. No.	Rate of transpiration					
	GN	Best performers	GN	Moderate performer's	GN	Least performers
1	620	6.3	359	5.6	24	4.7
2	616	6.3	213	5.6	205	4.7
3	598	6.3	326	5.6	25	4.7
4	600	6.3	317	5.6	351	4.7
5	604	6.3	209	5.6	73	4.7
6	618	6.3	349	5.6	431	4.7
7	599	6.3	519	5.6	86	4.7
8	590	6.3	348	5.6	112	4.7
9	594	6.3	405	5.6	78	4.7
10	607	6.3	333	5.6	93	4.7
11	592	6.3	177	5.6	97	4.7
12	596	6.3	553	5.6	15	4.7
13	610	6.3	153	5.6	91	4.7
14	614	6.3	432	5.6	33	4.7
15	611	6.3	409	5.6	81	4.7
16	601	6.3	541	5.6	107	4.7
17	595	6.3	492	5.6	272	4.7
18	597	6.3	440	5.6	32	4.7
19	613	6.3	441	5.6	143	4.7
20	606	6.3	276	5.6	204	4.7
21	622	6.3	253	5.6	219	4.6
22	608	6.3	369	5.6	212	4.6
23	591	6.3	414	5.6	21	4.6
24	624	6.3	246	5.6	458	4.6
25	593	6.3	423	5.6	215	4.6
26	602	6.3	298	5.6	456	4.6
27	623	6.3	556	5.6	267	4.6
28	615	6.3	394	5.6	36	4.6
29	605	6.3	203	5.6	370	4.6
30	609	6.3	416	5.6	17	4.6
31	501	6.3	583	5.6	452	4.6
32	520	6.3	335	5.6	34	4.6
33	554	6.3	278	5.6	84	4.6
34	484	6.3	450	5.5	96	4.6
35	585	6.3	338	5.5	144	4.6
36	561	6.3	536	5.5	287	4.6
37	479	6.2	223	5.5	274	4.6
38	374	6.2	387	5.5	503	4.5
39	557	6.2	318	5.5	445	4.5
40	574	6.2	378	5.5	87	4.5
41	567	6.2	443	5.5	275	4.5
42	513	6.2	135	5.5	173	4.5
43	538	6.2	168	5.5	228	4.5
44	436	6.2	238	5.5	22	4.5
45	544	6.2	301	5.5	1	4.5
46	552	6.2	426	5.5	29	4.5
47	555	6.2	222	5.5	285	4.5
48	573	6.2	483	5.5	303	4.5
49	512	6.2	176	5.5	23	4.5

Contd....

Sl. No.	Rate of transpiration					
	GN	Best performers	GN	Moderate performer's	GN	Least performers
50	419	6.2	332	5.5	248	4.5
51	421	6.2	363	5.5	103	4.5
52	410	6.2	373	5.5	146	4.5
53	489	6.2	316	5.5	45	4.5
54	570	6.2	393	5.5	384	4.5
55	532	6.2	447	5.5	39	4.5
56	411	6.2	312	5.5	77	4.4
57	562	6.2	353	5.5	252	4.4
58	391	6.2	376	5.5	418	4.4
59	362	6.2	385	5.5	85	4.4
60	580	6.2	427	5.5	47	4.4
61	547	6.2	288	5.5	221	4.4
62	525	6.2	310	5.5	124	4.4
63	619	6.2	539	5.5	182	4.4
64	621	6.2	281	5.4	193	4.4
65	612	6.2	344	5.4	65	4.4
66	603	6.2	543	5.4	136	4.4
67	617	6.2	527	5.4	2	4.4
68	589	6.2	437	5.4	49	4.4
69	559	6.2	237	5.4	52	4.4
70	588	6.2	255	5.4	395	4.4
71	476	6.1	152	5.4	104	4.4
72	506	6.1	397	5.4	63	4.4
73	568	6.1	457	5.4	402	4.4
74	371	6.1	256	5.4	27	4.4
75	586	6.1	306	5.4	44	4.4
76	498	6.1	523	5.4	9	4.3
77	560	6.1	192	5.4	148	4.3
78	477	6.1	296	5.4	211	4.3
79	505	6.1	413	5.4	322	4.3
80	475	6.1	516	5.4	56	4.3
81	473	6.1	546	5.4	110	4.3
82	389	6.1	300	5.4	169	4.3
83	540	6.1	345	5.4	268	4.3
84	558	6.1	181	5.3	35	4.3
85	550	6.1	226	5.3	293	4.3
86	565	6.1	314	5.3	290	4.3
87	530	6.1	132	5.3	297	4.3
88	584	6.1	277	5.3	8	4.3
89	466	6.1	187	5.3	119	4.3
90	587	6.1	354	5.3	188	4.3
91	522	6.1	323	5.3	79	4.3
92	537	6.1	258	5.3	167	4.3
93	375	6.1	286	5.3	217	4.3
94	531	6.1	242	5.3	20	4.3
95	576	6.1	366	5.3	28	4.3
96	406	6.1	428	5.3	141	4.3
97	478	6.1	201	5.3	225	4.2
98	545	6.1	470	5.3	94	4.2
99	487	6.1	534	5.3	202	4.2
100	399	6.0	339	5.3	279	4.2
101	582	6.0	230	5.3	117	4.2
102	514	6.0	138	5.2	259	4.2

Contd....

Sl. No.	Rate of transpiration					
	GN	Best performers	GN	Moderate performer's	GN	Least performers
103	337	6.0	336	5.2	4	4.2
104	356	6.0	455	5.2	100	4.2
105	364	6.0	150	5.2	438	4.2
106	524	6.0	396	5.2	90	4.2
107	526	6.0	241	5.2	61	4.2
108	572	6.0	309	5.2	19	4.2
109	262	6.0	368	5.2	120	4.2
110	471	6.0	195	5.2	224	4.2
111	579	6.0	289	5.2	422	4.2
112	180	6.0	575	5.2	130	4.2
113	533	6.0	265	5.2	67	4.2
114	459	6.0	433	5.2	207	4.2
115	319	6.0	346	5.2	10	4.2
116	386	6.0	313	5.2	58	4.1
117	390	6.0	448	5.2	50	4.1
118	577	6.0	194	5.2	191	4.1
119	380	6.0	218	5.2	99	4.1
120	325	6.0	485	5.2	162	4.1
121	367	6.0	340	5.1	165	4.1
122	564	6.0	183	5.1	352	4.1
123	509	6.0	481	5.1	439	4.1
124	420	6.0	200	5.1	250	4.1
125	482	6.0	220	5.1	377	4.1
126	408	6.0	196	5.1	48	4.1
127	446	6.0	284	5.1	101	4.1
128	551	6.0	11	5.1	357	4.1
129	392	6.0	41	5.1	108	4.1
130	175	5.9	460	5.1	31	4.1
131	563	5.9	140	5.1	89	4.1
132	321	5.9	160	5.1	106	4.1
133	401	5.9	535	5.1	54	4.1
134	495	5.9	139	5.1	174	4.1
135	521	5.9	245	5.1	189	4.1
136	361	5.9	232	5.1	59	4.0
137	497	5.9	266	5.0	80	4.0
138	454	5.9	403	5.0	13	4.0
139	529	5.9	264	5.0	114	4.0
140	425	5.9	14	5.0	145	4.0
141	486	5.9	307	5.0	128	4.0
142	504	5.9	291	5.0	5	4.0
143	360	5.9	206	5.0	184	4.0
144	467	5.9	358	5.0	76	4.0
145	499	5.9	347	5.0	122	4.0
146	500	5.9	82	5.0	113	4.0
147	328	5.9	311	5.0	197	4.0
148	449	5.9	172	5.0	305	4.0
149	569	5.9	240	5.0	46	4.0
150	581	5.9	430	5.0	66	4.0
151	502	5.9	247	5.0	190	4.0
152	330	5.9	355	5.0	69	4.0
153	254	5.9	251	5.0	92	3.9
154	474	5.9	429	5.0	292	3.9
155	488	5.9	257	5.0	6	3.9

Contd....

Sl. No.	Rate of transpiration					
	GN	Best performers	GN	Moderate performer's	GN	Least performers
156	435	5.9	270	5.0	40	3.9
157	490	5.9	329	5.0	260	3.9
158	566	5.9	304	5.0	62	3.9
159	342	5.9	464	5.0	12	3.9
160	404	5.9	415	5.0	75	3.9
161	472	5.9	43	5.0	243	3.9
162	494	5.9	126	5.0	263	3.9
163	424	5.9	30	5.0	98	3.9
164	507	5.9	60	5.0	294	3.9
165	548	5.9	261	5.0	74	3.9
166	463	5.9	186	5.0	109	3.9
167	528	5.8	468	5.0	343	3.9
168	381	5.8	236	4.9	444	3.9
169	515	5.8	496	4.9	88	3.9
170	407	5.8	38	4.9	71	3.9
171	331	5.8	324	4.9	116	3.9
172	233	5.8	320	4.9	115	3.9
173	365	5.8	185	4.9	147	3.9
174	461	5.8	161	4.9	315	3.9
175	571	5.8	299	4.9	102	3.8
176	383	5.8	508	4.9	105	3.8
177	334	5.8	216	4.9	118	3.8
178	382	5.8	235	4.9	142	3.8
179	462	5.8	239	4.9	18	3.8
180	493	5.8	208	4.9	417	3.8
181	214	5.8	549	4.8	51	3.8
182	350	5.8	244	4.8	149	3.8
183	434	5.8	83	4.8	542	3.8
184	517	5.7	53	4.8	271	3.8
185	388	5.7	123	4.8	70	3.8
186	469	5.7	234	4.8	282	3.8
187	156	5.7	269	4.8	95	3.8
188	578	5.7	442	4.8	229	3.7
189	451	5.7	3	4.8	198	3.7
190	491	5.7	125	4.8	26	3.7
191	379	5.7	111	4.8	72	3.7
192	480	5.7	327	4.8	295	3.7
193	400	5.7	37	4.8	68	3.7
194	511	5.7	280	4.8	127	3.7
195	453	5.7	57	4.8	283	3.7
196	42	5.7	16	4.8	302	3.7
197	308	5.6	158	4.8	163	3.7
198	341	5.6	121	4.8	64	3.7
199	510	5.6	273	4.7	249	3.7
200	518	5.6	412	4.7	7	3.7
	Mean	6.05		5.25		4.23

Note: (i) GN= Germplasm name

Note (ii): All the germplasm lines names start with prefix 'GPDWD'.

Table 11.6. Performance of the germplasm lines for different physiological traits at ARS Dharwad

Sl. No.	Performers	SPAD at 90 DAS		SPAD at 110 DAS		SLW (mg/cm ²) at 90 DAS		Rate of photosynthesis (μ mol CO ₂ /m ² /s) at 90 DAS		Rate of conductance (μ mol CO ₂ /m ² /s) at 90 DAS		Rate of transpiration (m mol H ₂ O/m ² /s) at 90 DAS	
		Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range
1	Best performers	43.1	45.1 to 40.4	48.9	50.1 to 47.5	10.5	10.8 to 10.2	32.6	33.4 to 31.6	0.41	0.45 to 0.38	6.05	6.3 to 5.7
2	Moderate performers	38.8	40.3 to 37.5	45.9	47.4 to 44.6	9.8	10.1 to 9.5	30.5	31.4 to 29.6	0.35	0.37 to 0.32	5.25	5.6 to 4.8
3	Least performers	36.3	37.4 to 35.5	43.2	44.4 to 41.6	9.1	9.4 to 8.8	28.6	29.4 to 27.6	0.29	0.31 to 0.26	4.23	4.7 to 3.7

4.2 Assessment of selected cotton genotypes for drought tolerance by biophysical, root architecture, yield and fibre properties

4.2.1 Evaluation of cotton genotypes for drought tolerance using PEG water stress by slanting glass plate technique

The effect of water potential on seed germination and seedling vigour were evaluated in slanting glass plate technique using Polyethyleneglycol-6000 (PEG) solutions with osmotic potentials of 0.0 MPa, -0.05 MPa, -0.148 MPa, -0.295 MPa, -0.491 MPa, -0.735 MPa and -0.846 MPa, these MPa values were equivalent to the PEG per cent concentrations of 0%, 5%, 10%, 15%, 20%, 25%, 27 per cent respectively.

4.2.1.1 Germination percentage (cf. Table 12.1)

Generally the cotton seed germination percentage was decreased with the decrease in water potential (or by increasing PEG concentration).

The mean seed germination percentage at PEG solutions with osmotic potentials of 0.0 MPa, -0.05 MPa, -0.148 MPa, -0.295 MPa, -0.491 MPa, -0.735 MPa and -0.846 MPa were 100%, 86%, 78%, 63%, 31%, 05 per cent and 0 per cent respectively.

The mean of germination percentage at all the PEG concentrations was higher in the genotype BS-279 (60%) and CNH-120MB (60%), followed by ARB-9701 (56%), GIHV-218 (56%) and CPD-750 (54%). Whereas, it was least in L-761 (44%), KH-155 (47%) and LH-2076 (47%).

All the twelve genotypes seeds were germinated at 0 per cent PEG concentrations. At 5 per cent PEG (-0.05 MPa) concentration the germination percentage was differed among the genotypes. The genotypes BS-279 (100%) and CNH-120MB (100%) recorded highest germination percentage followed by ARB-8908 (90%) and CPD-750 (90%). Whereas, L-761 (70%) followed by KH-155 (80%), F-2228 (80%) and GJHV-477 (80%) recorded lowest germination percentage.

At 10 per cent PEG (-0.05 MPa) concentration the germination percentage was differed among the genotypes. The genotypes BS-279 (90%) and CNH-120MB (90%) recorded highest germination percentage followed by CPD-750 (80%), Sahana (80%) and GIHV-218 (80%). Whereas L-761 (70%) followed by KH-155 (70%), LH-2076 (70%), GJHV-477 (70%) and F-2228 (80%) recorded least.

At 15 per cent PEG (-0.148 MPa) concentration the germination percentage was differed among the genotypes. The genotypes BS-279 (70%), ARB-9701 (70%), CNH-120MB (70%), CPD-750 (70%) and GIHV-218 (70%) recorded highest germination percentages, Whereas, L-761 (50%) recorded least followed by LH-2076 (60%), GJHV-477 (60%) and KH-155 (60%) recorded least.

At 20 per cent PEG (-0.148 MPa) concentration the germination percentage was differed among the genotypes. The genotypes CNH-120MB (40%), ARB-9701 (40%), GIHV-218 (40%), CPD-750 (40%) and BS-279 (40%) recorded highest germination percentages, whereas, L-761 (20%), LH-2076 (20%), GJHV-477 (20%) and KH-155 (20%) recorded least.

At 25 per cent PEG (-0.148 MPa) concentration only four genotypes germinated viz. BS-279 (20%) and CNH-120MB (20%) recorded highest germination percentage, followed by ARB-9701 (10%) and GIHV-218 (10%).

At 27 per cent PEG (-0.846 MPa) concentration there was none of the cotton genotypes was germinated.

4.2.1.2 Shoot length (cm) (cf. Table 12.2)

Generally, the cotton shoot length was decreased with the increase in PEG concentrations from 0 per cent to 27%.

The mean shoot length at all the PEG concentrations at both 12th and 18th DAS stages was higher in the genotype BS-279, followed by CNH-120MB, GIHV-218 and ARB-9701 Whereas, it was least in L-761, KH-155 and LH-2076.

At 12th day, the mean shoot length at PEG solutions with osmotic potentials of 0.0 MPa, -0.05 MPa, -0.148 MPa, -0.295 MPa, -0.491 MPa, -0.735 MPa and -0.846 MPa were 9.5cm, 8.9cm, 6.8cm, 6.1cm, 1.4cm, 0cm and 0cm respectively, whereas at 18th day the corresponding values were 12.2cm, 10.7cm, 8.9cm, 6.2cm, 3.7cm, 0cm and 0cm respectively.

Table 12.1. Effect of different concentrations of PEG-6000 on germination (%) of cotton

Sl. No.	Genotype	Germination (%)							
		PEG-6000 Concentrations							Mean
		0%	5%	10%	15%	20%	25%	27%	
1	CPD-750	100	90	80	70	40	0	0	54
2	Sahana	100	80	80	60	30	0	0	50
3	ARB-9701	100	90	80	70	40	10	0	56
4	CNH-120MB	100	100	90	70	40	20	0	60
5	L-761	100	70	70	50	20	0	0	44
6	LH-2076	100	80	70	60	20	0	0	47
7	GIHV-218	100	90	80	70	40	10	0	56
8	BS-279	100	100	90	70	40	20	0	60
9	RAH-101	100	90	80	60	30	0	0	51
10	GJHV-477	100	80	70	60	20	0	0	47
11	F-2228	100	80	80	60	30	0	0	50
12	KH-155	100	80	70	60	20	0	0	47
Mean		100	86	78	63	31	5	0	52

Table 12.2. Effect of different concentrations of PEG-6000 on cotton shoot length (cm) at different growth stages

Sl. No.	Genotype	12 th day								18 th day							
		PEG-6000 Concentrations							Mean	PEG-6000 Concentrations							Mean
		0%	5%	10%	15%	20%	25%	27%		0%	5%	10%	15%	20%	25%	27%	
1	CPD-750	10.0	10.0	7.6	6.5	1.7	0.0	0.0	5.1	12.4	11.1	9.2	6.5	4.1	0.0	0.0	6.2
2	Sahana	9.6	9.6	7.3	5.5	1.5	0.0	0.0	4.8	12.1	10.8	9.2	6.2	3.9	0.0	0.0	6.0
3	ARB-9701	10.0	10.0	7.8	6.5	1.8	0.0	0.0	5.2	12.4	11.2	9.3	6.7	4.2	0.0	0.0	6.3
4	CNH-120MB	11.3	10.6	8.1	8.0	2.0	0.0	0.0	5.7	13.3	11.3	9.4	6.7	4.2	0.0	0.0	6.4
5	L-761	7.3	6.5	4.5	3.5	0.7	0.0	0.0	3.2	10.7	9.3	7.2	4.7	2.2	0.0	0.0	4.9
6	LH-2076	7.8	7.3	4.8	4.4	1.0	0.0	0.0	3.6	11.7	10.2	8.5	5.7	3.2	0.0	0.0	5.6
7	GIHV-218	10.6	10.3	8.1	7.7	1.8	0.0	0.0	5.5	12.6	11.3	9.4	6.7	4.2	0.0	0.0	6.3
8	BS-279	12.4	10.7	8.5	9.8	2.1	0.0	0.0	6.2	13.8	11.4	9.4	6.8	4.3	0.0	0.0	6.5
9	RAH-101	9.9	9.7	7.4	6.4	1.5	0.0	0.0	5.0	12.4	10.9	9.2	6.3	4.0	0.0	0.0	6.1
10	GJHV-477	8.8	7.7	6.1	4.5	1.0	0.0	0.0	4.0	11.9	10.5	8.7	5.9	3.2	0.0	0.0	5.7
11	F-2228	9.2	8.2	6.8	5.3	1.2	0.0	0.0	4.4	12.0	10.8	9.1	6.2	3.7	0.0	0.0	6.0
12	KH-155	7.6	6.6	4.6	3.8	0.8	0.0	0.0	3.3	11.7	10.1	8.0	5.5	3.2	0.0	0.0	5.5
Mean		9.5	8.9	6.8	6.1	1.4	0.0	0.0	4.7	12.2	10.7	8.9	6.2	3.7	0.0	0.0	5.9

4.2.1.2.1 At 12th DAS

At 0 per cent PEG (0 MPa) concentration, the shoot length was differed among the genotypes. The genotypes BS-279 (12.4cm) recorded highest shoot length followed by CNH-120MB (11.3cm) and GIHV-218 (10.6cm). Whereas, L-761 (7.3cm) recorded lowest followed by KH-155 (7.6 cm) and LH-2076 (7.8 cm).

At 5 per cent PEG (-0.05 MPa) concentration the shoot length was differed among the genotypes. The genotypes BS-279 (10.7 cm) recorded highest shoot length followed by CNH-120MB (10.6 cm), GIHV-218 (10.3 cm), ARB-9701 (10.0 cm) and CPD-750 (10.0 cm). Whereas, L-761 (6.5 cm) followed by KH-155 (6.6 cm) and LH-2076 (7.3 cm) recorded least.

At 10 per cent PEG (-0.148 MPa) concentration the shoot length was differed among the genotypes. The genotypes BS-279 (8.5 cm) followed by CNH-120MB (8.1 cm), GIHV-218 (8.1 cm), ARB-9701 (7.8 cm) and CPD-750 (7.6 cm) recorded highest shoot length. Whereas L-761 (4.5 cm) followed by KH-155 (4.6 cm) and LH-2076 (4.8 cm) recorded least.

At 15 per cent PEG (-0.295 MPa) concentration the shoot length was differed among the genotypes. The genotypes BS-279 (9.8 cm) recorded highest shoot length followed by CNH-120MB (8.0 cm), GIHV-218 (7.7 cm) and ARB-9701 (6.5 cm). Whereas, L-761 (3.5 cm), KH-155 (3.8 cm) and LH-2076 (4.4 cm) recorded least.

At 20 per cent PEG (-0.491 MPa) concentration the shoot length was differed among the genotypes. The genotypes BS-279 (2.1 cm), followed by CNH-120MB (2.0 cm), ARB-9701 (1.8 cm) and GIHV-218 (1.8 cm) recorded highest shoot length, Whereas L-761 (0.7 cm), KH-155 (0.8 cm), GJHV-477 (1.0 cm), LH-2076 (1.0 cm) and F-2228 (1.2 cm) recorded least.

At 25 per cent PEG (-0.735 MPa) and 27 per cent PEG (-0.846 MPa) concentration none of the cotton genotypes were produced shoot growth.

4.2.1.2.2 At 18th DAS

At 0 per cent PEG (0 MPa) concentration, the shoot length was differed among the genotypes. The genotypes BS-279 (13.8 cm) recorded highest shoot length followed by followed by CNH-120MB (13.3 cm) and GIHV-218 (12.6 cm). Whereas, L-761 (10.7 cm) recorded lowest shoot length followed by KH-155 (11.7 cm) and LH-2076 (11.7 cm).

At 5 per cent PEG (-0.05 MPa) concentration the shoot length was differed among the genotypes. The genotypes BS-279 (11.4 cm) followed by CNH-120MB (11.3cm), ARB-9701 (11.2 cm), GIHV-218 (11.3 cm) recorded highest shoot length. Whereas L-761 (9.3cm) followed by KH-155 (10.1cm) and LH-2076 (10.2cm) recorded least.

At 10 per cent PEG (-0.148 MPa) concentration the shoot length was differed among the genotypes. The genotypes BS-279 (8.7 cm), CNH-120MB (9.4 cm), GIHV-218 (9.4 cm), ARB-9701 (9.3 cm) and CPD-750 (9.2 cm) recorded highest shoot length. Whereas, L-761 (7.2 cm) recorded least, followed by KH-155 (8.0 cm) and LH-2076 (8.5 cm) recorded least.

At 15 per cent PEG (-0.295 MPa) concentration the shoot length was differed among the genotypes. The genotypes BS-279 (6.8 cm) followed by ARB-9701 (6.7 cm), CNH-120MB (6.7 cm), GIHV-218 (6.7 cm) and CPD-750 (6.7 cm) recorded highest shoot length. Whereas, L-761 (4.7 cm) followed by KH-155 (5.5 cm) and LH-2076 (5.7 cm) recorded least.

At 20 per cent PEG (-0.491 MPa) concentration the shoot length was differed among the genotypes. The genotypes BS-279 (4.3 cm), ARB-9701 (4.2 cm), CNH-120MB (4.2 cm) and GIHV-218 (4.2 cm) recorded highest shoot length; Whereas, L-761 (2.2 cm), KH-155 (3.2 cm), GJHV-477 (3.2 cm) and LH-2076 (3.2 cm) recorded least.

At 25 per cent PEG (-0.735 MPa) and 27 per cent PEG (-0.846 MPa) concentration none of the cotton genotypes were produced shoots.

4.2.1.3 Root length (cf. Table 12.3)

Generally, in both 12th DAS and 18th DAS the cotton root length was increased with the decrease in water potential (by increasing PEG concentrations) up to 10% PEG concentrations thereafter it declined.

The mean root length at all the PEG concentrations at both 12th and 18th DAS stages was higher in the genotype BS-279 recorded highest, followed by CNH-120MB and GIHV-218 and ARB-9701. Whereas, it was least in L-761, KH-155 and LH-2076.

At 12th day, the mean root length at PEG solutions with osmotic potentials of 0.0 MPa, -0.05 MPa, -0.148 MPa, -0.295 MPa, -0.491 MPa, -0.735 MPa and -0.846 MPa were 7.0cm, 8.5cm, 13.1cm, 8.2cm, 4.4cm, 0.1cm and 0cm respectively, whereas at 18th day the corresponding values were 11.8cm, 13.8cm, 17.3cm, 12.9cm, 6.8cm, 0.5cm and 0cm respectively.

4.2.1.3.1 At 12th DAS

At 0 per cent PEG (0.0 MPa) concentration, the root length was differed among the genotypes. The genotypes BS-279 (8.8 cm) followed by CNH-120MB (8.5 cm) and ARB-9701 (8.2 cm) recorded highest root length. Whereas, L-761 (4.5 cm), LH-2076 (5.1 cm) and KH-155 (4.6 cm) recorded least.

At 5 per cent PEG (-0.05 MPa) concentration the root length was differed among the genotypes. The genotypes BS-279 (11.5 cm) recorded highest root length followed by CNH-120MB (10.0 cm) and GIHV-218 (9.9 cm). Whereas, L-761 (6.4 cm) and KH-155 (6.5 cm) recorded least.

At 10 per cent PEG (-0.148 MPa) concentration the root length was differed among the genotypes. The genotypes BS-279 (16.6cm) recorded highest root length followed by CNH-120MB (16.4cm) and ARB-9701 (13.4cm). Whereas, L-761 (10.6cm) and KH-155 (11.1cm) recorded least.

At 15 per cent PEG (-0.295 MPa) concentration the root length was differed among the genotypes. The genotypes BS-279 (9.7 cm) and CNH-120MB (9.5 cm) recorded highest root length followed by GIHV-218 (9.4 cm) and ARB-9701 (9.2 cm). Whereas, L-761 (6.2 cm) and KH-155 (6.3 cm) recorded least.

At 20 per cent PEG (-0.491 MPa) concentration the root length was differed among the genotypes. The genotypes BS-279 (6.1 cm), CNH-120MB (5.9 cm) and GIHV-218 (5.7 cm) recorded highest root length. Whereas the genotype L-761 (2.0 cm) recorded lowest root length, followed by KH-155 (2.4 cm) and LH-2076 (3.3 cm).

At 25 per cent PEG (-0.735 MPa) concentration the genotypes BS-279 (0.6 cm) followed by CNH-120MB (0.5 cm) and GIHV-218 (0.5 cm) genotypes produced roots.

At 27 per cent PEG (-0.846 MPa) concentration only none of the cotton genotypes were produced roots.

4.2.1.3.2 At 18th DAS

At 0 per cent PEG (0 MPa) concentration, the root length was differed among the genotypes. The genotypes BS-279 (15.1 cm), CNH-120MB (15.1 cm), GIHV-218 (13.0 cm) and ARB-9701 (12.9 cm) recorded highest root length. Whereas, L-761 (9.9 cm), KH-155 (10.5 cm) and LH-2076 (10.5 cm) recorded least.

At 5 per cent PEG (-0.05 MPa) concentration the root length was differed among the genotypes. The genotypes BS-279 (15.1 cm) followed by CNH-120MB (15.1 cm) and ARB-9701 (14.8 cm) recorded highest root length. Whereas, L-761 (12.3 cm) followed by KH-155 (12.5 cm) and LH-2076 (12.7 cm) recorded least.

At 10 per cent PEG (-0.148 MPa) concentration the root length was differed among the genotypes. The genotypes BS-279 (20.2 cm) and CNH-120MB (19.7 cm) recorded highest root length followed by GIHV-218 (19.3 cm) and ARB-9701 (19.2 cm). Whereas, L-761 (14.9 cm) and KH-155 (15.2 cm) recorded least.

At 15 per cent PEG (-0.295 MPa) concentration the root length was differed among the genotypes. The genotypes BS-279 (15.6 cm) recorded highest root length followed by CNH-120MB (15.4 cm) and GIHV-218 (14.7 cm). Whereas L-761 (10.0 cm) recorded lowest root length followed by KH-155 (10.6 cm) and LH-2076 (10.9 cm).

At 20 per cent PEG (-0.491 MPa) concentration the root length was differed among the genotypes. The genotypes BS-279 (11.4 cm) followed by CNH-120MB (11.3 cm) and GIHV-218 (10.3 cm) recorded highest root length. Whereas, L-761 (2.4 cm) recorded lowest root length followed by KH-155 (2.7 cm) and LH-2076 (3.0 cm).

At 25 per cent PEG (-0.735 MPa) concentration only the genotypes BS-279 (2.1 cm), GIHV-218 (1.8 cm), CNH-120MB (1.3 cm) and ARB-9701 (1.2 cm) genotypes were produced root growth.

At 27 per cent PEG (-0.846 MPa) concentration only none of the cotton genotypes were produced roots.

4.2.1.4 Root: shoot ratio (cf. Table 12.4)

At 12th DAS cotton root: shoot ratio was increased with the increase in PEG concentration upto 20%.

At 18th DAS the root: shoot ratio was increased with the increase in PEG concentrations up to 15% PEG, there after it declined.

The mean root: shoot ratio at all the PEG concentration at 18th DAS was higher in the genotypes CNH-120MB (1.3), BS-279 (1.3), GIHV-218 (1.3) and ARB-9701 (1.3). Whereas, it was least in KH-155 (1.0), LH-2076 (1.0) and F-2228 (1.0).

At 12th day, the mean root:shoot ratio at PEG solutions with osmotic potentials of 0.0 MPa, -0.05 MPa, -0.148 MPa, -0.295 MPa, -0.491 MPa, -0.735 MPa and -0.846 MPa were 0.7, 1.0, 2.0, 1.4, 3.1, 0.0 and 0.0 respectively, whereas at 18th day the corresponding values were 1.0, 1.3, 1.9, 2.11.8, 0.0 and 0.0 respectively.

4.2.1.5 Root length index (cf. Table 12.5)

In both stages viz. 12th DAS and 18th DAS the cotton root length index was maximum in 10 per cent PEG followed by 05% PEG, where as it was least in 27 per cent PEG followed by 25% PEG.

The mean root length index at all the PEG concentrations at 12th and 18th DAS was higher in the genotype BS-279, followed by CNH-120MB and GIHV-218. Whereas, it was least in L-761, KH-155 and LH-2076.

At 12th day, the mean root length index at PEG solutions with osmotic potentials of 0.0 MPa, -0.05 MPa, -0.148 MPa, -0.295 MPa, -0.491 MPa, -0.735 MPa and -0.846 MPa were 695, 744, 1035, 526, 146, 2.0 and 0.0 respectively, whereas at 18th day the corresponding values were 1180, 1182, 1355, 814, 210, 03 and 0.0 respectively.

4.2.1.6 Shoot vigour index (cf. Table 12.6)

In both stages viz. 12th DAS and 18th DAS in general, the shoot vigour index was decreased with the increase in PEG concentrations from 0% to 27%.

The mean shoot vigour index at all the PEG concentrations at 12th and 18th DAS was higher in the genotype BS-279, followed by CNH-120MB, GIHV-218 and ARB-9701. Whereas, it was least in L-761, KH-155 and LH-2076.

At 12th day, the mean shoot vigour index at PEG solutions with osmotic potentials of 0.0 MPa, -0.05 MPa, -0.148 MPa, -0.295 MPa, -0.491 MPa, -0.735 MPa and -0.846 MPa were 953, 778, 539, 388, 48, 0.0 and 0.0 respectively, whereas at 18th day the corresponding values were 1224, 921, 696, 391, 114, 0.0 and 0.0 respectively.

4.2.1.7 Seedling vigour index (cf. Table 12.7)

In both stages viz. 12th DAS and 18th DAS in general, the cotton seedling vigour index was decreased with the increase in PEG concentrations from 0 per cent to 27%.

The mean Seedling vigour index at all the PEG concentrations at both stages viz. 12th and 18th DAS was higher in the genotype BS-279, followed by CNH-120MB, GIHV-218 and ARB-9701. Whereas, it was least recorded in L-761, KH-155 and LH-2076.

At 12th day, the mean seedling vigour index at PEG solutions with osmotic potentials of 0.0 MPa, -0.05 MPa, -0.148 MPa, -0.295 MPa, -0.491 MPa, -0.735 MPa and -0.846 MPa were 1648, 1522, 1574, 914, 194, 2.0 and 0.0 respectively, whereas at 18th day the corresponding values were 2404, 2103, 2051, 1205, 324, 03 and 0.0 respectively.

4.2.2 Studies on drought tolerance under Rain out shelter

Based on the first year (2011-12) experimental results at two locations, out of thirty genotypes, ten genotypes (CPD-750, Sahana, ARB-9701, CNH-120MB, GIHV-218, BS-279, RAH-101, GJHV-477, F-2228 and KH-155) were identified as relatively best performer's and two genotypes (L-761 and LH-2076) as least performer's. These genotypes were evaluated in detail at rain out shelter for drought tolerance and the results are as follows.

Table 12.3. Effect of different concentrations of PEG-6000 on cotton root length (cm) at different growth stages

Sl. No.	Genotype	12 th day								18 th day							
		PEG-6000 Concentrations							Mean	PEG-6000 Concentrations							Mean
		0%	5%	10%	15%	20%	25%	27%		0%	5%	10%	15%	20%	25%	27%	
1	CPD-750	8.0	9.1	13.2	9.1	5.0	0.0	0.0	6.3	12.1	14.8	18.5	14.5	7.7	0.0	0.0	9.6
2	Sahana	7.4	8.3	12.9	8.4	4.8	0.0	0.0	6.0	11.7	13.5	15.8	11.5	5.5	0.0	0.0	8.3
3	ARB-9701	8.2	9.4	13.4	9.2	5.4	0.0	0.0	6.5	12.9	14.8	19.2	14.6	10.2	1.2	0.0	10.4
4	CNH-120MB	8.5	10.0	16.4	9.5	5.9	0.5	0.0	7.3	13.0	15.1	19.7	15.4	11.3	1.5	0.0	10.8
5	L-761	4.5	6.4	10.6	6.2	2.0	0.0	0.0	4.2	9.9	12.3	14.9	10.0	2.4	0.0	0.0	7.1
6	LH-2076	5.1	7.1	11.5	6.9	3.3	0.0	0.0	4.8	10.5	12.7	15.5	10.9	3.0	0.0	0.0	7.5
7	GIHV-218	8.3	9.9	13.4	9.4	5.7	0.4	0.0	6.7	13.0	15.1	19.3	14.7	10.3	1.3	0.0	10.5
8	BS-279	8.8	11.5	16.6	9.7	6.1	0.6	0.0	7.6	13.1	15.1	20.2	15.6	11.4	2.1	0.0	11.1
9	RAH-101	7.4	8.7	13.1	8.6	4.8	0	0.0	6.1	11.7	13.8	18.2	13.9	7.1	0.0	0.0	9.3
10	GJHV-477	5.7	7.4	11.9	7.6	3.6	0.0	0.0	5.2	11.6	12.7	15.6	11.3	4.8	0.0	0.0	8.0
11	F-2228	6.9	7.9	12.6	8.0	3.9	0.0	0.0	5.6	11.7	12.9	15.6	11.4	5.3	0.0	0.0	8.1
12	KH-155	4.6	6.5	11.1	6.3	2.4	0.0	0.0	4.4	10.5	12.5	15.2	10.6	2.7	0.0	0.0	7.3
Mean		7.0	8.5	13.1	8.2	4.4	0.1	0.0	5.9	11.8	13.8	17.3	12.9	6.8	0.5	0.0	9.0

Table 12.4. Effect of different concentrations of PEG-6000 on cotton root: shoot ratio at different growth stages

Sl. No.	Genotype	12 th day								18 th day							
		PEG-6000 Concentrations							Mean	PEG-6000 Concentrations							Mean
		0%	5%	10%	15%	20%	25%	27%		0%	5%	10%	15%	20%	25%	27%	
1	CPD-750	0.8	0.9	1.7	1.4	2.9	0.0	0.0	1.1	1.0	1.3	2.0	2.2	1.9	0.0	0.0	1.2
2	Sahana	0.8	0.9	1.8	1.5	3.2	0.0	0.0	1.2	1.0	1.3	1.7	1.8	1.4	0.0	0.0	1.0
3	ARB-9701	0.8	0.9	1.7	1.4	3.0	0.0	0.0	1.1	1.0	1.3	2.1	2.2	2.4	0.0	0.0	1.3
4	CNH-120MB	0.8	0.9	2.0	1.2	3.0	0.0	0.0	1.1	1.0	1.3	2.1	2.3	2.7	0.0	0.0	1.3
5	L-761	0.6	1.0	2.4	1.8	2.9	0.0	0.0	1.2	0.9	1.3	2.1	2.1	1.1	0.0	0.0	1.1
6	LH-2076	0.7	1.0	2.4	1.6	3.3	0.0	0.0	1.3	0.9	1.2	1.8	1.9	0.9	0.0	0.0	1.0
7	GIHV-218	0.8	1.0	1.7	1.2	3.2	0.0	0.0	1.1	1.0	1.3	2.1	2.2	2.4	0.0	0.0	1.3
8	BS-279	0.7	1.1	2.0	1.0	2.9	0.0	0.0	1.1	0.9	1.3	2.1	2.3	2.6	0.0	0.0	1.3
9	RAH-101	0.8	0.9	1.8	1.3	3.2	0.0	0.0	1.1	0.9	1.3	2.0	2.2	1.8	0.0	0.0	1.2
10	GJHV-477	0.6	1.0	2.0	1.7	3.6	0.0	0.0	1.3	1.0	1.2	1.8	1.9	1.5	0.0	0.0	1.1
11	F-2228	0.8	1.0	1.9	1.5	3.3	0.0	0.0	1.2	1.0	1.2	1.7	1.8	1.4	0.0	0.0	1.0
12	KH-155	0.6	1.0	2.4	1.7	3.0	0.0	0.0	1.2	0.9	1.2	1.9	1.9	0.8	0.0	0.0	1.0
Mean		0.7	1.0	2.0	1.4	3.1	0.0	0.0	1.2	1.0	1.3	1.9	2.1	1.8	0.0	0.0	1.1

Table 12.5. Effect of different concentrations of PEG-6000 on cotton root length index at different growth stages

Sl. No.	Genotype	12 th day								18 th day							
		PEG-6000 Concentrations							Mean	PEG-6000 Concentrations							Mean
		0%	5%	10%	15%	20%	25%	27%		0%	5%	10%	15%	20%	25%	27%	
1	CPD-750	800	817	1057	634	199	0	0	501	1209	1330	1476	1015	308	0	0	763
2	Sahana	740	666	1032	501	144	0	0	440	1170	1080	1260	687	165	0	0	623
3	ARB-9701	820	847	1072	641	215	0	0	513	1290	1334	1538	1019	408	12	0	800
4	CNH-120MB	850	1004	1479	667	236	10	0	607	1297	1506	1773	1078	452	30	0	877
5	L-761	450	450	742	308	41	0	0	284	994	861	1042	500	48	0	0	492
6	LH-2076	510	570	805	411	67	0	0	338	1053	1013	1085	653	60	0	0	552
7	GIHV-218	830	894	1072	655	229	4	0	526	1297	1356	1544	1031	412	13	0	808
8	BS-279	880	1153	1494	676	244	12	0	637	1310	1513	1815	1094	456	42	0	890
9	RAH-101	740	785	1049	513	145	0	0	462	1173	1245	1457	835	213	0	0	703
10	GJHV-477	570	591	832	453	71	0	0	360	1159	1016	1091	677	96	0	0	577
11	F-2228	690	628	1008	479	117	0	0	417	1165	1033	1247	684	159	0	0	613
12	KH-155	460	518	777	375	48	0	0	311	1046	998	1063	635	54	0	0	542
Mean		695	744	1035	526	146	2	0	450	1180	1182	1355	814	210	3	0	678

Table 12.6. Effect of different concentrations of PEG-6000 on shoot vigour index of cotton at different growth stages

Sl. No.	Genotype	12 th day								18 th day							
		PEG-6000 Concentrations							Mean	PEG-6000 Concentrations							Mean
		0%	5%	10%	15%	20%	25%	27%		0%	5%	10%	15%	20%	25%	27%	
1	CPD-750	1000	900	605	452	68	0	0	432	1237	1000	737	458	164	0	0	514
2	Sahana	960	771	581	330	45	0	0	384	1211	864	733	374	117	0	0	471
3	ARB-9701	1001	903	621	455	72	0	0	436	1239	1011	746	467	168	0	0	519
4	CNH-120MB	1125	1060	725	560	80	0	0	507	1330	1128	850	470	169	0	0	564
5	L-761	725	454	312	175	14	0	0	240	1067	648	506	234	45	0	0	357
6	LH-2076	783	586	339	264	20	0	0	285	1173	818	594	340	64	0	0	427
7	GIHV-218	1056	927	645	539	72	0	0	463	1259	1013	750	468	169	0	0	523
8	BS-279	1240	1070	761	686	84	0	0	549	1380	1136	850	476	173	0	0	574
9	RAH-101	986	873	589	384	45	0	0	411	1236	981	737	380	120	0	0	493
10	GJHV-477	880	616	424	270	20	0	0	316	1189	840	607	356	65	0	0	437
11	F-2228	919	652	541	317	36	0	0	352	1200	861	729	372	110	0	0	467
12	KH-155	764	528	325	225	16	0	0	265	1165	806	560	331	64	0	0	418
Mean		953	778	539	388	48	0	0	387	1224	921	696	391	114	0	0	478

Table 12.7. Effect of different concentrations of PEG-6000 on seedling vigour index of cotton at different growth stages

Sl. No.	Genotype	12 th day								18 th day							
		PEG-6000 Concentrations							Mean	PEG-6000 Concentrations							Mean
		0%	5%	10%	15%	20%	25%	27%		0%	5%	10%	15%	20%	25%	27%	
1	CPD-750	1800	1717	1662	1086	267	0	0	933	2445	2330	2213	1473	472	0	0	1276
2	Sahana	1700	1437	1613	831	189	0	0	824	2381	1944	1993	1061	282	0	0	1094
3	ARB-9701	1821	1750	1693	1096	287	0	0	949	2529	2345	2284	1485	576	12	0	1319
4	CNH-120MB	1975	2064	2204	1227	316	10	0	1114	2627	2634	2623	1548	621	30	0	1441
5	L-761	1175	904	1054	483	55	0	0	524	2060	1508	1548	734	93	0	0	849
6	LH-2076	1293	1156	1144	675	87	0	0	622	2225	1831	1679	993	124	0	0	979
7	GIHV-218	1886	1821	1717	1194	301	4	0	988	2556	2368	2294	1499	581	13	0	1330
8	BS-279	2120	2223	2255	1362	328	12	0	1186	2690	2649	2665	1569	629	42	0	1464
9	RAH-101	1726	1658	1638	897	190	0	0	872	2409	2226	2194	1215	333	0	0	1197
10	GJHV-477	1450	1207	1256	723	91	0	0	675	2348	1856	1698	1033	161	0	0	1014
11	F-2228	1609	1281	1549	796	153	0	0	769	2365	1894	1976	1056	269	0	0	1080
12	KH-155	1224	1046	1102	600	64	0	0	576	2211	1804	1623	966	118	0	0	960
Mean		1648	1522	1574	914	194	2	0	836	2404	2103	2051	1205	324	3	0	1156

4.2.2.1 Growth and morphological characters

4.2.2.1.1 Plant height (cm) (cf. Table 13)

In general, plant height increased with the age of the crop. The mean plant height was 43.2cm, 69.6cm and 85.8cm at 60 DAS, 90 DAS and 120 DAS respectively. There was significant difference among the moisture stress treatments, genotypes and their interaction for plant height recorded at all the crop stages *i.e.*, 60 DAS, 90 DAS and 120 DAS.

At 60 DAS, among different moisture stress a treatment, the increased water stress resulted in decreased plant height. Among different moisture stress treatments, control recorded significantly more plant height (48.9cm) compared to other stress treatments, followed by moderate moisture stress (42.8cm) and severe moisture stress (37.8cm). Among the genotypes, RAH-101 (55.4cm) showed significantly higher plant height over other genotypes, however, this was on par with GIHV-218 (53.5 cm) followed by ARB-9701 (51.6 cm). While, L-761 (30.6 cm) showed significantly less plant height over other genotypes, followed by LH-2076 (33.9 cm) and KH-155 (36.3 cm).

Among the interaction effects, the genotype RAH-101 (62.9 cm) under control condition showed significantly higher plant height over other genotypes; however, this was on par with GIHV-218 (58.8 cm), followed by ARB-9701 (57.3 cm) under control condition. While, L-761 (27.6 cm) and LH-2076 (28.0 cm) under severe moisture stress showed significantly less plant height over other genotypes and this was this was on par with KH-155 (31.5 cm).

At 90 DAS, among different moisture stress a treatments, the increased water stress resulting in decreased plant height. Among different moisture stress treatments, control (77.7cm) recorded significantly more plant height compared to other stress treatments, followed by moderate moisture stress (69.9cm) and severe moisture stress (61.3cm). Among the genotypes, RAH-101 showed significantly higher plant height (80.9 cm) over other genotypes, however, this was on par with GIHV-218 (79.5 cm) followed by ARB-9701 (77.3 cm), CNH-120MB (74.8 cm) and BS-279 (73.0 cm). While, L-761 (56.9 cm) showed significantly least plant height, followed by LH-2076 (60.4 cm) and KH-155 (63.3 cm).

Among the interaction effects, RAH-101 (90.3 cm) under control condition showed significantly higher plant height over other genotypes; however, this was on par with GIHV-218 (87.1 cm), followed by ARB-9701 (86.3 cm) under control condition. While, LH-2076 (51.7 cm) and L-761 (51.7 cm) under severe moisture stress showed significantly less plant height over other genotypes.

At 120 DAS, among different moisture stress treatments, as the water stress increased the plant height decreased significantly. Among different moisture stress treatments, control recorded significantly more plant height (100.5cm) compared to other stress treatments, followed by moderate moisture stress (86.0cm) and severe moisture stress (70.7cm). Among the genotypes, RAH-101 (96.8 cm) showed significantly higher plant height over other genotypes, however this was on par with GIHV-218 (94.3 cm) followed by ARB-9701 (93.1 cm) and CNH-120MB (90.8 cm). While, L-761 (71.6 cm) showed significantly least plant height, followed by LH-2076 (77.5 cm) and KH-155 (79.1 cm). Among the interaction effects, RAH-101 (114.2 cm) under control condition showed significantly higher plant height over other genotypes; however, this was on par with GIHV-218 (111.0 cm), followed by ARB-9701 (107.9 cm) and CNH-120MB (106.0 cm). While, L-761 (62.4 cm) under severe moisture stress recorded significantly less plant height over other genotypes, however, this was on par with LH-2076 (65.0 cm), KH-155 (65.4 cm) and F-2228 (66.3 cm).

4.2.2.1.2 Number of leaves per plant (cf. Table 14)

In general, the number of leaves per plant increased with the age of the crop up to 90 DAS and decreased thereafter. The mean number of leaves per plant was 43.7, 101.7 and 95.5 at 60 DAS, 90 DAS and 120 DAS respectively. There was significant difference among the moisture stress treatments, genotypes and their interaction for number of leaves per plant at all the stages *i.e.*, 60 DAS, 90 DAS and 120 DAS.

At 60 DAS, among different moisture stress treatments, as the water stress increased the number of leaves per plant decreased significantly. Among different moisture stress treatments, control recorded significantly more number of leaves per plant (47.6) compared to other stress treatments, followed by moderate moisture stress (44.0) and severe moisture stress (39.4). Among the genotypes, RAH-101 (51.3) showed significantly more number of leaves per plant followed by GIHV-218 (47.9), CNH-120MB (46.8) and ARB-9701 (46.3). While, L-761 (38.4) and LH-2076 (39.0) showed significantly least and was on par with KH-155 (39.7) and F-2228 (40.0). Among the

interaction effects, RAH-101 (58.3) under control condition showed significantly more number of leaves per plant followed by GIHV-218 (54.5), however, this was on par with CNH-120MB (52.3) and ARB-9701 (51.4) under control condition and RAH-101 (52.0) in moderate moisture stress condition. While, L-761 (34.0) and LH-2076 (34.5) under severe moisture stress showed significantly less number of leaves per plant among the genotypes, however, these were on par with KH-155 (36.5) and F-2228 (36.8).

At 90 DAS, among different moisture stress treatments, as the water stress increased the number of leaves per plant decreased significantly. Among different moisture stress treatments, control recorded significantly more number of leaves per plant (107.8) over other stress treatments, followed by moderate moisture stress (101.2) and severe moisture stress (96.1). Among the genotypes, RAH-101 (105.8) showed significantly more number of leaves per plant over other genotypes followed by CNH-120MB (103.4), however this was on par with GIHV-218 (103.2), ARB-9701 (103.2) and CPD-750 (102.7). While, L-761 (97.4) and LH-2076 (98.5) showed significantly least followed by F-2228 (100.5). Among the interaction effects, CPD-750 (111.5) and RAH-101 (111.5) under control condition showed significantly more number of leaves per plant over other genotypes followed by CNH-120MB (109.2), however, this was on par with ARB-9701 (109.0). While, L-761 (91.3) under severe moisture stress showed significantly less number of leaves per plant among the genotypes, however, this was on par with LH-2076 (92.6), KH-155 (94.3) and F-2228 (94.8).

At 120 DAS, among different moisture stress treatments, as the water stress increased the number of leaves per plant decreased significantly. Among different moisture stress treatments, control recorded significantly more number of leaves per plant (100.9) compared to other stress treatments, followed by moderate moisture stress (94.9) and severe moisture stress (90.8). Among the genotypes, RAH-101 showed significantly more number of leaves per plant (99.4) over other genotypes followed by GIHV-218 (98.0), however, this was on par with CNH-120MB (97.3). While, L-761 (91.3) and LH-2076 (92.2) showed significantly least, followed by KH-155 (94.1) and F-2228 (94.7). Among the interaction effects, RAH-101 (97.7) under control condition showed significantly more number of leaves per plant over other genotypes, however, this was on par with GIHV-218 (103.3); followed by CNH-120MB (102.2) this was on par with ARB-9701 (102.0) and BS-279 (101.6). While, L-761 (86.2) under severe moisture stress showed significantly less number of leaves per plant among the genotypes, however, this was on par with LH-2076 (87.6) followed by KH-155 (88.6).

4.2.2.2 Phenological characters

4.2.2.2.1 Number of days to 50 per cent squaring (days) (cf. Table 15)

There was a significant difference among the moisture stress treatments and genotypes; however, their interaction effect was non-significant. Among different moisture stress treatments, as the water stress increased the number of days to 50 per cent squaring decreased significantly. Among different moisture stress treatments, control recorded significantly more number of days to 50 per cent squaring (65.8 days) compared to other stress treatments, followed by moderate moisture stress (65.2 days) and severe moisture stress (64.3 days). Among the genotypes, F-2228 (67.0 days) showed significantly more number of days to 50 per cent squaring over other genotypes, however this was on par with LH-2076 (66.9 days), GJHV-477 (66.2 days), L-761 (66.2 days) and KH-155 (66.1 days). While, GIHV-218 (63.6 days) took significantly less number of days to 50 per cent squaring over all the genotypes, however this was on par with ARB-9701 (63.1 days), RAH-101 (63.8 days), BS-279 (64.0 days) and Sahana (64.0 days).

4.2.2.2.2 Number of days to 50 per cent flowering (days) (cf. Table 15)

There was a significant difference among the moisture stress treatments and genotypes; however, their interaction effect was non-significant.

Among different moisture stress treatments, as the water stress increased the number of days to 50 per cent flowering decreased significantly. Among different moisture stress treatments, control recorded significantly more number of days to 50 per cent flowering (81.1 days) compared to other stress treatments, followed by moderate moisture stress (80.2 days) and severe moisture stress (78.6 days). Among the genotypes, L-761 (81.5 days) showed significantly more number of days to 50 per cent flowering over all others, followed by KH-155 (80.6 days), however, this was on par with CPD-750 (80.3 days), RAH-101 (80.3 days), LH-2076 (80.3 days), GJHV-477 (80.2 days) and F-2228 (80.2 days). While, GIHV-218 (79.7 days) took significantly less number of days to 50 per cent flowering over all the genotypes, followed by BS-279 (79.4 days), ARB-9701 (79.6 days) and Sahana (79.7 days).

Table 13. Effect of different levels of moisture stresses on plant height (cm) in cotton genotypes at different growth stages

Sl. No.	Genotypes	60 DAS				90 DAS				120 DAS			
		M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean
1	CPD-750	43.2	40.5	33.4	39.0	72.3	70.7	57.9	67.0	98.2	82.6	67.6	82.8
2	Sahana	47.7	41.7	34.7	41.4	78.2	67.8	58.7	68.2	100.7	85.4	67.8	84.6
3	ARB-9701	57.3	49.6	47.7	51.6	86.3	76.9	68.7	77.3	107.9	93.5	78.1	93.1
4	CNH-120MB	53.3	47.3	42.1	47.6	83.6	74.7	66.1	74.8	106.0	91.4	75.0	90.8
5	L-761	32.1	32.2	27.6	30.6	59.5	59.3	51.7	56.9	79.7	72.6	62.4	71.6
6	LH-2076	41.0	32.6	28.0	33.9	70.3	59.3	51.7	60.4	90.9	76.7	65.0	77.5
7	GIHV-218	58.8	53.2	48.5	53.5	87.1	80.5	70.8	79.5	111.0	93.6	78.3	94.3
8	BS-279	53.3	46.2	41.8	47.1	81.6	72.6	64.7	73.0	105.7	90.2	73.8	89.9
9	RAH-101	62.9	54.6	48.7	55.4	90.3	81.0	71.3	80.9	114.2	96.8	79.5	96.8
10	GJHV-477	53.0	44.8	36.8	44.9	80.4	70.7	60.0	70.4	105.1	88.4	69.2	87.6
11	F-2228	41.9	35.4	33.2	36.8	71.5	62.7	57.2	63.8	95.7	80.8	66.3	80.9
12	KH-155	41.7	35.6	31.5	36.3	71.0	62.3	56.7	63.3	91.6	80.2	65.4	79.1
Mean		48.9	42.8	37.8	43.2	77.7	69.9	61.3	69.6	100.5	86.0	70.7	85.8
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.729		2.864		1.017		3.992		0.468		1.839	
Sub		0.769		2.172		0.929		2.623		0.988		2.789	
M x S		1.333		3.763		1.609		4.543		1.711		4.830	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress, DAS= Days after sowing

Table 14. Effect of different levels of moisture stresses on number of leaves/plant in cotton genotypes at different growth stages

Sl. No.	Genotypes	60 DAS				90 DAS				120 DAS			
		M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean
1	CPD-750	43.3	41.0	40.8	41.7	111.5	101.0	95.6	102.7	100.4	94.9	90.2	95.2
2	Sahana	46.7	44.2	40.8	43.9	106.7	101.2	96.0	101.3	100.6	95.0	90.5	95.4
3	ARB-9701	51.4	46.2	41.2	46.3	109.0	103.3	97.3	103.2	102.0	96.4	92.3	96.9
4	CNH-120MB	52.3	46.5	41.5	46.8	109.2	103.3	97.7	103.4	102.2	97.0	92.7	97.3
5	L-761	42.1	39.2	34.0	38.4	104.8	96.0	91.3	97.4	97.8	89.9	86.2	91.3
6	LH-2076	42.2	40.2	34.5	39.0	106.7	96.3	92.6	98.5	98.8	90.2	87.6	92.2
7	GIHV-218	54.5	47.5	41.8	47.9	107.1	103.7	98.8	103.2	103.3	97.6	93.2	98.0
8	BS-279	48.2	45.7	41.0	45.0	108.3	101.7	97.2	102.4	101.6	95.3	91.3	96.1
9	RAH-101Yc	58.3	52.0	43.6	51.3	111.5	104.5	101.3	105.8	104.3	97.7	96.1	99.4
10	GJHV-477	47.5	45.2	41.0	44.6	105.7	101.3	96.8	101.3	101.0	95.2	90.8	95.6
11	F-2228	42.4	40.7	36.8	40.0	105.8	101.0	94.8	100.5	99.7	94.8	89.6	94.7
12	KH-155	42.3	40.2	36.5	39.7	107.6	100.8	94.3	100.9	99.1	94.6	88.6	94.1
Mean		47.6	44.0	39.4	43.7	107.8	101.2	96.1	101.7	100.9	94.9	90.8	95.5
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.596		2.342		0.269		1.056		0.236		0.928	
Sub		0.704		1.989		0.541		1.526		0.321		0.908	
M x S		1.220		3.445		0.936		2.644		0.557		1.572	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress, DAS= Days after sowing

Table 15. Effect of different levels of moisture stresses on Days to 50% squaring and Days to 50% flowering in cotton genotypes

Sl. No.	Genotypes	Days to 50% squaring				Days to 50% flowering			
		M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean
1	CPD-750	66.0	66.0	64.7	65.6	81.3	80.4	79.0	80.3
2	Sahana	65.0	64.0	63.0	64.0	80.3	80.0	78.8	79.7
3	ARB-9701	63.7	63.0	62.7	63.1	80.3	79.7	78.8	79.6
4	CNH-120MB	65.0	64.7	63.7	64.4	79.7	77.8	76.5	78.0
5	L-761	66.7	66.3	65.7	66.2	83.0	81.7	79.9	81.5
6	LH-2076	67.7	67.0	66.0	66.9	82.0	80.7	78.2	80.3
7	GIHV-218	64.3	63.7	62.7	63.6	80.0	79.7	79.4	79.7
8	BS-279	65.0	64.0	63.0	64.0	80.3	79.7	78.0	79.4
9	RAH-101	64.3	64.0	63.0	63.8	81.3	80.4	79.1	80.3
10	GJHV-477	67.3	66.3	65.0	66.2	81.7	80.7	78.1	80.2
11	F-2228	67.7	67.0	66.3	67.0	81.3	80.7	78.5	80.2
12	KH-155	66.7	66.3	65.3	66.1	82.3	80.4	79.1	80.6
Mean		65.8	65.2	64.3	65.1	81.1	80.2	78.6	80.0
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.185		0.726		0.065		0.254	
Sub		0.309		0.873		0.275		0.775	
M x S		0.535		NS		0.475		NS	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress NS= Non-significant

4.2.2.2.3 Number of days to maturity (days) (cf. Table 16)

There was a significant difference among the moisture stress treatments and genotypes; however, their interaction effect was non-significant.

Among different moisture stress treatments, as the water stress increased the number of days taken to maturity decreased significantly. Among different moisture stress treatments, control recorded significantly more number of days taken to maturity (165.7 days) compared to other stress treatments, followed by moderate moisture stress (164.1 days) and severe moisture stress (163.6 days). Among the genotypes, LH-2076 (165.7 days) took more number of days to maturity over other genotypes; however, this was on par with L-761 (165.6 days), KH-155 (165.5 days) and F-2228 (165.3 days). While, GIHV-218 (163.9 days) took significantly less number of days to maturity over all the genotypes, however, this was on par with ARB-9701 (163.6 days), Sahana (163.6 days) and RAH-101 (163.8 days).

4.2.2.3 Morpho physiological parameters

4.2.2.3.1 Total dry matter production (TDM) (g/plant) (cf. Table 17)

The mean total dry matter was $34.3 \text{ g plant}^{-1}$ and $87.9 \text{ g plant}^{-1}$ at 90 DAS and 120 DAS respectively. There was significant difference among the moisture stress treatments, genotypes and their interaction at all the stages *i.e.*, 90 DAS and 120 DAS.

At 90 DAS, among different moisture stress treatments, as the water stress increased the TDM decreased significantly. Among different moisture stress treatments, control recorded significantly more TDM (43.4 g/plant) compared to other stress treatments, followed by moderate moisture stress (31.8 g/plant) and severe moisture stress (27.8 g/plant). Among the genotypes, GIHV-218 (38.2 g/plant) and CNH-120MB (37.5 g/plant) recorded significantly more TDM per plant over other genotypes followed by BS-279 (36.1 g/plant), however, this was on par with ARB-9701 (35.8 g/plant). While, L-761 (30.3 g/plant) recorded significantly lesser followed by LH-2076 (32.0 g/plant) and was on par with F-2228 (33.0 g/plant) and KH-155 (32.9 g/plant).

At 120 DAS, among different moisture stress treatments, as the water stress increased the TDM decreased significantly. Among different moisture stress treatments, control (99.8 g/plant) recorded significantly more TDM compared to other stress treatments, followed by moderate moisture stress (84.9 g/plant) and severe moisture stress (79.1 g/plant). Among the genotypes, GIHV-218 (91.8 g/plant) and CNH-120MB (91.1 g/plant) recorded significantly more TDM per plant over other genotypes followed by BS-279 (89.7 g/plant) and ARB-9701 (89.4 g/plant). While, L-761 (83.9 g/plant) recorded significantly less TDM, followed by LH-2076 (85.6 g/plant), however, this was on par with KH-155 (86.5 g/plant) and F-2228 (86.6 g/plant).

Among the interaction effects GIHV-218 ($47.2 \text{ g plant}^{-1}$ at 90 DAS, $103.6 \text{ g plant}^{-1}$ at 120 DAS) under control condition showed significantly more TDM over other genotypes, however, this was on par with CNH-120MB ($46.9 \text{ g plant}^{-1}$ at 90 DAS, $103.3 \text{ g plant}^{-1}$ at 120 DAS); followed by BS-279 ($46.49 \text{ g plant}^{-1}$ at 90 DAS, $102.8 \text{ g plant}^{-1}$ at 120 DAS) and ARB-9701 ($45.3 \text{ g plant}^{-1}$ at 90 DAS, $101.7 \text{ g plant}^{-1}$ at 120 DAS) under control condition. While ($25.3 \text{ g plant}^{-1}$ at 90 DAS, $76.6 \text{ g plant}^{-1}$ at 120 DAS) ($25.4 \text{ g plant}^{-1}$ at 90 DAS, $76.7 \text{ g plant}^{-1}$ at 120 DAS) and ($25.7 \text{ g plant}^{-1}$ at 90 DAS, $77.0 \text{ g plant}^{-1}$ at 120 DAS) under severe moisture stress showed less TDM among the genotypes.

4.2.2.3.2 Net assimilation rate (NAR) ($\text{g/dm}^2/\text{day}$) (cf. Table 18)

The mean net assimilation rate was $0.040 \text{ g/dm}^2/\text{day}$. There was significant difference among the moisture stress treatments and genotypes; however, their interaction effect was non-significant.

Among different moisture stress treatments, as the water stress increased the net assimilation rate was decreased. Among different moisture stress treatments, control ($0.041 \text{ g/dm}^2/\text{day}$) and moderate moisture stress ($0.041 \text{ g/dm}^2/\text{day}$) recorded significantly more NAR followed by and severe moisture stress ($0.037 \text{ g/dm}^2/\text{day}$). Among the genotypes, GIHV-218 ($0.044 \text{ g/dm}^2/\text{day}$), CNH-120MB ($0.044 \text{ g/dm}^2/\text{day}$) and ARB-9701 ($0.044 \text{ g/dm}^2/\text{day}$) recorded significantly more total NAR over all others followed by RAH-101 ($0.043 \text{ g/dm}^2/\text{day}$). While, KH-155 ($0.034 \text{ g/dm}^2/\text{day}$), LH-2076 ($0.034 \text{ g/dm}^2/\text{day}$) L-761 ($0.035 \text{ g/dm}^2/\text{day}$) and F-2228 ($0.035 \text{ g/dm}^2/\text{day}$) recorded NAR among the genotypes.

Table 16. Effect of different levels of moisture stresses on Days to maturity (days), Ginning out turn (%) in cotton genotypes

Sl. No.	Genotypes	Days to maturity				Ginning out turn			
		M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean
1	CPD-750	165.7	164.3	163.7	164.6	38.7	37.3	35.9	37.3
2	Sahana	165.0	163.3	162.3	163.6	39.0	36.0	35.9	37.0
3	ARB-9701	165.0	163.0	162.7	163.6	39.3	37.3	36.6	37.7
4	CNH-120MB	165.3	163.7	163.7	164.2	39.5	38.0	36.8	38.1
5	L-761	166.7	165.7	164.3	165.6	36.0	35.0	34.6	35.2
6	LH-2076	166.7	165.7	164.7	165.7	36.2	35.1	34.9	35.4
7	GIHV-218	165.0	163.3	163.3	163.9	39.6	38.6	37.0	38.4
8	BS-279	165.0	163.0	162.3	163.4	39.3	37.7	36.6	37.9
9	RAH-101	165.0	163.7	162.7	163.8	38.3	36.0	36.2	36.8
10	GJHV-477	166.0	164.0	163.3	164.4	38.3	35.4	35.7	36.5
11	F-2228	166.0	165.0	165.0	165.3	37.5	35.2	35.3	36.0
12	KH-155	166.7	165.0	164.8	165.5	37.0	35.3	35.2	35.8
Mean		165.7	164.1	163.6	164.5	38.2	36.4	35.9	36.8
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.104		0.408		0.089		0.351	
Sub		0.147		0.415		0.190		0.537	
M x S		0.255		NS		0.329		0.930	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress NS= Non-significant

Table 17. Effect of different levels of moisture stresses on total dry matter (g/plant) in cotton genotypes at different growth stages

Sl. No.	Genotypes	90 DAS				120 DAS			
		M1	M2	M3	Mean	M1	M2	M3	Mean
1	CPD-750	44.3	31.6	26.7	34.2	100.7	84.7	78.0	87.8
2	Sahana	44.6	31.6	26.9	34.4	100.0	84.7	78.2	87.6
3	ARB-9701	45.3	32.2	30.0	35.8	101.7	85.3	81.3	89.4
4	CNH-120MB	46.9	34.2	31.4	37.5	103.3	87.3	82.7	91.1
5	L-761	35.8	29.9	25.3	30.3	92.2	83.0	76.6	83.9
6	LH-2076	40.7	29.9	25.4	32.0	97.1	83.0	76.7	85.6
7	GIHV-218	47.2	35.2	32.2	38.2	103.6	88.3	83.5	91.8
8	BS-279	46.4	32.2	29.7	36.1	102.8	85.3	81.0	89.7
9	RAH-101	43.3	31.9	27.1	34.1	99.7	85.0	78.4	87.7
10	GJHV-477	43.0	31.2	26.5	33.6	99.4	84.3	77.8	87.2
11	F-2228	41.7	31.2	26.2	33.0	98.1	84.3	77.5	86.6
12	KH-155	42.2	30.9	25.7	32.9	98.6	84.0	77.0	86.5
Mean		43.4	31.8	27.8	34.3	99.8	84.9	79.1	87.9
For comparing		S.E.m±		CD at 5%		S.E.m±		CD at 5%	
Main		0.146		0.572		0.188		0.738	
Sub		0.383		1.081		0.457		1.291	
M × S		0.663		1.873		0.792		2.236	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress NS= Non-significant

4.2.2.3.3 Relative growth rate (RGR) (g/g/day) (cf. Table 19)

The mean relative growth rate was 0.0170 and 0.0192 at 0-90 DAS and 90-120 DAS respectively.

In present study, as the water stress increased the relative growth rate was decreased. At 0-90 DAS among different moisture stress treatments, control (0.0182 g/g/day) recorded significantly more RGR compared to other stress treatments, followed by moderate moisture stress (0.0167 g/g/day) and severe moisture stress (0.0160 g/g/day). Among the genotypes, GIHV-218 (0.0175 g/g/day) followed by CNH-120MB (0.0174 g/g/day) and ARB-9701 (0.0172 g/g/day) recorded significantly more RGR over other genotypes. While, L-761 (0.0164 g/g/day) and LH-2076 (0.0166 g/g/day) recorded least.

At 90-120 DAS There was significant difference among the moisture stress treatments, whereas among genotypes and their interaction effect was non-significant. At 90-120 DAS among different moisture stress treatments, control (0.0195 g/dm²/day) recorded significantly more RGR compared to other stress treatments, followed by moderate moisture stress (0.0192 g/dm²/day) and severe moisture stress (0.0190 g/dm²/day).

4.2.2.3.4 Specific leaf weight (SLW) (mg/cm²) (cf. Table 20)

In general, SLW increased with the age of the crop. The mean SLW was 8.4 mg/cm² and 8.8 mg/cm² at 90 DAS and 120 DAS respectively. There was significant difference among treatments, genotypes and their interaction effect at all the stages *i.e.*, 60 DAS, 90 DAS and 120 DAS.

At 90 DAS, among different moisture stress treatments, as the water stress increased the SLW decreased significantly. Among different moisture stress treatments, control recorded significantly more SLW (9.3 mg/cm²) over other stress treatments, followed by moderate moisture stress (8.4 mg/cm²) and severe moisture stress (7.3 mg/cm²). Among the genotypes, GIHV-218 (9.4 mg/cm²) showed significantly more SLW over other genotypes followed by BS-279 (9.0 mg/cm²), however this was on par with CNH-120MB (8.9 mg/cm²). While, LH-2076 (7.5 mg/cm²) showed significantly less SLW, however this was on par with L-761 (7.6 mg/cm²) followed by KH-155 (7.7 mg/cm²). Among the interaction effects, GIHV-218 (10.2 mg/cm²) under control condition showed significantly more SLW over other genotypes, however, this was on par with ARB-9701 (10.1 mg/cm²) followed by BS-279 (9.8 mg/cm²) under control condition. While, LH-2076 (6.8 mg/cm²) under severe moisture stress showed significantly less SLW over other genotypes, however, this was on par with L-761 (6.9 mg/cm²) and KH-155 (6.9 mg/cm²).

At 120 DAS, among different moisture stress treatments, as the water stress increased the SLW decreased significantly. Among different moisture stress treatments, control recorded significantly more SLW (9.9 mg/cm²) compared to other stress treatments, followed by moderate moisture stress (8.9 mg/cm²) and severe moisture stress (7.6 mg/cm²). Among the genotypes, GIHV-218 (9.9) showed significantly more SLW over other genotypes followed by BS-279 (9.4), however, this was on par with ARB-9701 (9.3) and CNH-120MB (9.3). While, LH-2076 (7.8) and L-761 (7.9) showed significantly less SLW followed by KH-155 (8.1).

Among the interaction effects, GIHV-218 (10.7) under control condition showed significantly more SLW over other genotypes, however, this was on par with ARB-9701 (10.6) followed by GIHV-218 (10.3) under moderate moisture stress condition. While, LH-2076 (6.5) under severe moisture stress showed significantly less SLW, however, this was on par with L-761 (6.7) and KH-155 (6.9).

4.2.2.3.5 Leaf area index (LAI) (cf. Table 21)

In general, LAI increased with the age of the crop up to 90 DAS and decreased thereafter. The mean LAI was 1.4, 3.3 and 2.4 at 60 DAS, 90 DAS and 120 DAS respectively. There was significant difference among the moisture stress treatments, genotypes and their interaction at all stages.

At 60 DAS, among different moisture stress treatments, as the water stress increased the LAI decreased significantly. Among different moisture stress treatments, control recorded significantly more LAI (1.6) compared to other stress treatments, followed by moderate moisture stress (1.4) and severe moisture stress (1.2). Among the genotypes, CNH-120MB (1.7) showed significantly more LAI over other genotypes, however, this was on par with GIHV-218 (1.6), followed by BS-279 (1.5), ARB-9701 (1.5) and RAH-101 (1.5). While, L-761 (1.2) showed significantly less LAI, however this was on par with KH-155 (1.3) and LH-2076 (1.3). Among the interaction effects, CNH-120MB (1.9) under control condition showed significantly more LAI over other genotypes; however, this was on par with CPD-750 (1.8) and ARB-9701 (1.8). While, L-761 (1.0) under severe moisture stress showed significantly less LAI over other genotypes, followed by KH-155 (1.1) and LH-2076 (1.1).

At 90 DAS, among different moisture stress treatments, as the water stress increased the LAI decreased significantly. Among different moisture stress treatments, control recorded significantly more LAI (3.4) over other stress treatments, followed by moderate moisture stress (2.6) and severe moisture stress (2.2). Among the genotypes, GIHV-218 (3.5) showed significantly more LAI over other genotypes, followed by BS-279 (3.1), however, this was on par with CNH-120MB (3.1) and ARB-9701 (3.0). While, LH-2076 (2.0) and L-761 (2.1) showed significantly less LAI over other genotypes. Among the interaction effects, GIHV-218 (4.2) under control condition showed significantly more LAI over other genotypes; however, this was on par with CNH-120MB (4.0), BS-279 (4.0) and ARB-9701 (3.9) under control condition. While, L-761 (1.6) and LH-2076 (1.7) under severe moisture stress showed significantly less LAI over other genotypes, however, these were on par with KH-155 (1.9), F-2228 (2.1) and GJHV-477 (2.1).

At 120 DAS, among different moisture stress treatments, as the water stress increased the LAI decreased significantly. Among different moisture stress treatments, control recorded significantly more LAI (3.0) compared to other stress treatments, followed by moderate moisture stress (2.3) and severe moisture stress (1.9). Among the genotypes, GIHV-218 (3.1) showed significantly more LAI over other genotypes, followed by BS-279 (2.8), CNH-120MB (2.8) and ARB-9701 (2.6). While, L-761 (1.6) and LH-2076 (1.7) showed significantly less LAI, followed by KH-155 (2.2), F-2228 (2.3) and GJHV-477 (2.4). Among the interaction effects, GIHV-218 (3.9) under control condition showed significantly more LAI over other genotypes; and it was on par with CNH-120MB (3.8) and BS-279 (3.7). While, L-761 (1.2) and LH-2076 (1.3) under severe moisture stress showed significantly less LAI over other genotypes, followed by KH-155 (2.2).

4.2.2.4 Biophysical and biochemical characters

4.2.2.4.1 Rate of photosynthesis ($\mu \text{ mol CO}_2/\text{m}^2/\text{s}$) (cf. Table 22)

The mean rate of photosynthesis was $25.9 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$ and $22.7 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$ at 90 DAS and 120 DAS respectively. There was significant difference among the moisture stress treatments, genotypes and their interaction effect at all the crop stages *i.e.*, 90 DAS and 120 DAS.

At 90 DAS, among different moisture stress treatments, as the water stress increased the rate of photosynthesis decreased significantly. Among different moisture stress treatments, control ($30.2 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) recorded significantly more rate of photosynthesis over other stress treatments, followed by moderate moisture stress ($25.6 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) and severe moisture stress ($21.8 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$). The treatment severe moisture stress significantly affects the rate of photosynthesis, which records least ($21.8 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) over other moisture stress treatments. Among the genotypes, GIHV-218 ($28.8 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) followed by CNH-120MB ($28.6 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$), BS-279 ($28.5 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) and ARB-9701 ($28.4 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) showed significantly highest rate of photosynthesis over other genotypes, however, these genotypes were on par with each other. While, L-761 ($20.8 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) showed significantly less rate of photosynthesis over other genotypes, followed by LH-2076 ($22.2 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) and KH-155 ($23.3 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$). Among the interaction effects, GIHV-218 ($33.8 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) under control condition showed significantly highest rate of photosynthesis over other genotypes, however, this was on par with CNH-120MB ($33.4 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$), BS-279 ($33.4 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$), ARB-9701 ($33.3 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) and CPD-750 ($33.1 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) under control condition. While, L-761 ($17.7 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) under severe moisture stress showed significantly less rate of photosynthesis over other genotypes, however, this was on par with LH-2076 ($17.9 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) and KH-155 ($18.2 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$).

At 120 DAS, among different moisture stress treatments, as the water stress increased the rate of photosynthesis decreased significantly. The control recorded significantly more rate of photosynthesis ($26.8 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) compared to other stress treatments, followed by moderate moisture stress ($22.9 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) and severe moisture stress ($18.4 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$). Among the genotypes, GIHV-218 ($26.4 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) showed significantly highest rate of photosynthesis over other genotypes, followed by BS-279 ($25.0 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$), however, this genotype was on par with CNH-120MB ($25.0 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) and ARB-9701 ($24.6 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$). While, L-761 ($19.1 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$), LH-2076 ($19.6 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) and KH-155 ($20.2 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) showed significantly less rate of photosynthesis over other genotypes, however these genotypes were on par with each other. Among the interaction effects, GIHV-218 ($31.2 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) followed by BS-279 ($30.5 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$), CNH-120MB ($29.8 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) and ARB-9701 ($29.5 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) under control condition recorded highest rate of photosynthesis over other genotypes. While, L-761 ($14.9 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) under severe moisture stress showed significantly less over other genotypes, however this was on par with LH-2076 ($15.2 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$) and KH-155 ($16.6 \mu \text{ mol CO}_2/\text{m}^2/\text{s}$).

Table 18. Effect of different levels of moisture stresses on net assimilation rate (g/dm²/day) in cotton genotypes

Sl. No.	Genotypes	NAR at 90-120 DAS			
		M1	M2	M3	Mean
1	CPD-750	0.040	0.038	0.032	0.036
2	SAHANA	0.043	0.042	0.038	0.041
3	ARB-9701	0.045	0.045	0.042	0.044
4	CNH120MB	0.045	0.045	0.042	0.044
5	L-761	0.037	0.038	0.030	0.035
6	LH-2076	0.035	0.039	0.030	0.034
7	GIHV-218	0.044	0.045	0.042	0.044
8	BS-279	0.043	0.044	0.040	0.042
9	RAH-101	0.043	0.045	0.041	0.043
10	GJHV-477	0.044	0.044	0.040	0.043
11	F-2228	0.038	0.035	0.033	0.035
12	KH-155	0.035	0.032	0.035	0.034
Mean		0.041	0.041	0.037	0.040
For comparing		S.E.m $\pm$		CD at 5%	
Main		0.000396		0.001554	
Sub		0.001269		0.003582	
M x S		0.002197		NS	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress NS= Non-significant

Table 19. Effect of different levels of moisture stresses on relative growth rate (g/g/day) in cotton genotypes at different growth stages

Sl. No.	Genotypes	0-90 DAS				90-120 DAS			
		M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean
1	CPD-750	0.0183	0.0167	0.0159	0.0169	0.0195	0.0192	0.0190	0.01921
2	Sahana	0.0183	0.0167	0.0159	0.0170	0.0194	0.0192	0.0190	0.01918
3	ARB-9701	0.0184	0.0168	0.0164	0.0172	0.0195	0.0192	0.0190	0.01921
4	CNH-120MB	0.0186	0.0170	0.0166	0.0174	0.0195	0.0192	0.0190	0.01921
5	L-761	0.0173	0.0164	0.0156	0.0164	0.0195	0.0192	0.0190	0.01921
6	LH-2076	0.0179	0.0164	0.0156	0.0166	0.0195	0.0192	0.0190	0.01921
7	GIHV-218	0.0186	0.0172	0.0167	0.0175	0.0195	0.0192	0.0190	0.01921
8	BS-279	0.0185	0.0168	0.0164	0.0172	0.0195	0.0192	0.0190	0.01921
9	RAH-101	0.0182	0.0167	0.0159	0.0169	0.0195	0.0192	0.0190	0.01921
10	GJHV-477	0.0182	0.0166	0.0158	0.0169	0.0195	0.0192	0.0190	0.01921
11	F-2228	0.0180	0.0166	0.0158	0.0168	0.0195	0.0192	0.0190	0.01921
12	KH-155	0.0181	0.0166	0.0157	0.0168	0.0195	0.0192	0.0190	0.01921
Mean		0.0182	0.0167	0.0160	0.0170	0.0195	0.0192	0.0190	0.01921
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.000023		0.000089		0.0000214		0.0000838	
Sub		0.000056		0.000157		0.0000402		NS	
M x S		0.000096		0.000272		0.0000696		NS	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress NS= Non-significant, DAS= Days after sowing

Table 20. Effect of different levels of moisture stresses on specific leaf weight (mg/cm²) in cotton genotypes at different growth stages

Sl. No.	Genotypes	90 DAS				120 DAS			
		M1	M2	M3	Mean	M1	M2	M3	Mean
1	CPD-750	9.7	8.7	7.1	8.5	10.1	9.2	7.3	8.9
2	Sahana	9.7	8.6	7.3	8.5	10.1	9.1	7.8	9.0
3	ARB-9701	10.1	8.8	7.5	8.8	10.6	9.2	8.2	9.3
4	CNH-120MB	9.7	9.0	8.1	8.9	10.2	9.3	8.4	9.3
5	L-761	8.5	7.5	6.9	7.6	9.1	7.9	6.7	7.9
6	LH-2076	8.4	7.4	6.8	7.5	9.0	7.9	6.5	7.8
7	GIHV-218	10.2	9.7	8.3	9.4	10.7	10.3	8.8	9.9
8	BS-279	9.8	9.6	7.7	9.0	10.2	9.6	8.3	9.4
9	RAH-101	9.3	8.6	7.5	8.5	10.1	8.9	8.1	9.0
10	GJHV-477	9.0	8.1	7.1	8.0	9.6	8.7	7.2	8.5
11	F-2228	9.0	7.7	7.0	7.9	9.5	8.6	6.9	8.3
12	KH-155	8.7	7.6	6.9	7.7	9.2	8.2	6.9	8.1
Mean		9.3	8.4	7.3	8.4	9.9	8.9	7.6	8.8
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.010		0.041		0.022		0.087	
Sub		0.070		0.199		0.068		0.191	
M × S		0.122		0.344		0.117		0.330	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress NS= Non-significant, DAS= Days after sowing

Table 21. Effect of different levels of moisture stresses on Leaf area index in cotton genotypes at different growth stages

Sl. No.	Genotypes	60 DAS				90 DAS				120 DAS			
		M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean
1	CPD-750	1.8	1.2	1.2	1.4	3.6	2.6	2.3	2.8	3.2	2.3	2.0	2.5
2	Sahana	1.7	1.4	1.2	1.4	3.5	2.6	2.3	2.8	3.2	2.3	2.0	2.5
3	ARB-9701	1.8	1.5	1.3	1.5	3.9	2.8	2.4	3.0	3.2	2.4	2.1	2.6
4	CNH-120MB	1.9	1.5	1.5	1.7	4.0	2.6	2.6	3.1	3.8	2.3	2.2	2.8
5	L-761	1.3	1.4	1.0	1.2	2.3	2.5	1.6	2.1	1.9	1.8	1.2	1.6
6	LH-2076	1.5	1.5	1.1	1.3	2.3	2.1	1.7	2.0	2.0	1.9	1.3	1.7
7	GIHV-218	1.3	1.7	1.7	1.6	4.2	3.3	2.9	3.5	3.9	3.0	2.5	3.1
8	BS-279	1.8	1.5	1.3	1.5	4.0	2.8	2.6	3.1	3.7	2.4	2.2	2.8
9	RAH-101	1.6	1.6	1.3	1.5	3.5	2.7	2.3	2.8	3.1	2.4	2.0	2.5
10	GJHV-477	1.6	1.3	1.2	1.4	3.4	2.6	2.1	2.7	3.0	2.3	1.9	2.4
11	F-2228	1.6	1.4	1.2	1.4	3.1	2.6	2.1	2.6	2.7	2.2	1.9	2.3
12	KH-155	1.5	1.4	1.1	1.3	3.0	2.5	1.9	2.5	2.6	2.2	1.8	2.2
Mean		1.6	1.4	1.2	1.4	3.4	2.6	2.2	2.8	3.0	2.3	1.9	2.4
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.020		0.077		0.090		0.355		0.110		0.431	
Sub		0.057		0.161		0.094		0.264		0.088		0.247	
M x S		0.099		0.279		0.162		0.458		0.152		0.429	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress, DAS= Days after sowing

Table 22. Effect of different levels of moisture stresses on rate of photosynthesis (μ mol CO₂/m²/s), stomatal conductance (μ mol CO₂/m²/s) in cotton genotypes at different growth stages

Sl. No.	Genotypes	Rate of photosynthesis at 90 DAS				Rate of photosynthesis at 120 DAS				Conductance at 90 DAS				Conductance at 120 DAS			
		M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean
1	CPD-750	33.1	27.8	22.7	27.9	29.3	24.1	17.6	23.7	0.39	0.30	0.14	0.28	0.23	0.18	0.13	0.18
2	Sahana	31.1	25.8	23.1	26.6	26.2	23.6	19.5	23.1	0.37	0.28	0.15	0.27	0.23	0.17	0.13	0.18
3	ARB-9701	33.3	27.9	24.1	28.4	29.5	24.2	19.9	24.6	0.40	0.30	0.16	0.29	0.24	0.18	0.14	0.19
4	CNH-120MB	33.4	28.1	24.3	28.6	29.8	24.7	20.5	25.0	0.42	0.32	0.19	0.31	0.25	0.19	0.15	0.20
5	L-761	22.9	22.0	17.7	20.8	23.0	19.4	14.9	19.1	0.24	0.15	0.08	0.16	0.18	0.13	0.04	0.12
6	LH-2076	25.3	23.5	17.9	22.2	23.4	20.2	15.2	19.6	0.27	0.16	0.09	0.17	0.19	0.14	0.05	0.13
7	GIHV-218	33.8	28.2	24.4	28.8	31.2	26.1	21.9	26.4	0.44	0.34	0.21	0.33	0.28	0.21	0.16	0.21
8	BS-279	33.4	28.0	24.2	28.5	30.5	24.4	20.1	25.0	0.44	0.31	0.18	0.31	0.26	0.19	0.14	0.20
9	RAH-101	30.9	25.3	24.0	26.7	25.7	22.8	19.9	22.8	0.36	0.27	0.15	0.26	0.21	0.15	0.13	0.17
10	GJHV-477	29.3	23.8	21.1	24.7	25.1	22.4	17.2	21.5	0.34	0.25	0.14	0.24	0.21	0.15	0.11	0.16
11	F-2228	28.5	23.7	20.2	24.1	25.0	22.2	17.2	21.5	0.31	0.24	0.13	0.23	0.20	0.15	0.08	0.14
12	KH-155	28.0	23.6	18.2	23.3	23.4	20.7	16.6	20.2	0.28	0.19	0.10	0.19	0.20	0.14	0.07	0.14
Mean		30.2	25.6	21.8	25.9	26.8	22.9	18.4	22.7	0.36	0.26	0.14	0.25	0.22	0.16	0.11	0.17
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.340		1.336		0.203		0.799		0.003		0.013		0.004		0.016	
Sub		0.435		1.229		0.390		1.102		0.008		0.023		0.005		0.014	
M x S		0.754		2.129		0.676		1.908		0.014		0.039		0.009		0.025	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress

4.2.2.4.2 Stomatal conductance ($\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) (cf. Table 22)

The mean stomatal conductance was $0.25\mu\text{ mol CO}_2/\text{m}^2/\text{s}$ and $0.17\mu\text{ mol CO}_2/\text{m}^2/\text{s}$ at 90 DAS and 120 DAS respectively. There was significant difference among the moisture stress treatments, genotypes and their interaction for stomatal conductance recorded at 90 DAS and 120 DAS.

At 90 DAS, among different moisture stress treatments, as the water stress increased the stomatal conductance decreased significantly. Among different moisture stress treatments, control ($0.36\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) recorded significantly more stomatal conductance over other stress treatments, followed by moderate moisture stress ($0.26\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) and severe moisture stress ($0.14\mu\text{ mol CO}_2/\text{m}^2/\text{s}$). Among the genotypes, GIHV-218 ($0.33\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) in control condition showed significantly highest stomatal conductance over other genotypes, however, this was on par with BS-279 ($0.31\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) and CNH-120MB ($0.31\mu\text{ mol CO}_2/\text{m}^2/\text{s}$). While, L-761 ($0.16\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) showed significantly less stomatal conductance over other genotypes, however, this was on par with LH-2076 ($0.17\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) and KH-155 ($0.19\mu\text{ mol CO}_2/\text{m}^2/\text{s}$).

Among the interaction effects, GIHV-218 ($0.44\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) and BS-279 ($0.44\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) under control condition showed significantly highest stomatal conductance over other genotypes, however, these were on par with CNH-120MB ($0.42\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) under control condition. While, L-761 ($0.08\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) under severe moisture stress showed significantly less stomatal conductance over other genotypes, however, this was on par with LH-2076 ($0.09\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) and KH-155 ($0.10\mu\text{ mol CO}_2/\text{m}^2/\text{s}$).

At 120 DAS, among different moisture stress treatments, as the water stress increased the stomatal conductance decreased significantly. Among different moisture stress treatments, control ($0.22\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) recorded significantly more stomatal conductance compared to other stress treatments, followed by moderate moisture stress ($0.16\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) and severe moisture stress ($0.11\mu\text{ mol CO}_2/\text{m}^2/\text{s}$). Among the genotypes, GIHV-218 ($0.21\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) showed significantly highest stomatal conductance over other genotypes, however, this was on par with BS-279 ($0.20\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) and CNH-120MB ($0.20\mu\text{ mol CO}_2/\text{m}^2/\text{s}$). While, L-761 ($0.12\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) showed significantly less stomatal conductance over other genotypes, however, this was on par with LH-2076 ($0.13\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) and KH-155 ($0.14\mu\text{ mol CO}_2/\text{m}^2/\text{s}$).

Among the interaction effects, GIHV-218 ($0.28\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) under control condition showed significantly highest stomatal conductance over other genotypes, however, this was on par with BS-279 ($0.28\mu\text{ mol CO}_2/\text{m}^2/\text{s}$), CNH-120MB ($0.25\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) and ARB-9701 ($0.24\mu\text{ mol CO}_2/\text{m}^2/\text{s}$). While, L-761 ($0.04\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) under severe moisture stress showed significantly less stomatal conductance over other genotypes, however, this was on par with LH-2076 ($0.05\mu\text{ mol CO}_2/\text{m}^2/\text{s}$) and KH-155 ($0.07\mu\text{ mol CO}_2/\text{m}^2/\text{s}$).

4.2.2.4.3 Rate of transpiration ($\text{m mol H}_2\text{O}/\text{m}^2/\text{s}$) (cf. Table 23)

The mean rate of transpiration was $4.9\text{ m mol CO}_2/\text{m}^2/\text{s}$ and $4.2\text{ m mol CO}_2/\text{m}^2/\text{s}$ at 90 DAS and 120 DAS respectively. There was significant difference among the moisture stress treatments, genotypes and their at 90 DAS and 120 DAS.

At 90 DAS, among different moisture stress treatments, as the water stress increased the rate of transpiration decreased significantly. Among different moisture stress treatments, control ($6.4\text{ m mol CO}_2/\text{m}^2/\text{s}$) recorded significantly more rate of transpiration over other stress treatments, followed by moderate moisture stress ($4.6\text{ m mol CO}_2/\text{m}^2/\text{s}$) and severe moisture stress ($3.7\text{ m mol CO}_2/\text{m}^2/\text{s}$). Among the genotypes, GIHV-218 ($5.9\text{ m mol CO}_2/\text{m}^2/\text{s}$) and BS-279 ($5.8\text{ m mol CO}_2/\text{m}^2/\text{s}$) showed significantly highest rate of transpiration over other genotypes, however, these genotypes were on par with ARB-9701 ($5.7\text{ m mol CO}_2/\text{m}^2/\text{s}$) and CNH-120MB ($5.7\text{ m mol CO}_2/\text{m}^2/\text{s}$). While L-761 ($3.7\text{ m mol CO}_2/\text{m}^2/\text{s}$) and LH-2076 ($3.8\text{ m mol CO}_2/\text{m}^2/\text{s}$) showed significantly less rate of transpiration over other genotypes, however this was on par with KH-155 ($4.0\text{ m mol CO}_2/\text{m}^2/\text{s}$).

Among the interaction effects, under control condition GIHV-218 ($7.4\text{ m mol CO}_2/\text{m}^2/\text{s}$) followed by BS-279 ($7.4\text{ m mol CO}_2/\text{m}^2/\text{s}$), CNH-120MB ($7.3\text{ m mol CO}_2/\text{m}^2/\text{s}$) and CPD-750 ($7.2\text{ m mol CO}_2/\text{m}^2/\text{s}$) showed significantly high rate of transpiration over other genotypes. While, L-761 ($2.5\text{ m mol CO}_2/\text{m}^2/\text{s}$) and LH-2076 ($2.6\text{ m mol CO}_2/\text{m}^2/\text{s}$) under severe moisture stress showed significantly less rate of transpiration over other genotypes.

At 120 DAS, among different moisture stress treatments, as the water stress increased the rate of transpiration decreased significantly. Among different moisture stress treatments, control recorded significantly more rate of transpiration ($5.2\text{ m mol CO}_2/\text{m}^2/\text{s}$) compared to other stress treatments, followed by moderate moisture stress ($4.3\text{ m mol CO}_2/\text{m}^2/\text{s}$) and severe moisture stress ($3.2\text{ m mol CO}_2/\text{m}^2/\text{s}$). Among the genotypes, GIHV-218 ($4.9\text{ m mol CO}_2/\text{m}^2/\text{s}$) showed significantly highest rate of transpiration over other genotypes, however, this was on par with BS-279 ($4.7\text{ m mol CO}_2/\text{m}^2/\text{s}$).

CO₂/m²/s) and CNH-120MB (4.7 m mol CO₂/m²/s). While, L-761 (3.5 m mol CO₂/m²/s) showed significantly less rate of transpiration over other genotypes, however, this was on par with LH-2076 (3.6 m mol CO₂/m²/s), followed by KH-155 (3.8 m mol CO₂/m²/s).

Among the interaction effects, GIHV-218 (6.1 m mol CO₂/m²/s) under control condition showed significantly highest rate of transpiration over other genotypes, however, this was on par with BS-279 (6.0 m mol CO₂/m²/s) and CNH-120MB (5.9 m mol CO₂/m²/s) in control condition. While, L-761 (2.2 m mol CO₂/m²/s) and LH-2076 (2.3 m mol CO₂/m²/s) under severe moisture stress showed significantly less over other genotypes.

4.2.2.4.4 Leaf temperature (°C) (cf. Table 23)

The mean leaf temperature was 34.4°C and 37.2°C at 90 DAS and 120 DAS respectively. There was significant difference among the moisture stress treatments, genotypes and their interaction at 90 and 120 DAS.

At 90 DAS, among different moisture stress treatments, as the water stress increased the leaf temperature increased significantly. Among different moisture stress treatments, control maintained significantly less leaf temperature (33.7°C) over other stress treatments, followed by moderate moisture stress (34.4°C) and severe moisture stress (35.1°C). Among the genotypes, L-761 (35.0°C) and LH-2076 (35.0°C) maintained significantly highest leaf temperature over other genotypes; however, these were on par with KH-155 (34.8°C). While, GIHV-218 maintained significantly less leaf temperature (33.6°C) over other genotypes, however, this was on par with BS-279 (33.9°C) and CNH-120MB (33.9°C).

Among the interaction effects, L-761 (35.8°C) and LH-2076 (35.7°C) under severe moisture stress maintained significantly highest leaf temperature over other genotypes; followed by KH-155 (35.5°C) and F-2228 (35.2°C). While GIHV-218 under control condition maintained significantly less leaf temperature (32.4°C) over other genotypes, however, this was on par with BS-279 (32.7°C) and CNH-120MB (32.9°C).

At 120 DAS, among different moisture stress treatments, as the water stress increased the leaf temperature decreased significantly. Among different moisture stress treatments, control (36.1°C) recorded significantly more leaf temperature compared to other stress treatments, followed by moderate moisture stress (37.1°C) and severe moisture stress (38.4°C). Among the genotypes, L-761 (38.2°C) maintained significantly highest leaf temperature over other genotypes; however, this was on par with LH-2076 (38.0°C) followed by KH-155 (37.8°C). While, GIHV-218 (36.2°C) maintained significantly less leaf temperature over other genotypes, however, this was on par with CNH-120MB (36.4°C) and BS-279 (36.6°C).

Among the interaction effects, L-761 (39.5°C) under severe moisture stress maintained significantly highest leaf temperature over other genotypes; however this was on par with LH-2076 (39.3°C) and KH-155 (39.1°C). While, GIHV-218 (35.2°C) under control condition maintained significantly less leaf temperature over other genotypes, however, this was on par with BS-279 (35.3°C), CNH-120MB (35.5°C) and ARB-9701 (35.7°C).

4.2.2.4.5 Water use efficiency (WUE) (μ mol CO₂/m mol H₂O) (cf. Table 24)

The mean WUE was 0.201 μ mol CO₂/m mol H₂O and 0.345 μ mol CO₂/m mol H₂O at 90 DAS and 120 DAS respectively. There was significant difference among the moisture stress treatments and genotypes; however, their interaction effect was non-significant at 90 DAS.

At 90 DAS, among different moisture stress treatments, as the water stress increased the WUE increased significantly. Among different moisture stress treatments, control maintained significantly less WUE (0.17 μ mol CO₂/m mol H₂O) over other stress treatments, followed by moderate moisture stress (0.20 μ mol CO₂/m mol H₂O) and severe moisture stress (0.23 μ mol CO₂/m mol H₂O). Among the genotypes, GIHV-218 (0.213 μ mol CO₂/m mol H₂O) followed by CNH-120MB (0.213 μ mol CO₂/m mol H₂O) and BS-279 (0.211 μ mol CO₂/m mol H₂O) maintained significantly highest WUE over other genotypes. While, L-761 (0.188 μ mol CO₂/m mol H₂O) followed by LH-2076 (0.189 μ mol CO₂/m mol H₂O) and KH-155 (0.190 μ mol CO₂/m mol H₂O) maintained significantly less WUE over other genotypes.

At 120 DAS, among different moisture stress treatments, as the water stress increased the WUE decreased significantly. Among different moisture stress treatments, control (0.32 μ mol CO₂/m mol H₂O) recorded significantly more WUE compared to other stress treatments, followed by moderate moisture stress (0.35 μ mol CO₂/m mol H₂O) and severe moisture stress (0.37 μ mol CO₂/m mol H₂O). Among the genotypes, GIHV-218 (0.364 μ mol CO₂/m mol H₂O) followed by CNH-120MB (0.360 μ mol CO₂/m mol H₂O) and BS-279 (0.359 μ mol CO₂/m mol H₂O) maintained significantly highest WUE over other genotypes. While, L-761 (0.327 μ mol CO₂/m mol H₂O) followed by LH-2076 (0.328 μ mol CO₂/m mol H₂O) and KH-155 (0.336 μ mol CO₂/m mol H₂O) maintained significantly less WUE.

Table 23. Effect of different levels of moisture stresses on rate of transpiration (m mol H₂O/m²/s), leaf temperature (°C) in cotton genotypes at different growth stages

Sl. No.	Genotypes	Rate of transpiration at 90 DAS				Rate of transpiration at 120 DAS				Leaf temperature at 60 DAS				Leaf temperature at 120 DAS			
		M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean
1	CPD-750	7.2	5.1	3.1	5.1	5.8	4.4	3.2	4.5	33.4	34.3	35.0	34.2	35.8	37.0	38.6	37.1
2	Sahana	6.9	5.0	4.4	5.4	5.0	4.3	3.4	4.2	33.8	34.5	34.9	34.4	35.9	37.2	38.6	37.2
3	ARB-9701	7.2	5.2	4.5	5.7	5.9	4.4	3.5	4.6	33.2	34.2	34.9	34.1	35.7	37.0	37.8	36.9
4	CNH-120MB	7.3	5.4	4.6	5.7	5.9	4.6	3.7	4.7	32.9	34.1	34.7	33.9	35.5	36.4	37.3	36.4
5	L-761	5.1	3.5	2.5	3.7	4.4	3.9	2.2	3.5	34.5	34.8	35.8	35.0	37.2	37.7	39.5	38.2
6	LH-2076	5.2	3.6	2.6	3.8	4.5	4.1	2.3	3.6	34.5	34.7	35.7	35.0	37.0	37.6	39.3	38.0
7	GIHV-218	7.4	5.7	4.6	5.9	6.1	4.8	3.8	4.9	32.4	33.8	34.6	33.6	35.2	36.1	37.3	36.2
8	BS-279	7.4	5.3	4.5	5.8	6.0	4.5	3.5	4.7	32.7	34.1	34.9	33.9	35.3	36.8	37.6	36.6
9	RAH-101	6.4	4.9	4.5	5.3	5.0	4.3	3.5	4.2	33.9	34.5	34.9	34.4	36.0	37.2	38.0	37.0
10	GJHV-477	6.1	4.2	3.1	4.5	4.9	4.2	3.2	4.1	34.1	34.5	35.0	34.5	36.1	37.3	38.7	37.4
11	F-2228	5.6	4.1	3.1	4.3	4.8	4.2	3.2	4.0	34.2	34.6	35.2	34.6	36.3	37.4	38.7	37.5
12	KH-155	5.6	3.8	2.7	4.0	4.7	4.2	2.5	3.8	34.3	34.6	35.5	34.8	36.8	37.5	39.1	37.8
Mean		6.4	4.6	3.7	4.9	5.2	4.3	3.2	4.2	33.7	34.4	35.1	34.4	36.1	37.1	38.4	37.2
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.076		0.299		0.044		0.174		0.072		0.282		0.059		0.232	
Sub		0.116		0.327		0.071		0.201		0.130		0.368		0.128		0.360	
M x S		0.201		0.567		0.124		0.349		0.226		NS		0.221		NS	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress NS= Non-significant, DAS= Days after sowing

Table 24. Effect of different levels of moisture stresses on Water use efficiency (μ mol CO₂/m mol H₂O) and Proline content (mg/g fresh weight) in cotton genotypes at different growth stages

Sl. No.	Genotypes	WUE at 90 DAS				WUE at 120 DAS				Proline content at 120DAS			
		M1	M2	M3	Mean	M1	M2	M3	Mean	M1	M2	M3	Mean
1	CPD-750	0.17	0.21	0.23	0.203	0.32	0.35	0.37	0.347	0.063	0.067	0.074	0.068
2	Sahana	0.17	0.21	0.23	0.203	0.32	0.35	0.37	0.347	0.062	0.067	0.074	0.068
3	ARB-9701	0.18	0.21	0.24	0.209	0.32	0.36	0.38	0.354	0.063	0.069	0.078	0.070
4	CNH-120MB	0.18	0.21	0.24	0.213	0.33	0.36	0.39	0.360	0.063	0.069	0.078	0.070
5	L-761	0.16	0.19	0.22	0.188	0.30	0.33	0.35	0.327	0.055	0.065	0.074	0.065
6	LH-2076	0.16	0.19	0.22	0.189	0.30	0.34	0.34	0.328	0.057	0.065	0.072	0.065
7	GIHV-218	0.18	0.21	0.24	0.213	0.33	0.36	0.40	0.364	0.063	0.069	0.079	0.070
8	BS-279	0.18	0.21	0.24	0.211	0.33	0.36	0.39	0.359	0.063	0.070	0.078	0.071
9	RAH-101	0.17	0.20	0.24	0.201	0.31	0.35	0.38	0.348	0.062	0.067	0.075	0.068
10	GJHV-477	0.17	0.19	0.23	0.196	0.31	0.34	0.37	0.338	0.061	0.067	0.074	0.067
11	F-2228	0.16	0.19	0.23	0.194	0.31	0.34	0.36	0.336	0.059	0.066	0.073	0.066
12	KH-155	0.16	0.19	0.22	0.190	0.30	0.34	0.36	0.336	0.059	0.066	0.072	0.066
Mean		0.17	0.20	0.23	0.201	0.32	0.35	0.37	0.345	0.061	0.067	0.075	0.068
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.002		0.009		0.005		0.018		0.0001		0.0006	
Sub		0.004		0.012		0.009		0.025		0.0003		0.0009	
M x S		0.007		NS		0.016		NS		0.0006		0.0016	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress NS= Non-significant, DAS= Days after sowing

4.2.2.4.6 SPAD values (cf. Table 25)

In general, SPAD value increased with the age of the crop up to 90 DAS and decreased thereafter. The mean SPAD values were 41.4, 45.0 and 41.5 at 60 DAS, 90 DAS and 125 DAS respectively. There was significant difference among the moisture stress treatments, genotypes and their interaction at all the stages *i.e.*, 60 DAS, 90 DAS and 120 DAS.

At 60 DAS, among different moisture stress treatments, as the water stress increased the SPAD values were decreased significantly. Among different moisture stress treatments, control recorded significantly more SPAD values (45.0) compared to other stress treatments, followed by moderate moisture stress (41.5) and severe moisture stress (37.8). Among the genotypes, GIHV-218 (44.1) showed significantly more SPAD value over other genotypes; however, this was on par with CNH-120MB (43.7) and BS-279 (43.5). While, L-761 (37.2) showed significantly less SPAD value followed by LH-2076 (38.1) and KH-155 (39.2).

Among the interaction effects, GIHV-218 (47.8) and BS-279 (47.2) under control condition showed significantly more SPAD value over other genotypes; however, these genotypes were on par with CNH-120MB (46.8), ARB-9701 (46.5) and CPD-750 (46.4) under control condition. While, L-761 (32.0) and LH-2076 (33.2) under severe moisture stress showed significantly less SPAD value over other genotypes followed by KH-155 (35.8) under severe moisture stress.

At 90 DAS, among different moisture stress treatments, as the water stress increased the SPAD values decreased significantly. Among different moisture stress treatments, control (50.9) recorded significantly more SPAD values over other stress treatments, followed by moderate moisture stress (43.7) and severe moisture stress (40.3). Among the genotypes, GIHV-218 (50.2) showed significantly more SPAD value over other genotypes, however, this was on par with CNH-120MB (48.8) followed by BS-279 (47.9). While, L-761 (39.3) and LH-2076 (41.2) recorded significantly less SPAD value followed by KH-155 (42.6). Among the interaction effects, GIHV-218 (57.4) under control condition showed significantly more SPAD value over other genotypes; however, this was on par with BS-279 (55.9) and CNH-120MB (55.1). While, L-761 (36.2) under moderate moisture stress showed significantly less SPAD value over other genotypes however, this was on par with L-761 (38.0), LH-2076 (38.3), KH-155 and (38.6).

At 120 DAS, among different moisture stress treatments, as the water stress increased the SPAD values decreased significantly. Among different moisture stress treatments, control recorded significantly more SPAD values (46.4) compared to other stress treatments, followed by moderate moisture stress (41.2) and severe moisture stress (36.9). Among the genotypes, GIHV-218 (46.4) showed significantly more SPAD value over other genotypes, followed by BS-279 (44.6) however; this was on par with ARB-9701 (44.0) and CNH-120MB (43.7). While, L-761 (35.6) showed significantly less SPAD value over other genotypes followed by LH-2076 (37.7), however, this was on par with KH-155 (38.8). Among the interaction effects, GIHV-218 (54.1) and BS-279 (52.6) under control condition showed significantly more SPAD value over other genotypes followed by CNH-120MB (49.5), CPD-750 (48.2) and ARB-9701 (48.2). While, L-761 (30.1) under severe moisture stress showed significantly less SPAD value over other genotypes however, followed by LH-2076 (33.5) and KH-155 (35.6).

4.2.2.4.7 Proline content (mg/g fresh weight) (cf. Table 24)

The mean proline content was 0.068 mg/g fresh weight. There was significant difference among the moisture stress treatments, genotypes and their interaction effect.

Among different moisture stress treatments, as the water stress increased the proline content increased significantly. The treatment control recorded significantly less proline (0.061 mg/g fresh weight) over other stress treatments, followed by moderate moisture stress (0.067 mg/g fresh weight) and severe moisture stress (0.075 mg/g fresh weight). Among the genotypes, BS-279 (0.071 mg/g fresh weight) followed by GIHV-218 (0.070 mg/g fresh weight) and ARB-9701 (0.070 mg/g fresh weight) and CNH-120MB (0.070 mg/g fresh weight) recorded significantly highest proline content over other genotypes. While, L-761 (0.065 mg/g fresh weight) followed by LH-2076 (0.065 mg/g fresh weight) and KH-155 (0.066 mg/g fresh weight) recorded least. Among the interaction effects, GIHV-218 (0.079 mg/g fresh weight), BS-279 (0.078 mg/g fresh weight), ARB-9701 (0.078 mg/g fresh weight) and CNH-120MB (0.078 mg/g fresh weight) under severe moisture stress recorded significantly highest proline content over other genotypes. While, L-761 (0.055 mg/g fresh weight), LH-2076 (0.057 mg/g fresh weight) and KH-155 (0.059 mg/g fresh weight) under control condition recorded significantly least.

Table 25. Effect of different levels of moisture stresses on SPAD values in cotton genotypes at different growth stages

Sl. No.	Genotypes	60 DAS				90 DAS				120 DAS			
		M1	M2	M3	Mean	M1	M2	M3	Mean	M1	M2	M3	Mean
1	CPD-750	46.4	42.9	38.9	42.7	51.9	44.2	39.5	45.2	48.2	40.7	37.4	42.1
2	Sahana	45.2	42.0	39.0	42.1	51.7	44.0	39.9	45.2	46.4	40.2	37.9	41.5
3	ARB-9701	46.5	43.3	39.6	43.1	53.5	45.9	40.7	46.7	48.2	45.5	38.5	44.0
4	CNH-120MB	46.8	44.1	40.1	43.7	55.1	47.7	43.8	48.8	49.5	43.0	38.7	43.7
5	L-761	41.8	37.9	32.0	37.2	43.7	36.2	38.0	39.3	39.4	37.3	30.1	35.6
6	LH-2076	42.5	38.5	33.2	38.1	44.8	40.5	38.3	41.2	41.4	38.2	33.5	37.7
7	GIHV-218	47.8	44.3	40.3	44.1	57.4	48.7	44.7	50.2	54.1	44.4	40.5	46.4
8	BS-279	47.2	43.7	39.7	43.5	55.9	46.3	41.7	47.9	52.6	42.6	38.5	44.6
9	RAH-101	44.6	41.6	39.3	41.9	50.9	43.2	40.5	44.9	45.6	41.5	38.0	41.7
10	GJHV-477	44.3	40.4	38.4	41.1	49.9	43.1	39.3	44.1	45.1	40.2	37.2	40.8
11	F-2228	44.0	40.2	37.8	40.7	48.3	42.7	39.1	43.4	45.0	41.1	36.4	40.8
12	KH-155	42.7	39.0	35.8	39.2	47.5	41.7	38.6	42.6	41.6	39.3	35.6	38.8
Mean		45.0	41.5	37.8	41.4	50.9	43.7	40.3	45.0	46.4	41.2	36.9	41.5
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.085		0.332		0.211		0.827		0.293		1.149	
Sub		0.318		0.899		0.590		1.665		0.502		1.417	
MXS		0.552		1.557		1.021		2.883		0.869		2.455	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress NS= Non-significant, DAS= Days after sowing

4.2.2.5 Root architecture study

4.2.2.5.1 Root length (cm) (cf. Table 26)

The mean root length was 31.8cm recorded at 80 DAS. There was significant difference among the moisture stress treatments, genotypes and their interaction.

Among different moisture stress treatments, as the water stress increased the root length increased significantly. Among different moisture stress treatments, the treatment severe moisture stress (38.0cm) recorded significantly less root length over other stress treatments, followed by moderate moisture stress (30.9cm) and control (26.5cm). Among the genotypes, BS-279 (43.0cm) recorded significantly highest root length over other genotypes and was on par with CNH-120MB (42.0 cm). While, L-761 (26.2 cm) and LH-2076 (25.9 cm) recorded significantly less root length over other genotypes, followed by KH-155 (27.5 cm) and F-2228 (28.3 cm).

Among the interaction effects, BS-279 (47.0 cm) under severe moisture stress recorded significantly highest root length over other genotypes; however, this was on par with GIHV-218 (47.0 cm) and CNH-120MB (45.7 cm) under severe moisture stress and BS-279 (47.0 cm) under moderate moisture stress. While, L-761 (19.0 cm) under control condition followed by LH-2076 (20.3 cm), KH-155 (20.5 cm) and F-2228 (20.6 cm) recorded significantly less root length over other genotypes.

4.2.2.5.2 Number of lateral roots (per plant) (cf. Table 26)

The mean number of lateral roots was 15.1 recorded at 80 DAS. There was significant difference among the moisture stress treatments, genotypes and their interaction.

Among different moisture stress treatments, as the water stress increased the number of lateral roots increased significantly. Among different moisture stress treatments, the treatment severe moisture stress (17.0) recorded significantly less number of lateral roots over other stress treatments, followed by moderate moisture stress (15.4) and control (13.0). Among the genotypes, BS-279 (19.8) and CNH-120MB (19.1) recorded significantly highest numbers of lateral roots over other genotypes, followed by GIHV-218 (18.8) and ARB-9701 (17.0). While, LH-2076 (11.7) followed by L-761 (12.0), KH-155 (12.0) and F-2228 (12.4) recorded significantly less number of lateral roots.

Among the interaction effects, GIHV-218 (22.0) under severe moisture stress recorded significantly highest numbers of lateral roots over other genotypes, however, this was on par with BS-279 (21.3) and CNH-120MB (21.0) under severe moisture stress. While, L-761 (10.0) under control condition followed by LH-2076 (10.0), KH-155 (10.0) and F-2228 (10.3) recorded significantly least.

4.2.2.5.3 Root volume (ml³) (cf. Table 26)

The mean root volume was 9.8ml³ recorded at 80 DAS. There was significant difference among the moisture stress treatments, genotypes and their interaction.

Among different moisture stress treatments, as the water stress increased the root volume increased significantly. Among different moisture stress treatments, the treatment severe moisture stress (10.4 ml³) recorded significantly less root volume over other stress treatments, followed by moderate moisture stress (9.8 ml³) and control (9.3 ml³). Among the genotypes, BS-279 (11.3 ml³) recorded significantly root volume over other genotypes, however, this was on par with CNH-120MB (11.0 ml³). While, L-761 (8.3 ml³) and LH-2076 (8.3 ml³) recorded significantly less root volume over other genotypes, followed by KH-155 (8.7 ml³) and F-2228 (9.0 ml³). Among the interaction effects, BS-279 (11.7 ml³) under severe moisture stress recorded significantly more root volume over other genotypes; however it was on par with GIHV-218 (11.7 ml³), CNH-120MB (11.5 ml³) and ARB-9701 (10.7 ml³) under severe moisture stress, while BS-279 (11.5 ml³), CNH-120MB (11.3 ml³) in moderate moisture stress condition. While, L-761 under control condition recorded significantly less root volume (7.5 ml³) over other genotypes, however this was on par with KH-155 (8.0 ml³).

4.2.2.6 Yield and yield components

4.2.2.6.1 Number of bolls per plant (cf. Table 27)

There was significant difference among the moisture stress treatments, genotypes and their interaction for number of bolls per plant.

Among different moisture stress treatments, as the water stress increased the number of bolls per plant decreased significantly. Among different moisture stress treatments, control recorded significantly more number of bolls per plant (25.3) compared to other stress treatments, followed by moderate moisture stress (21.8) and severe moisture stress (17.6). Among the genotypes, BS-279 (25.1) and CNH-120MB (24.6) recorded significantly highest number of bolls per plant over other genotypes followed by GIHV-218 (23.5) and ARB-9701 (22.5). While, L-761 recorded significantly less number of bolls per plant (19.6) over other genotypes and was on par with KH-155 (19.9). Among the interaction effects, BS-279 (28.7) and CNH-120MB (28.4) under control condition recorded significantly highest number of bolls per plant over other genotypes, followed by GIHV-218 (26.4) and ARB-9701 (25.9) under control condition while, CNH-120MB (26.5) and BS-279 (27.1) in moderate stress condition. While, LH-2076 (15.0) under severe moisture stress recorded significantly less number of bolls per plant over other genotypes, however, this was on par with KH-155 (15.6) and F-2228 (16.2).

Table 26. Effect of different levels of moisture stresses on root volume (ml³), root length (cm), and number of lateral roots in cotton genotypes at 80 DAS

Sl. No.	Genotypes	Root length				No of lateral roots				Root volume			
		M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean
1	CPD-750	30.3	39.3	34.0	34.5	14.7	16.0	15.0	15.2	10.0	10.4	10.0	10.2
2	Sahana	26.2	38.6	38.6	34.5	13.3	15.7	16.0	15.0	9.5	9.9	10.0	9.8
3	ARB-9701	32.5	44.6	44.8	40.6	15.0	17.0	19.0	17.0	10.1	10.9	11.1	10.7
4	CNH-120MB	34.1	46.2	45.7	42.0	16.7	19.7	21.0	19.1	10.2	11.3	11.5	11.0
5	L-761	19.0	27.5	32.2	26.2	10.0	11.3	14.7	12.0	7.5	7.8	9.7	8.3
6	LH-2076	20.3	29.8	27.5	25.9	10.0	12.3	12.7	11.7	8.2	8.3	8.3	8.3
7	GIHV-218	32.8	44.8	47.0	41.6	15.7	18.7	22.0	18.8	10.2	10.9	11.7	10.9
8	BS-279	35.0	47.0	47.0	43.0	17.0	21.0	21.3	19.8	10.8	11.5	11.7	11.3
9	RAH-101	23.3	34.0	44.6	34.0	12.3	15.0	19.0	15.4	9.8	9.8	10.6	10.1
10	GJHV-477	23.0	32.6	32.6	29.4	12.0	13.7	15.0	13.6	9.4	9.6	9.9	9.6
11	F-2228	20.6	32.2	32.2	28.3	10.3	12.7	14.3	12.4	8.3	9.3	9.5	9.0
12	KH-155	20.5	32.2	29.8	27.5	10.0	12.3	13.7	12.0	8.0	8.9	9.3	8.7
Mean		26.5	37.4	38.0	34.0	13.1	15.4	17.0	15.2	9.3	9.9	10.3	9.8
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.070		0.273		0.049		0.191		0.117		0.461	
Sub		0.123		0.348		0.390		1.100		0.268		0.756	
M x S		0.213		0.602		0.675		1.906		0.464		1.310	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress, DAS= Days after sowing

Table 27. Effect of different levels of moisture stresses on Seed cotton yield (kg/ha), Number of bolls per plant and Boll weight (g/boll) in cotton genotypes

Sl. No.	Genotypes	Seed cotton yield				Number of bolls/plant				Boll weight			
		M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean
1	CPD-750	2477	1815	1406	1900	25.3	22.5	17.8	21.9	4.9	3.7	3.2	3.9
2	Sahana	2450	1742	1453	1882	25.1	22.2	17.9	21.7	4.8	3.6	3.2	3.9
3	ARB-9701	2542	1875	1584	2000	25.9	23.3	18.4	22.5	5.0	3.7	3.3	4.0
4	CNH-120MB	2598	2066	1619	2094	28.4	26.5	18.8	24.6	5.1	3.9	3.4	4.1
5	L-761	1702	1204	1335	1414	23.2	18.6	17.0	19.6	3.4	2.8	2.9	3.0
6	LH-2076	1758	1237	986	1327	23.3	19.3	15.0	19.2	3.5	2.8	2.3	2.9
7	GIHV-218	2585	1880	1715	2060	26.4	23.7	20.5	23.5	5.0	3.8	3.5	4.1
8	BS-279	2606	2097	1677	2127	28.7	27.1	19.4	25.1	5.2	4.0	3.4	4.2
9	RAH-101	2431	1657	1505	1864	24.9	21.1	18.0	21.3	4.7	3.4	3.2	3.8
10	GJHV-477	2390	1621	1374	1795	24.5	20.2	17.1	20.6	4.6	3.4	3.0	3.7
11	F-2228	2386	1599	1237	1740	24.3	19.9	16.2	20.1	4.2	3.4	2.7	3.4
12	KH-155	2192	1460	1201	1618	24.3	19.9	15.6	19.9	4.1	2.9	2.4	3.1
Mean		2343	1688	1424	1818	25.4	22.0	17.6	21.7	4.5	3.4	3.0	3.7
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		4.407		17.305		0.130		0.510		0.039		0.152	
Sub		10.708		30.234		0.252		0.712		0.062		0.175	
M x S		18.546		52.366		0.437		1.234		0.107		0.303	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress

4.2.2.6.2 Mean boll weight (g/boll) (cf. Table 27)

There was a significant difference among the moisture stress treatments, genotypes and their interaction for mean boll weight recorded.

Among different moisture stress treatments, as the water stress increased the mean boll weight decreased significantly. Among different moisture stress treatments, control (4.5g/boll) recorded significantly more mean boll weight compared to other stress treatments, followed by moderate moisture stress (3.4 g/boll) and severe moisture stress (3.0 g/boll). Among the genotypes, BS-279 (4.2 g/boll) recorded significantly highest boll weight over other genotypes, however, this was on par with GIHV-218 (4.1 g/boll) and CNH-120MB (4.1g/boll). While, LH-2076 (2.9 g/boll) recorded significantly less boll weight over other genotypes, however, this was on par with L-761 (3.0 g/boll) and KH-155 (3.1 g/boll).

Among the interaction effects, BS-279 (5.2 g/boll) under control condition recorded significantly highest boll weight over other genotypes, however, this was on par with CNH-120MB (5.1 g/boll) and ARB-9701 (5.0 g/boll) in control condition. While, LH-2076 (2.3 g/boll) under severe moisture stress recorded significantly less boll weight over other genotypes, however, this was on par with KH-155 (2.4 g/boll).

4.2.2.6.3 Seed cotton yield (kg/ha) (cf. Table 27)

There was significant difference among the moisture stress treatments, genotypes and their interaction for seed cotton yield.

Among different moisture stress treatments, as the water stress increased the seed cotton yield decreased significantly. Among different moisture stress treatments, control (2343 kg/ha) recorded significantly more seed cotton yield compared to other stress treatments, followed by moderate moisture stress (1693 kg/ha) and severe moisture stress (1424kg/ha). The treatment severe moisture stress affects the seed cotton yield significantly, which recorded less (1424 kg/ha) over other moisture stress treatments. Among the genotypes, BS-279 (2127kg/ha) recorded significantly highest seed cotton yield over other genotypes followed by CNH-120MB (2094 kg/ha), GIHV-218 (2060 kg/ha) and ARB-9701 (2000 kg/ha). While, LH-2076 (1327 kg/ha) recorded significantly less seed cotton yield over other genotypes, followed by L-761 (1414 kg/ha) and KH-155 (1618 kg/ha).

Among the interaction effects, BS-279 (2606 kg/ha) under control condition recorded significantly highest seed cotton yield over other genotypes, however, this was on par with CNH-120MB (2598 kg/ha) and GIHV-218 (2585 kg/ha). While, LH-2076 (986) under severe moisture stress recorded significantly less seed cotton yield over other genotypes, followed by KH-155 (1201 kg/ha) and F-2228 (1237 kg/ha) under severe moisture stress, while L-761 (1204 kg/ha), LH-2076 (1237 kg/ha).

4.2.2.7 Fibre properties in cotton genotypes

4.2.2.7.1 Staple length (mm) (cf. Table 28)

There was significant difference among the moisture stress treatments and genotypes; however, their interaction was non-significant.

Among different moisture stress treatments, as the water stress increased the staple length decreased significantly. Among different moisture stress treatments, control (29.9mm) recorded significantly more staple length compared to other stress treatments, followed by moderate moisture stress (29.3mm) and severe moisture stress (28.5 mm). Among the genotypes, CPD-750 (30.3 mm), ARB-9701 (30.3 mm) and RAH-101 (30.3 mm) maintained significantly highest fibre length over other genotypes followed by F-2228 (29.6 mm). While, L-761 (27.9 mm) and GJHV-477 (28.0 mm) maintained significantly less fibre length over all the genotypes and were on par with BS-279 (28.5 mm) and LH-2076 (28.6 mm).

Among the interaction effects, RAH-101 (31.4 mm) under control condition produced significantly highest fibre length over other genotypes; however, these genotypes were on par with CPD-750 (30.7 mm), ARB-9701 (30.4 mm) under control condition. While, GJHV-477 (26.8 mm) under severe moisture stress produced significantly less fibre length over all the genotypes and was on par with L-761 (26.9 mm), KH-155 (27.3 mm) and LH-2076 (27.5 mm).

4.2.2.7.2 Fibre strength (g/tex) (cf. Table 28)

There was a significant difference among the moisture stress treatments and genotypes; however, their interaction for fibre strength was non-significant.

Among different moisture stress treatments, as the water stress increased the fibre strength decreased significantly. Among different moisture stress treatments, control (22.2 g/tex) recorded significantly more fibre strength compared to other stress treatments, followed by moderate moisture stress (21.0 g/tex) and severe moisture stress (19.8 g/tex). Among the genotypes, GIHV-218 (23.9 g/tex) maintained significantly highest fibre strength over other genotypes, however, this was on par with Sahana (23.0 g/tex) and RAH-101 (22.9 g/tex) and ARB-9701 (22.2 g/tex). While, L-761 (18.7 g/tex) maintained significantly less fibre strength over all the genotypes, however, this was on par with LH-2076 (19.2 g/tex), KH-155 (19.3 g/tex) and F-2228 (19.7 g/tex).

Among the interaction effects, Sahana (25.4 g/tex) under control condition maintained significantly highest fibre strength over other genotypes however, this was on par with GIHV-218 (25.2), RAH-101 (24.3 g/tex), ARB-9701 (24.3 g/tex) under control condition, while, GIHV-218 (24.9 g/tex) and RAH-101 (23.5 g/tex) under moderate moisture stress condition. While, LH-2076 (17.3 g/tex) under severe moisture stress produced significantly less fibre strength over all the genotypes, however, this was on par with F-2228 (17.5 g/tex), L-761 (18.1 g/tex) and KH-155 (18.6 g/tex).

4.2.2.7.3 Micronair (cf. Table 28)

There was a no significant difference among the moisture stress treatments for micronair. However, there was significant difference found among genotypes. But the interaction was non-significant. The genotypes which showed significantly best fibre fineness were CNH-120MB (3.6) and GIHV-218 (3.5) followed by Sahana (3.4) and CPD-750 (3.4). The least performer's were KH-155 (3.0) and F-2228 (3.1).

4.2.2.7.4 Ginning out turn (%) (cf. Table 16)

There was a significant difference among the moisture stress treatments, genotypes and their interaction for ginning out turn.

Among different moisture stress treatments, as the water stress increased the ginning out turn decreased significantly. Among different moisture stress treatments, control recorded significantly more ginning out turn (38.2%) compared to other stress treatments, followed by moderate moisture stress (36.4%) and severe moisture stress (35.9%). Among the genotypes, GIHV-218 (38.4%) recorded significantly highest ginning out turn over other genotypes; however, this was on par with CNH-120MB (38.1%), BS-279 (37.9%), and ARB-9701 (37.7%). While, L-761 (35.2%) recorded significantly less ginning out turn over all the genotypes and was on par with LH-2076 (35.4%) and KH-155 (35.8%).

Among the interaction effects, GIHV-218 (39.6%) under control condition recorded significantly highest ginning out turn over other genotypes; however, this was on par with CNH-120MB (39.5%), ARB-9701 (39.3%) and BS-279 (39.3%) under control condition. While, L-761 (34.6%) under severe moisture stress recorded significantly less ginning out turn over all the genotypes and was on par with LH-2076 (34.9%), L-761 (35.0%) and LH-2076 (35.1%).

4.2.2.8 Correlation studies (r) (cf. Table 29)

The correlation studies of seed cotton yield versus all the physiological traits at rain out shelter revealed that all the traits were positively correlated with yield except WUE at 120DAS, root length, number of lateral roots, root volume, days to 50% squaring, days to 50% flowering, and number of days to 50% maturity.

4.3 Genetic polymorphism of selected cotton genotypes using suitable molecular markers (SSR/suitable marker)

RAPD (Random Amplified Polymorphic DNA) technique uses a polymerase chain reaction (PCR) method to amplify DNA with random primers. Using PCR, random primers of arbitrary nucleotide sequence binds to the DNA at two different sites on opposite strands of the DNA template. If the primer sites were located at a closer amplifiable distance from each other, it results in a DNA product by a thermocyclic reaction. In the present study this technique was used to detect the molecular polymorphism/genetic diversity among cotton genotypes by using 79 RAPD markers. RAPD-analysis was performed on twelve cotton genotypes with 79 RAPD primers 76 primers indicated genetic polymorphism and the pooled results were used for further analysis.

Table 28. Effect of different levels of moisture stresses on Fibre length (mm), Fibre strength (g/tex) and Micronair in cotton genotypes

Sl. No.	Genotypes	Fibre length				Fibre strength				Micronair			
		M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean	M ₁	M ₂	M ₃	Mean
1	CPD-750	30.7	30.2	30.1	30.3	20.8	19.3	20.6	20.2	3.5	3.2	3.4	3.4
2	Sahana	30.2	29.7	28.5	29.5	25.4	21.9	21.6	23.0	3.4	3.2	3.5	3.4
3	ARB-9701	30.4	30.3	30.1	30.3	24.3	21.5	20.9	22.2	3.4	3.2	3.4	3.3
4	CNH-120MB	30.1	29.1	28.5	29.2	21.2	20.8	20.4	20.8	3.6	3.6	3.5	3.6
5	L-761	28.8	28.1	26.9	27.9	19.0	19.0	18.1	18.7	3.2	3.3	3.3	3.3
6	LH-2076	29.3	28.9	27.5	28.6	20.4	19.8	17.3	19.2	3.3	3.3	3.3	3.3
7	GIHV-218	29.7	29.8	28.7	29.4	25.2	24.9	21.8	23.9	3.5	3.7	3.2	3.5
8	BS-279	29.1	28.2	28.3	28.5	22.2	21.3	20.8	21.4	3.5	3.3	3.2	3.3
9	RAH-101	31.4	29.9	29.6	30.3	24.3	23.5	21.0	22.9	3.1	3.4	3.5	3.3
10	GJHV-477	29.2	28.0	26.8	28.0	22.3	20.8	18.9	20.7	3.5	3.4	3.2	3.3
11	F-2228	29.4	29.7	29.6	29.6	21.3	20.4	17.5	19.7	3.1	3.2	3.1	3.1
12	KH-155	30.3	29.1	27.3	28.9	20.1	19.3	18.6	19.3	2.9	3.0	3.0	3.0
Mean		29.9	29.3	28.5	29.2	22.2	21.0	19.8	21.0	3.3	3.3	3.3	3.3
For comparing		S.Em±		CD at 5%		S.Em±		CD at 5%		S.Em±		CD at 5%	
Main		0.128		0.504		0.388		1.523		0.022		NS	
Sub		0.235		0.664		0.430		1.215		0.058		0.163	
M x S		0.408		NS		0.745		NS		0.100		NS	

M₁= Control, M₂= Moderate moisture stress, M₃= Severe moisture stress NS= Non-significant

Table 29. Correlation co-efficient (r) between seed cotton yield versus growth and other physiological attributes in cotton at ROS (pooled)

Sl. No.	Parameters	'r' value
1	Seed cotton yield	--
2	LAI at 60 DAS	0.762**
3	LAI at 90 DAS	0.928**
4	LAI at 120 DAS	0.919**
5	Plant height at 60 DAS	0.771**
6	Plant height at 90 DAS	0.856**
7	Plant height at 120 DAS	0.917**
8	No. of leaves at 60 DAS	0.772**
9	No. of leaves at 90 DAS	0.895**
10	No. of leaves at 120 DAS	0.916**
11	SPAD at 60 DAS	0.923**
12	SPAD at 90 DAS	0.963**
13	SPAD at 120 DAS	0.913**
14	SLW at 90 DAS	0.927**
15	SLW at 120 DAS	0.919**
16	WUE at 90 DAS	0.582**
17	Photosynthesis at 90 DAS	0.954**
18	Conductance at 90 DAS	0.943**
19	Transpiration at 90 DAS	0.958**
20	Leaf temperature at 90 DAS	0.892**
21	WUE at 120 DAS	0.497**
22	Photosynthesis at 120 DAS	0.926**
23	Conductance at 120 DAS	0.925**
24	Transpiration at 120 DAS	0.901**
25	Leaf temperature at 120 DAS	0.924**
26	Root volume at 80 DAS	0.209
27	Root length at 80 DAS	0.132
28	No. of lateral roots at 80 DAS	0.030
29	No. of bolls/plant	0.925**
30	Boll weight	0.987**
31	Days to 50% Squaring	0.036
32	Days to 50% Flowering	0.341
33	Days to maturity	0.284
34	TDM at 90 DAS	0.936**
35	TDM at 120 DAS	0.92**
36	RGR at 0-90 DAS	0.935**
37	RGR at 90-120 DAS	0.818**
38	Fibre length	0.581**
39	Fibre strength	0.700**
40	Micronair	0.467**
41	GOT%	0.930**

* Correlation is significant at 0.01% level.

Table 30. Scorable DNA bands generated by different RAPD primer through PCR

Primer Name	Total bands produced	Number of polymorphic bands	Per cent polymorphism
OPI 1	3	2	66.66
OPI 2	2	1	50.00
OPI 3	8	2	25.00
OPI 4	4	1	25.00
OPI 5	3	3	100.00
OPI 7	6	5	83.33
OPI 9	6	6	100.00
OPI 12	6	6	100.00
OPI 15	2	2	100.00
OPI 17	4	3	75.00
OPI 19	5	5	100.00
OPN 5	4	3	75.00
OPN 7	5	5	100.00
OPN 8	3	2	66.66
OPN13	3	3	100.00
OPN16	5	5	100.00
OPN19	3	3	100.00
OPE3	4	3	75.00
OPE4	3	3	100.00
OPL04	6	0	0.00
OPL09	4	4	100.00
OPL10	3	3	100.00
OPL14	4	4	100.00
OPL 19	1	1	100.00
OLIGO623	5	5	100.00
OLIGO 647	3	2	66.66
OLIGO 652	3	1	33.33
OLIGO 656	4	4	100.00
OLIGO 667	3	3	100.00
OLIGO 676	1	0	0.00
OLIGO 677	5	4	80.00

Contd....

Primer Name	Total bands produced	Number of polymorphic bands	Per cent polymorphism
OLIGO 686	3	0	0.00
UBC 757	5	4	80.00
OPP07	3	2	66.66
OPI 16	2	1	50.00
OPI 18	4	2	50.00
OPI 20	5	5	100.00
OPN 4	3	3	100.00
BNL 2634	3	3	100.00
BNL 3563	3	3	100.00
BNL 3090	1	1	100.00
BNL 2895	4	4	100.00
BNL 3441	2	2	100.00
BNL 2895	2	2	100.00
OPN 9	5	3	60.00
OPE2	1	1	100.00
OPE13	5	4	80.00
OPL05	8	3	37.5
OPL07	5	5	100.00
OPL13	2	2	100.00
OPL18	4	2	50.00
OPAP 01	3	3	100.00
OLIGO 626	3	3	100.00
OLIGO 640	1	1	100.00
OLIGO 644	1	1	100.00
OLIGO 662	2	1	50.00
OLIGO 678	1	1	100.00
OLIGO 685	1	1	100.00
OLIGO 612	3	3	100.00
OPI 6	8	8	100.00
OPI 8	2	1	50.00
OLIGO 688	4	3	75.00
UBC 431	4	4	100.00
BNL 2572	1	1	100.00

Contd....

Primer Name	Total bands produced	Number of polymorphic bands	Per cent polymorphism
BNL 3441	5	5	100.00
BNL 3599	1	1	100.00
BNL 2634	3	3	100.00
A1A13	1	1	100.00
A9B7	1	1	100.00
BNL 3792	3	3	100.00
BNL 3599	4	4	100.00
BNL2572	1	1	100.00
BNL 3090	2	2	100.00
BNL 3563	2	2	100.00
BNL 3792	3	2	66.66
OPI 10	5	5	100.00
OPI 11	6	4	66.66
OPI 13	7	4	57.14
OPI 14	5	3	60.00
Total	274	218	6521.26
Mean	3.47	2.76	82.55

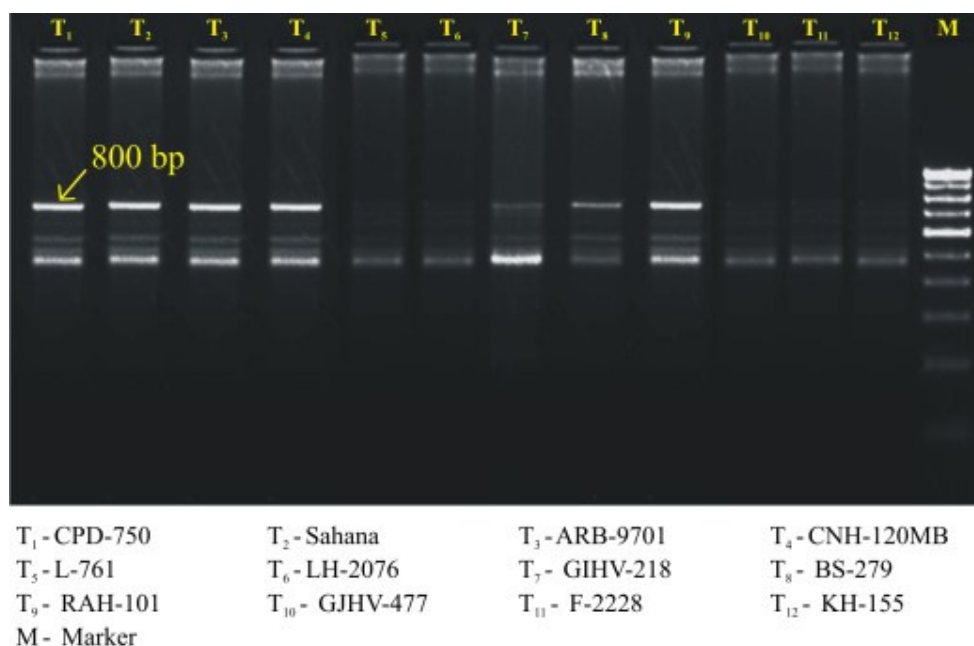


Plate 4.1: RAPD profile of different genotypes for the primer OPI 4

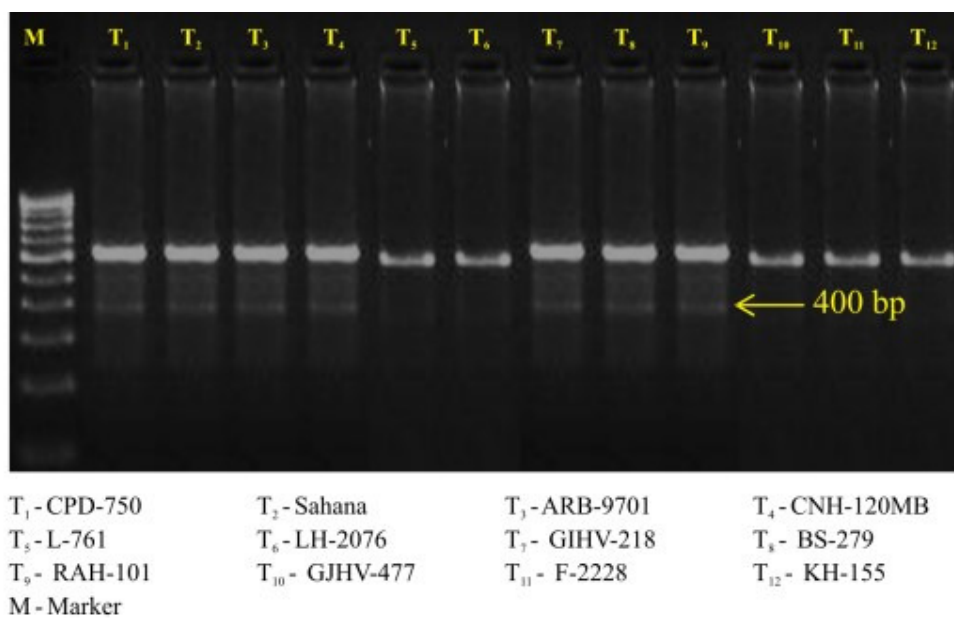
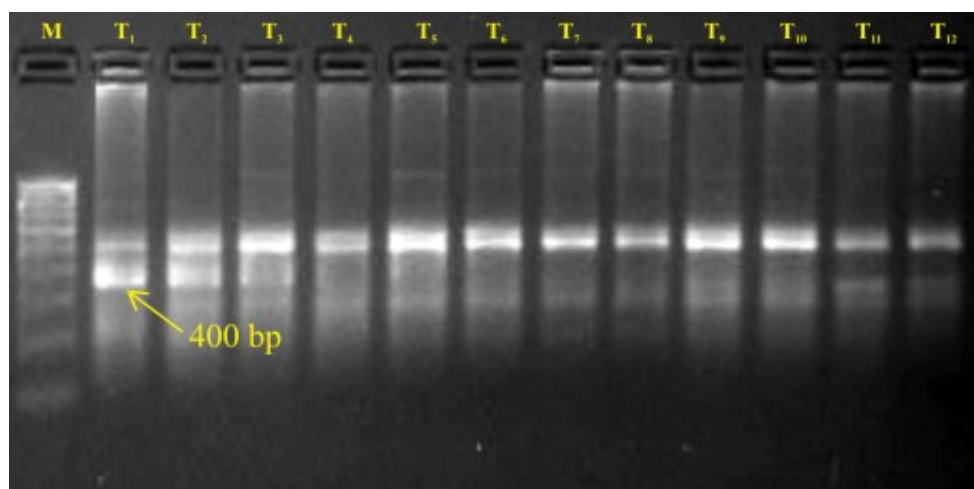
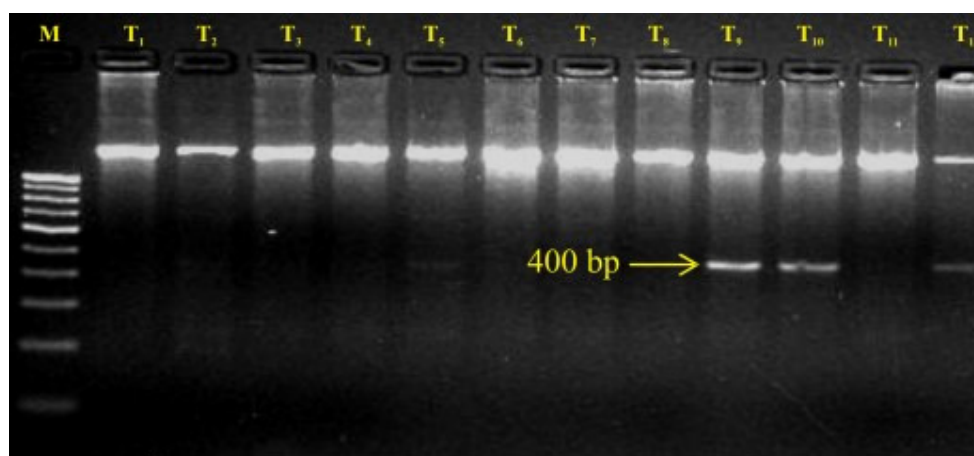


Plate 4.2: RAPD profile of different genotypes for the primer OLIGO 652



T ₁ - CPD-750	T ₂ - Sahana	T ₃ - ARB-9701	T ₄ - CNH-120MB
T ₅ - L-761	T ₆ - LH-2076	T ₇ - GIHV-218	T ₈ - BS-279
T ₉ - RAH-101	T ₁₀ - GJHV-477	T ₁₁ - F-2228	T ₁₂ - KH-155
M - Marker			

Plate 4.3: RAPD profile of different genotypes for the primer OPE3



T ₁ - CPD-750	T ₂ - Sahana	T ₃ - ARB-9701	T ₄ - CNH-120MB
T ₅ - L-761	T ₆ - LH-2076	T ₇ - GIHV-218	T ₈ - BS-279
T ₉ - RAH-101	T ₁₀ - GJHV-477	T ₁₁ - F-2228	T ₁₂ - KH-155
M - Marker			

Plate 4.4: RAPD profile of different genotypes for the primer OPI16

4.3.1 RAPD-profiles

4.3.1.1 Genetic polymorphism (cf. Table 30)

In the present study, the total of 79 cotton specific RAPD primers was used to study genetic polymorphism among the twelve cotton genotypes. All these 79 RAPD primers were cotton specific primers.

In total, 274 scorable bands were produced in twelve genotypes with 79 primers. This data was utilized for further computations. The average number of bands per primer was 3.47. Out of 274 bands, 218 bands were polymorphic (79.56%). The average number of polymorphic RAPD bands was 2.76 per primer. Out of total 79 RAPD primers 48 primers showed 100 per cent polymorphism for twelve cotton genotypes (Table 30).

The 48 primers viz. OPI 5, OPI 9, OPI 12, OPI 15, OPI 19, OPN 7, OPN13, OPN16, OPN19, OPE4, OPL09, OPL10, OPL14, OPL 19, OLIGO623, OLIGO 656, OLIGO 667, OPI 20, OPN 4, BNL 2634, BNL 3563, BNL 3090, BNL 2895, BNL 3441, BNL 2895, OPE2, OPL07, OPL13, OPAP 01, OLIGO 626, OLIGO 640, OLIGO 644, OLIGO 678, OLIGO 685, OLIGO 612, OPI 6, UBC 431, BNL 2572, BNL 3441, BNL 3599, BNL 2634, A1A13, A9B7, BNL 3792, BNL 3599, BNL2572, BNL 3090 and BNL 3563 produced 100 per cent polymorphism with all the identifiable RAPD bands being polymorphic.

The three primers viz. OPL04, OLIGO 676 and OLIGO 686 not produced any polymorphism bands with all the identifiable RAPD bands.

4.3.1.2 Genotype specific bands (cf. Plate 4)

The primer OPI 4 and OLIGO 652 amplified 800 bp (Plate 4.1) and 400 bp (Plate 4.2) respectively were specific to drought tolerant genotypes viz. CPD-750, Sahana, ARB-9701, CNH-120MB, GIHV-218, BS-279 and RAH-101 specific bands. These primers could be drought tolerance specific RAPD makers in cotton, since they amplified only in drought tolerant genotypes. The primer OPE3 amplified at 400bp which was specific only to the genotypes CPD-750, Sahana and ARB-9701 (Plate 4.3). While, the primer OPI16 produced band 450bp this was specific to the genotypes RAH-101, GJHV-477 and KH-155 (Plate 4.4).

4.3.2 Genetic similarity for pooled data (cf. Table 31 and Fig. 6)

The genetic similarity was computed considering all the genotypes from the pooled data and the dendrogram was constructed. The dendrogram was constructed using NTSYSpc programme. On the basis of this analysis, the populations were grouped into three major clusters (Fig. 6).

In first major cluster consists of the genotypes CPD-750 and GIHV-218. In second cluster consists of Sahana, CNH-120MB, L-761, LH-2076, ARB-9701, RAH-101 and GJHV-477. Whereas, in third cluster consists of the genotypes BS-279, F-2228 and KH-155.

Among all the twelve genotypes from the pooled data, the genetic similarity was ranged from 63.8 per cent to 82.1 per cent. The maximum genetic similarity of 82.1 per cent was found between LH-2076 and L-761 (hence they were grouped in same sub cluster in dendrogram), followed by 79.9 per cent between LRA-2076 and CNH-120MB followed by 78.8 per cent GJHV-477 and LH-2076. The lower genetic similarity of 62.8 per cent recorded between BS-279 and Sahana hence they grouped in different major clusters, followed by 63.5 per cent recorded between BS-279 and L-761 and between BS-279 and CNH-120MB (Table 31).

Table 31. Genetic similarity (%) based on RAPD pooled over the 79 primers in twelve cotton genotypes

	CPD-750	Sahana	ARB-9701	CNH-120MB	L-761	LH-2076	GIHV-218	BS-279	RAH-101Yc	GJHV-477	F-2228	KH-155
CPD-750	100.0											
Sahana	69.7	100.0										
ARB-9701	70.4	74.5	100.0									
CNH-120MB	67.5	75.2	76.6	100.0								
L-761	63.9	71.5	71.5	74.5	100.0							
LH-2076	70.1	77.0	74.8	79.9	82.1	100.0						
GIHV-218	74.1	73.0	73.0	71.5	73.0	76.3	100.0					
BS-279	67.5	62.8	67.9	63.5	63.5	66.8	67.2	100.0				
RAH-101Yc	68.6	72.6	73.4	68.2	68.2	75.2	74.1	73.4	100.0			
GJHV-477	65.7	70.4	68.2	69.7	71.9	78.8	71.2	67.5	76.6	100.0		
F-2228	68.6	69.0	73.4	71.2	70.4	73.0	71.9	74.8	70.8	75.9	100.0	
KH-155	72.3	69.7	64.6	65.3	73.4	68.6	67.5	66.8	67.9	71.5	75.9	100.0

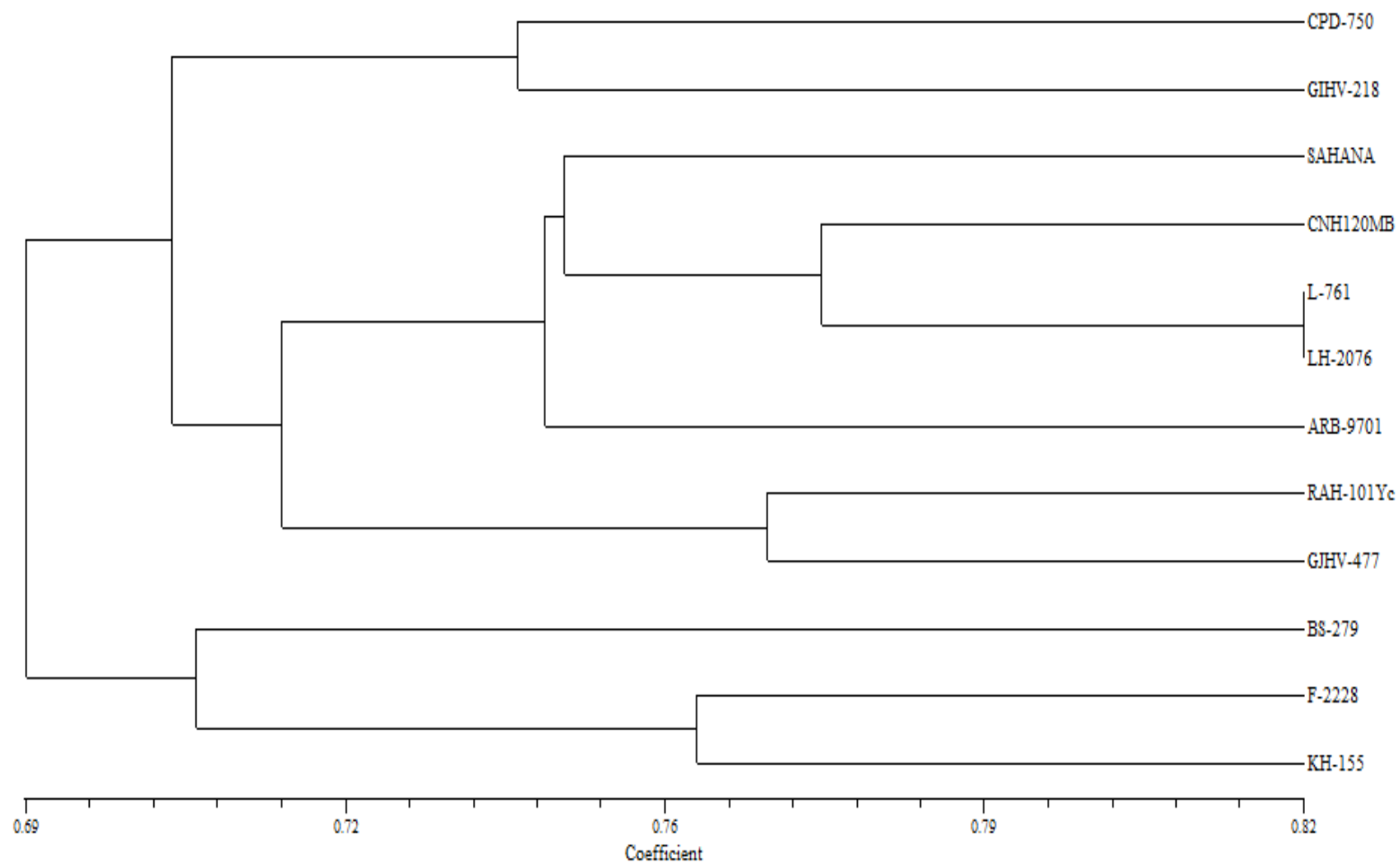


Fig. 6. Dendrogram depicting twelve cotton genotypes based on the genetic similarity generated by 79 random primers

DISCUSSION

Amongst the abiotic stresses reducing crop productivity, aridity and/or shortage of irrigation water is a primary limiting factor in many regions of the world (Turner, 1997; Sinclair, 2005). As a result of increasing demand and competition from environmental, industrial and domestic sectors, supply of fresh water to agriculture sector is likely to be reduced in the coming years. With the increase in world's population, production of food and cash crops has become a top endeavor and the major challenge for agriculture sector. It has been reported that most of the crops are sensitive to water stress, particularly during flowering to seed development stage (Salter and Goode, 1967). Thus keeping in view the current situation of water supply in rivers and canals, it has become indispensable to breed drought tolerant varieties of various crops through selection and breeding.

Cotton (*Gossypium hirsutum* L.) is the most important textile fibre crop and the world's second important oil seed crop after soybean. Although cotton is considered to be a drought tolerant crop, its sensitivity varies greatly among genotypes (Naidu *et al.*, 1995). Water stress affects the growth and thereby limiting kapas yield and lint quality, necessitating the development of drought tolerant cultivars to get economic yield in water deficit areas. Hence, in this direction we worked on cotton varieties to identify the best genotypes for drought tolerance based on physiological traits and molecular approaches.

Many scientists earlier have been successful in screening/identifying the genotypes for drought tolerance on the basis of physiology and genetics. Mahmood (2006) evaluated eight cotton varieties for drought tolerance using various physiological, growth and productivity traits.

Similarly, Muhammad *et al.* (2011) evaluated the performance of 31 cotton genotypes under two irrigation regimes *i.e.*, seven irrigations (Control) and two irrigations (Stress), for growth and physiological traits. They found that few genotypes maintained highest performance for all the parameters studied under high drought conditions.

Traditional plant breeding efforts aim to improve drought tolerance in crop species using solely yield *per se* have met only with limited success. Yield is a complex trait and is end product of various developmental and physiological processes. Therefore, the heritability of yield, particularly under drought, is low which hampers the progress in improving yield and its stability under water stress conditions. Moreover, large genotype x environment interaction for yield under drought is another major reason for slow progress. Indirect selection for the secondary physiological traits exhibiting high correlation with yield may complement empirical breeding efforts to improve drought tolerance in crop plants (Cooper, 1999).

Taking into consideration the historic data on performance of cotton, we chose ARS Annigeri as Hot spot/drought prone and ARS Dharwad as normal/unstressed environment for the study. Features (including soil and climate) have been presented in the previous chapter.

Hence the present study was aimed at identifying drought tolerant cotton genotypes from the field studies, germination studies under osmotic stress linking to molecular studies in an integrated way.

5.1 Field experiment at ARS Dharwad and ARS Annigeri

Thirty *Gossypium hirsutum* genotypes were evaluated during 2011-12 *kharif* at ARS Dharwad and ARS Annigeri under rainfed condition which represented normal and water stress conditions respectively.

ARS Dharwad received 827.6mm rainfall during 2011 *kharif* season. Whereas, ARS Annigeri represented comparatively arid location received 23 per cent less rainfall (636.4mm) over ARS Dharwad (827.6mm). This lower moisture availability resulted in poor performance of the genotypes grown at ARS Annigeri compared to ARS Dharwad. The lower moisture availability representing arid condition at ARS Annigeri affected the water relations of the cotton particularly reducing the water potential at all the growth stages of the plant affected the growth thereby limiting the cotton yield as compared to ARS Dharwad.

The rainfall in 2011 at ARS Annigeri during July, August, September, October, and November was 68.1, 185.2, 34.5, 101, and 0.0 with number of rainy days were 8, 11, 4, 9, and 0 respectively. Cotton crop experienced moisture stress during September, November and December. At ARS Annigeri lower rainfall in september and no rainfall in subscequent months was coincided with critical

water requirement of cotton at flowering to reproductive stage. However, in ARS Dharwad there was no rainfall shortage.

Thus the effect of moisture stress at ARS Annigeri recorded lower SLW, SPAD values, and the leaf water potential was reduced considerably. The impact of water potential was predominant on gas exchange parameters (rate of photosynthesis, stomatal conductance, rate of transpiration and Leaf temperature) and seed cotton yield.

5.1.1 Physiological attributes

Genetically equivalent cotton plant populations, when subjected to water deficits, showed reductions in yield of up to 50 per cent compared to those that have been irrigated, especially when the stress is imposed during the period between flowering and fructification (Araújo *et al.*, 2003). This study showed the impact of drought on the physiology and the development of the cotton plant. Thus, the tolerance of cotton genotypes to water deficits has been the target of various studies on both at physiological and the molecular levels (Levi *et al.*, 2009; Lubbers *et al.*, 2007; Saranga *et al.*, 2004).

In the present study, the effect of water stress on cotton at ARS Annigeri caused the significant reduction in physiological attributes viz. SLW, SPAD values, leaf water potential and gas exchange parameters at all growth stages compared to the same genotypes grown under assured rainfall at ARS Dharwad. There was a significant genotypic difference among the genotypes at both locations for physiological traits.

Ullah *et al.* (2008) reported that seed cotton yield and biological yield were distinctly affected in all cultivars except few which proved their superiority to others in drought tolerance. Ihsan ullah *et al.* (2006) evaluated 32 upland cotton (*Gossypium hirsutum* L.) for drought tolerance traits. He found large genotypic variation among genotypes for drought susceptibility index with seed cotton yield, boll number, net assimilation rate, stomatal conductance and transpiration rate.

Genotypic variation for physiological attributes had been reported in cotton. Inhibition of photosynthesis and stomatal conductance due to water stress is well documented (Pettigrew, 2004; Athar and Ashraf, 2005).

In the present study the mean SLW values of all the genotypes at ARS Dharwad was 8.5 mg/cm², 8.8 mg/cm², 9.9 mg/cm² at 60 DAS, 90 DAS and 125 DAS respectively. Whereas in ARS Annigeri corresponding values were 7.7 mg/cm², 8.4 mg/cm², 8.9 mg/cm². Along with the decrease in SLW decrease in seed cotton yield was significant at ARS Annigeri.

The results in the present investigation indicate that higher SLW had influence on the higher yield. These results are in conformity with the results of Landiver *et al.* (1983).

The mean SPAD values all the genotypes at ARS Dharwad was 35.5, 39.75 and 33.5 at 60 DAS, 90 DAS and 125 DAS respectively. Whereas in ARS Annigeri corresponding values were 29.6, 35.1 and 28.1 respectively. Reddy *et al.* (2003) also reported significantly positive correlation between Chlorophyll stability index and grain yield.

Similarly Yi *et al.* (2000) reported that the chlorophyll content in cotton leaves in all cultivars decreased with increased water stress. Kar *et al.* (2001) reported that moisture deficit affected the total chlorophyll as well as proline content in cotton leaves irrespective of varieties.

The leaf water potential in plants is the result of interaction between soil moisture and plant ability to maintain it to the required level. It depends on atmospheric RH and temperature. As a evidence to this in the present study the leaf water potential decreased with an increase in crop growth and decrease in soil moisture content. Similar results were obtained by Singh *et al.* (1990). In the present study the mean leaf water potential values of the genotypes grown at ARS Dharwad ranged from -0.97 MPa to -2.05 MPa during the growth period. Whereas in ARS Annigeri corresponding values ranged from -1.17 MPa to -2.45 MPa during crop growth. The corresponding value of relative water content in plants varies with the water potential at both locations. So also the other processes like rate of photosynthesis, transpiration, stomatal conductance also recorded significantly high at ARS Dharwad compared to ARS Annigeri. Because of higher transpiration rate lower leaf temperature recorded at ARS Dharwad compared to Annigeri. Lower leaf temperature maintenance has made the plant canopy cooler and helped to maintain normal metabolic activity at ARS Dharwad.

Higher mean photosynthesis rate (31.4 μ mol CO₂/m²/s), stomatal conductance (0.30 μ mol CO₂/m²/s) and transpiration rate (4.4 m mol H₂O/m²/s) were recorded at ARS Dharwad. The

corresponding values at ARS Annigeri were 25.5 μ mol CO₂/m²/s, 0.23 μ mol CO₂/m²/s and 2.9 m mol H₂O/ m²/s respectively. But comparatively low leaf temperature was recorded at ARS Dharwad (29.6^oC) than ARS Annigeri (31.0^oC).

These results are in conformity with the results of Landiver *et al.* (1983) who found that lint yield could be increased by increasing photosynthetic rate to the extent that can remain photosynthetically active up to 70 DAS of their age.

The reduction in the rate of photosynthesis and stomatal conductance under water stress might be due to lower chlorophyll content and decrease in turgor pressure causes closure of stomata to avoid transpirational water loss. Patil (2011) reported that, water stress reduced plant height, number of leaves, leaf area, total dry matter, photosynthetic rate, stomatal conductance, transpiration, NAR and leaf area duration in all the genotypes under water stressed condition compared with well watered control.

At ARS Dharwad the genotypes which performed significantly superior for physiological traits were GIHV-218 followed by CNH-120MB, BS-30, KH-155, ARB-9701, CPD-168, GSHV-01/26, Sahana, GJHV-477, CPD-23, CPD-446, RAH-101, ARB-8908, RAH-30 and CPD-750. While, the water stress sensitive genotypes L-761, H-1353, LH-2076, KH-138, F-186, GSHV-97/13 and L-763 performed least.

At ARS Annigeri the relatively drought tolerant genotypes which performed significantly superior for physiological traits (*viz.* SLW, SPAD, leaf water potential and gas exchange parameters) were GIHV-218 followed by CNH-120MB, KH-155, ARB-9701, CPD-750, Sahana, RAH-101 and RAH-30. While, LH-2076, L-761, H-1353 and KH-138 performed least. Landiver *et al.* (1983) who reported that lint yield could be increased by increasing photosynthetic rate to the extent of 30 per cent through thicker leaves which can remain photosynthetically active for a period up to 70 days.

5.1.1 Seed cotton yield (cf. Fig. 7)

The conclusion from the field experiment revealed that water stress affects adversely on the cotton physiological traits and gas exchange parameters in cotton during crop growth which ultimately resulted in reduced seed cotton yield at water stressed area (ARS Annigeri). The mean yield at ARS Dharwad was significantly higher (2155kg/ha) than ARS Annigeri (1616kg/ha). The reduction in seed cotton yield was 25 per cent at ARS Annigeri compared to ARS Dharwad.

Similarly Karademir *et al.* (2011) sown the 12 cotton genotypes during kharif season (with annual mean temperature of 33^oc), when they were subjected to water stress, there was a significant reduction in cotton yield upto 48% compared to well watered condition.

5.2 Field experiment at ARS Dharwad to evaluate 600 cotton germplasm lines for drought tolerance (cf. Fig. 8)

The 600 cotton germ plasm lines representing larger genetic diversity had variation in morphological traits and physiological traits.

Similar greater diversity was observed in cotton at seedling stage under water stressed and non-stressed conditions by Khalid Iqbal *et al.* (2011).

The physiological traits *viz.* SLW, SPAD values and gas exchange parameters differed significantly. Similar larger genetic variation/diversity was noticed by Mahmood *et al.* (2006).

The analysis of variance obtained by statistical analysis using windostat version 8.5 software indicated the presence of significantly higher difference among the germplasm lines for SPAD Values, specific leaf weight and gas exchange parameters.

The ANOVA for augmented analysis for these traits revealed that, there was highly significant genotypic difference observed for all the physiological traits (SLW, SPAD values and gas exchange traits). There was also highly significant difference was observed for the interaction between checks and varieties.

Among the germplasms GPDWD 613, GPDWD 606, GPDWD 622, GPDWD 608, GPDWD 501, GPDWD 520, GPDWD 484, GPDWD 561, GPDWD 607, GPDWD 592, GPDWD 596, GPDWD 610, GPDWD 614, GPDWD 611, GPDWD 601, GPDWD 620, GPDWD 598, GPDWD 602, GPDWD 620, GPDWD 616, GPDWD 600, GPDWD 624, GPDWD 590 and GPDWD 618 which were having

statistically significant higher values for most of the recorded physiological traits hence these are the superior genotypes which might be drought tolerance lines.

Further, based on the physiological observations (*viz.* SLW, SPAD values and gas exchange parameters), the germplasm lines were broadly categorized into three groups containing 200 germplasm lines each which were named as the best, moderate and least performers. These germplasm lines were grouped based on their highest to lowest values. These performers group was varied for different physiological traits.

The best performers group (consists of 200 germplasm lines) recorded the mean SPAD value of 43.1 and 48.9 at 90 DAS and 110 DAS respectively. In moderate performers corresponding SPAD values were 38.8 and 45.9 at 90 DAS and 110 DAS respectively. Whereas in least performers it was 36.3 and 43.2 at 90 DAS and 110 DAS respectively.

In the present study the mean SLW of the 600 cotton germplasm lines at 90 DAS ranged from 10.8 mg/cm² to 8.8 mg/cm². The best performers recorded highest SLW of 10.5 mg cm⁻² followed by moderate performers (9.8 mg/cm²) and least performers (9.1 mg/cm²). The SLW indicates the thickness of the leaf and is known to have a positive correlation with photosynthetic rate (Rasulov and Assrrov, 1982).

5.2.1 Gas exchange parameters/biophysical parameters

In the present study among 600 germplasm lines, the best performers recorded highest mean rate of photosynthesis (32.6 μ mol CO₂/m²/s) followed by medium performers (30.5 μ mol CO₂/m²/s) and least performers (28.6 μ mol CO₂/m²/s). Similarly, best performers recorded highest stomatal conductance (0.41 μ mol CO₂/m²/s), followed by medium performers (0.35 μ mol CO₂/m²/s) and least performers (0.29 μ mol CO₂/m²/s).

Out of 600 germplasm lines, the best performers (200 germplasm lines) recorded highest mean rate of transpiration (6.05 m mol H₂O/m²/s) followed by medium performers (5.25 m mol H₂O/m²/s) and least performers (4.23 m mol H₂O/m²/s). This indicates the presence of lot of genetic variability in the genotypes for these physiological traits.

Photosynthetic rate could be a selection criterion for plant breeders, especially if lines with superior photosynthesis could be identified and coupled with those lines with suitable partitioning of photosynthates between reproductive and vegetative parts (Pettigrew *et al.*, 1993). The single leaf photosynthetic rate increased as the sink to source ratios increased (Quisenberry *et al.*, 1994). Genotypic variation for physiological attributes had been reported in cotton. Inhibition of photosynthesis and stomatal conductance due to water stress is well documented (Pettigrew, 2004; Athar and Ashraf, 2005).

In the present study the best performer's germplasm lines were found to be drought tolerance having relatively higher SLW, SPAD and gas exchange parameters compared to least performers. Since similar trend was also found in the drought tolerant genotypes which were evaluated at ARS Dharwad and ARS Annigeri locations.

5.3 Evaluation of cotton genotypes for drought tolerance using PEG water stress by slanting glass plate technique

Since the 1980s, researchers have been working to establish the screening methods for evaluation and identification of drought-tolerant plants (Chen and Liu 1997, Karamanos 1984, Maiti *et al.*, 2002), particularly in wheat (Islam *et al.*, 1998), Barley (Olsoyska *et al.*, 2001), maize (Bolanos *et al.*, 1993), sorghum (Okonkwo and Onoenyi, 1998) and so on. The main identification methods include field identification method, managed drought stress, biochemical identification method and natural desiccation stress method. Field identification method is simple and reliable, but restricted by the season, labor-intensive, slow and poorly repetitive; manual control drought stress, including drought stress of repeated and continuously drying methods, has the similar shortages to field identification method. Under this circumstances biochemical identification method with polyethylene glycol (PEG) which creates osmotic stress, can overcome the limitations of the two methods above (LV X H, 1990). Hence in recent days PEG water stress method for screening genotypes for drought traits has been widely used in many crops.

Mahmood *et al.* (2006) reported that juvenile stages of cotton were more susceptible to water deficit. Hence the juvenile/seedling stage was considered in the present study for screening the genotypes through slanting glass plate technique using PEG water stress.

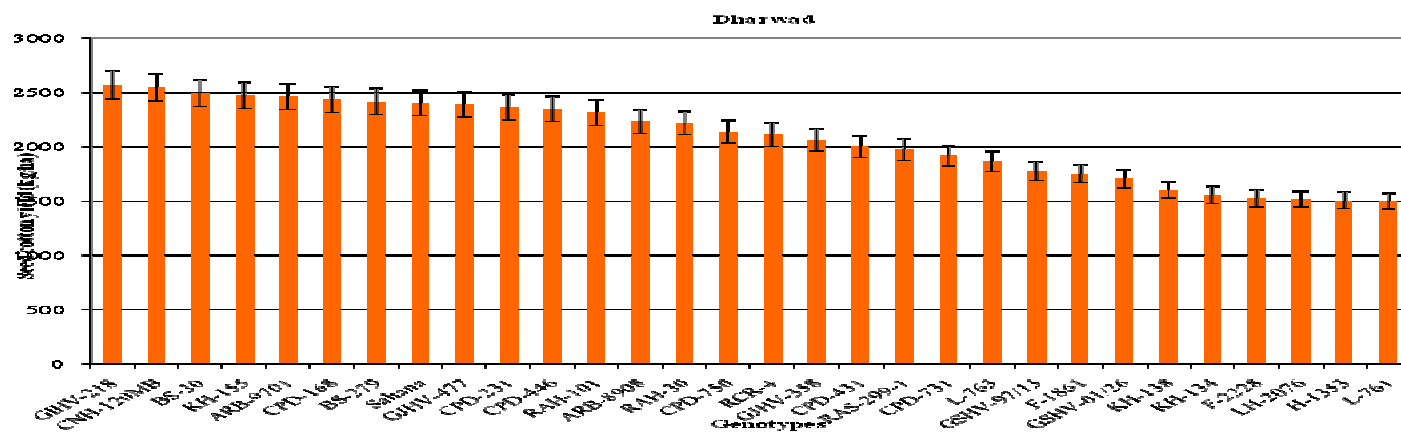


Fig. 7: Genotypic differences in cotton genotypes for seed cotton yield (kg/ha) at Dharwad and

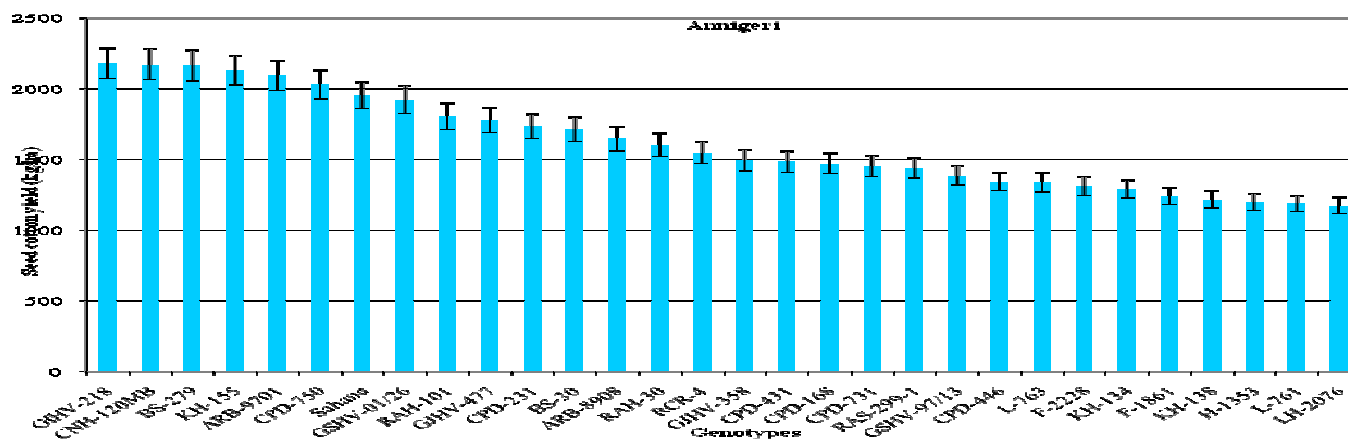


Fig.7: Genotypic differences in cotton genotypes for seed cotton yield (kg/ha) at Dharwad and Annigeri locations

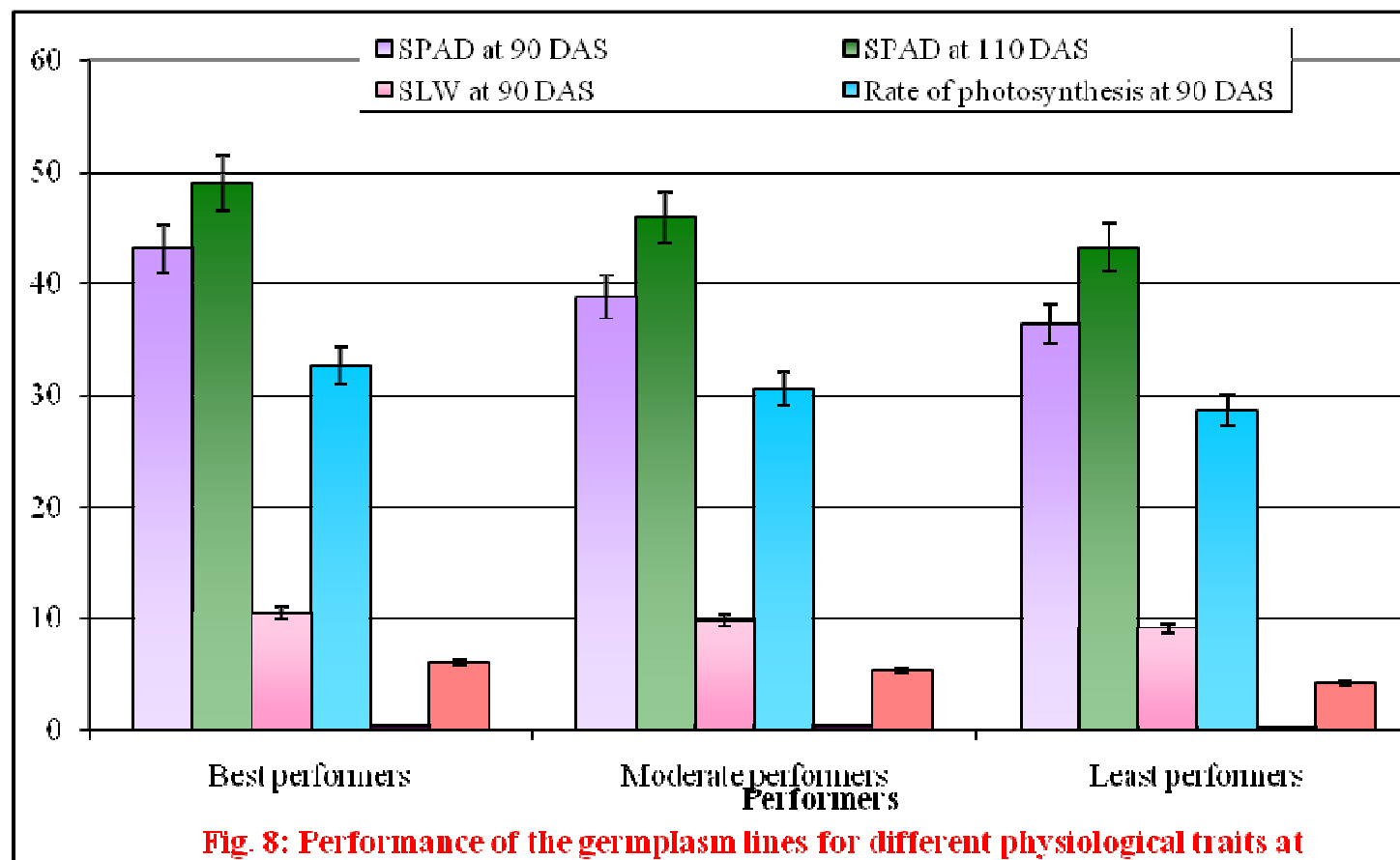


Fig.8: Performance of the germplasm lines for different physiological traits at ARS Dharwad

5.3.1 Germination percentage (cf. Fig. 9)

The germination percentage decreased as the PEG 6000 concentration increased from 0% to 27%. The mean seed germination percentage at PEG solutions with osmotic potentials of 0.0 MPa, -0.05 MPa, -0.148 MPa, -0.295 MPa, -0.491 MPa, -0.735 MPa and -0.846 MPa was, 100%, 86%, 78%, 63%, 31%, 05 per cent and 0 per cent respectively. The decrease in germination due to the increased osmotic stress subjected the plant to water deficit which damaged cellular machinery. At 25% - 27% PEG concentration was found lethal water potential for the germination of cotton seeds, hence the germination was ceased in that concentration.

The PEG stress tolerant genotypes which germinated relatively superior are BS-279 (60%) and CNH-120MB (60%), followed by ARB-9701 (56%), GIHV-218 (56%) and CPD-750 (54%) under all the PEG concentrations. These genotypes appeared to be PEG osmotic stress tolerant genotypes. Whereas, L-761 (44%), KH-155 (47%) and LH-2076 (47%) are PEG stress sensitive genotypes. From the present experiment it was found that, the maximum level of PEG 6000 concentration for cotton seed germination was 25 per cent PEG (-0.735 MPa), above this concentrations the seed germination was inhibited in all twelve genotypes. Similar observations are found by Bohnert (1998), who reported more injurious effects of initial moisture stress, however, extended drought periods allowed plants to cope better.

5.3.2 Shoot length (cf. Fig. 10)

In general the cotton shoot length decreased with the increase in PEG concentrations from 0 per cent to 27%. The decreased shoot length may be at the cost of increased the root length, root volume, root weight and lateral roots to absorb water from deeper surfaces under moisture stress, caused the decreased shoot biomass. The decreased shoot organs helps in reducing transpiration water loss from shoot surfaces. The best performed genotypes for shoot length at all the PEG concentrations were BS-279, CNH-120MB, GIHV-218 and ARB-9701. It was found that at 25 per cent PEG (-0.735 MPa) the cotton shoot growth was completely inhibited in all twelve genotypes.

5.3.3 Root length (cf. Fig. 11)

In the present study the cotton root length increased with the increasing PEG concentrations up to 10 per cent and declined thereafter. The increased root length might be due to preferential partitioning of more photosynthates for the growth of roots rather than shoots, which helps in absorbing more water from deeper layers.

The roots are water absorbing organs and shoot is meant for photosynthesis and transpiration. Thus the moisture absorption of plants occurs by modifying the growth of shoot morphology to mitigate the water stress. The decreased shoot organs helps in reducing transpirational water loss from shoot surfaces.

Similarly, Taylor and Klepper (1971) observed that water extraction per unit length of root was greater in wet soil and decreased exponentially with soil water potential. In general they found that deep roots were effective in extracting water from soil. Zhang Xue-yan *et al.* (2007) evaluated eight upland cotton cultivars, two sea island cotton and three Asian cotton with varied levels of drought. They indicated that 3-6 leaf stage is the key period related to cotton drought tolerance and is associated with the osmotic adjustment of the genotypes.

The best performed genotypes for root length at all the PEG concentrations were BS-279, CNH-120MB, GIHV-218 and ARB-9701 which had better root length at all the PEG concentrations.

5.3.4 Root: shoot ratio

Higher cotton root: shoot ratio observed with increase in PEG concentrations up to 20 per cent PEG at 12th DAS. Whereas at 18th DAS, it was observed up to 15 per cent PEG, and decreased thereafter. The mean root: shoot ratio at all the PEG concentrations at 18th DAS was higher in the genotypes CNH-120MB (1.3), BS-279 (1.3), GIHV-218 (1.3) and ARB-9701 (1.3). Whereas, it was least in KH-155 (1.0), LH-2076 (1.0) and F-2228 (1.0). The increased root:shoot ratio could be due to absolute increase in root weight and the plant spends more photosynthates for root biomass development to absorb more water under water stress. Decreased shoot biomass helps plant to save water loss by transpirational loss.

Similarly Carlos *et al.* (2011) evaluated the physiological quality of cotton cultivar seeds (*Gossypium hirsutum* var. *latifolium* L.) in laboratory by the simulation of water potentials with PEG

and the study revealed that effect of water stress on seed viability and on plantlet vigor was severe at potentials below -0.4 MPa.

From the present study it was found that at 12th DAS and 18th DAS the cotton root length index was maximum in 10 per cent PEG followed by 05% PEG, 27 % PEG and 25% PEG. Similarly, cotton shoot vigour index decreased with the increase in PEG concentrations. This reduced shoot vigour might be due to increase in root: shoot ratio and also due to decreased leaf numbers, reduced plant height and other shoot organs.

5.3.5 Seedling vigour index (cf. Fig. 12)

The vigour index is a computed value of root and shoots length of seedlings. Hence the cotton seedling vigour index decreased with the increased in PEG concentrations. The mean seedling vigour index at all the PEG concentrations at 12th and 18th DAS was higher in the genotype BS-279, followed by CNH-120MB, GIHV-218 and ARB-9701. Whereas, it was least in the genotypes L-761, KH-155 and LH-2076.

Zhang Xue-yan *et al.* (2007) found that osmotic adjustment of cotton could be used to evaluate the drought tolerance of cotton. This method is simple, fast and easily operated, could be used to evaluate the drought tolerance of cotton.

The results of the present study also fall in line with these results thus concluding that one of the best methods to evaluate cotton genotypes for drought tolerance which is fast and reliable.

5.4 Studies on drought tolerance under Rain out shelter

Based on the first year (2011-12) field experimental results, out of thirty genotypes, ten genotypes viz., CPD-750, Sahana, ARB-9701, CNH-120MB, GIHV-218, BS-279, RAH-101, GJHV-477, F-2228 and KH-155 were identified as relatively drought tolerant (best performers) and two genotypes (L-761 and LH-2076) as water stress sensitive lines. These twelve genotypes were further evaluated in detail under rain out shelter for drought tolerance. Later these genotypes were further studied for genetic polymorphism and genetic diversity assay using RAPD molecular markers. The results obtained from these are discussed below.

5.4.1 Growth and morphological characters

Water stress caused a reduction in the whole plant leaf area by decreasing the initiation of new leaves, with no significant changes in leaf size or leaf abscission. Both the main stem and sympodial branches developed significantly less leaves; however, the effect was less severe on the main-stem leaves (Krieg and Sung, 1986).

Radin and Mauney (1986) found that the expansion of leaves declines parallel to the decreasing water supply during a drying cycle, while stomatal closure occurs after some threshold water deficit (McMichael and Hesketh, 1982).

Water stress decreased partitioning of plant biomass into leaves and increased partitioning into roots (Patterson, 1988). Genotypes exhibited significant difference in plant height, number of leaves, branches and other morphological characters. The studies made earlier also noticed the existence of varietal differences in plant height (Bharadwaj and Singh, 1988). The number of leaves is an important character because it can be used as an indicator of growth stages for applying management practices (Shao *et al.*, 1994).

In the present study water stress reduced plant height and number of leaves in all the genotypes at all growth stages in comparison with control. In general, plant height was increased with the age of the crop. Whereas number of leaves per plant increased with the age of the crop up to 90 DAS thereafter decreased. The mean plant height was 43.2cm, 69.6cm and 85.8cm at 60 DAS, 90 DAS and 120 DAS respectively. The mean number of leaves per plant was 43.7, 101.7 and 95.5 at 60 DAS, 90 DAS and 120 DAS respectively. The genotypes which found higher plant height and number of leaves under moderate and severe water stresses at all growth stages were RAH-101 followed by GIHV-218, ARB-9701, CNH-120MB and BS-279. While, the genotype L-761 followed by LH-2076 and KH-155 found adversely affected by water deficit moisture regimes. The plant height and number of leaves was correlated significantly with yield. These results were in agreement with the findings of Patil (2011).

Singh and Gupta (1970) reported that increase in plant height in irrigated condition was accompanied by increase in sympodial branches and number of bolls per plant. Basu and Bhatt

(1987) observed that plant height and number of monopodial branches have no influence on harvest index unlike sympodial branches and seed cotton yield. Water stress showed decreased plant height. The genotypes that maintained higher plant height at the increased moisture stress levels gave better yields compared to other genotypes (Ahuja and Tuteja, 2001 and Ansari *et al.*, 1989).

Genotypes exhibited significant difference in plant height, number of leaves, branches and other morphological characters. The studies made earlier also noticed the existence of varietal differences in plant height (Bharadwaj and Singh, 1988). The genotypes that maintained higher plant height at the increased moisture stress levels gave better yields compared to other genotypes (Ahuja and Tuteja, 2001 and Ansari *et al.*, 1989).

5.4.2 Phenological characters

Sikka and Joshi (1960) reported that time taken from sowing to the commencement of flowering indicate the earliness or lateness of a variety.

Effect of water stress on squaring and flowering behaviour in cotton under water stress revealed that, water stress significantly reduced the number of days taken to 50 per cent squaring and flowering. Among the different moisture stress treatments, the treatment control took more number of days to 50 per cent squaring and flowering (65.8 days for squaring and 81.1 days for flowering) compared to other stress treatments, followed by moderate moisture stress (65.2 days for squaring and 80.2 days for flowering). The treatment severe moisture stress affects significantly, which took least (64.3 days for squaring and 78.6 days for flowering) over other moisture stress treatments. Among the genotypes, F-2228, LH-2076, GJHV-477 and KH-155 took more days to 50 per cent squaring and flowering, while, the genotypes GIHV-218, ARB-9701, BS-279 and Sahana took relatively less days, which is desirable trait under moisture stress environments. The days taken to 50 per cent squaring and flowering was not correlated significantly with yield.

Effect of water stress on maturity period in cotton under water stress revealed that, water stress significantly reduced the number of days taken to maturity. Among the different moisture stress treatments, the treatment control took more number of days to maturity (165.7 days), followed by moderate moisture stress (164.1 days) and severe moisture stress (163.6 days). The genotypes ARB-9701, Sahana and RAH-101 took less number of days to maturity over other genotypes.

The earliness in squaring and flowering may be due to sensing of the water deficit signal at early stage of growth, which made preponement of squaring and flowering to escape from the drought damage at later stages of the crop.

5.4.3 Morpho-physiological and biochemical parameters

The present study of the evaluation of cotton genotypes under water stress condition revealed that, moisture stress significantly reduced total dry matter relative growth rate, net assimilation rate, SLW, leaf area index and SPAD values at all growth stages.

5.4.3.1 Specific leaf weight (SLW)

Leaf thickness is the one of the important traits of plants as leaf is the major metabolically active organ of the plant involved in gas exchange process. The variation in the thickness is indicated by the SLW, higher the SLW higher is the number of cells per plant volume and compactness of the cells. When SLW under moisture stress increases its water use efficiency also increases there by the photosynthetic rate. The genotypes GIHV-218, ARB-9701 and BS-279 had higher SLW along with the higher WUE and seed cotton yield.

It has indicated that higher SLW had influence on the higher yield. These results are in conformity with the results of Landiver *et al.* (1983).

5.4.3.2 Total dry matter (TDM) (cf. Fig. 13)

In the present study TDM was increased with the age of the crop. There was significant difference among the moisture stress treatments, genotypes and their interaction for TDM was recorded at all stages. Higher TDM was maintained by the genotypes GIHV-218, BS-279, CNH-120MB, ARB-9701 and CPD-750 under control, moderate and severe water stresses at all growth stages. While, the genotypes LH-2076, L-761 and KH-155 were least performed. The TDM was positively correlated with yield.

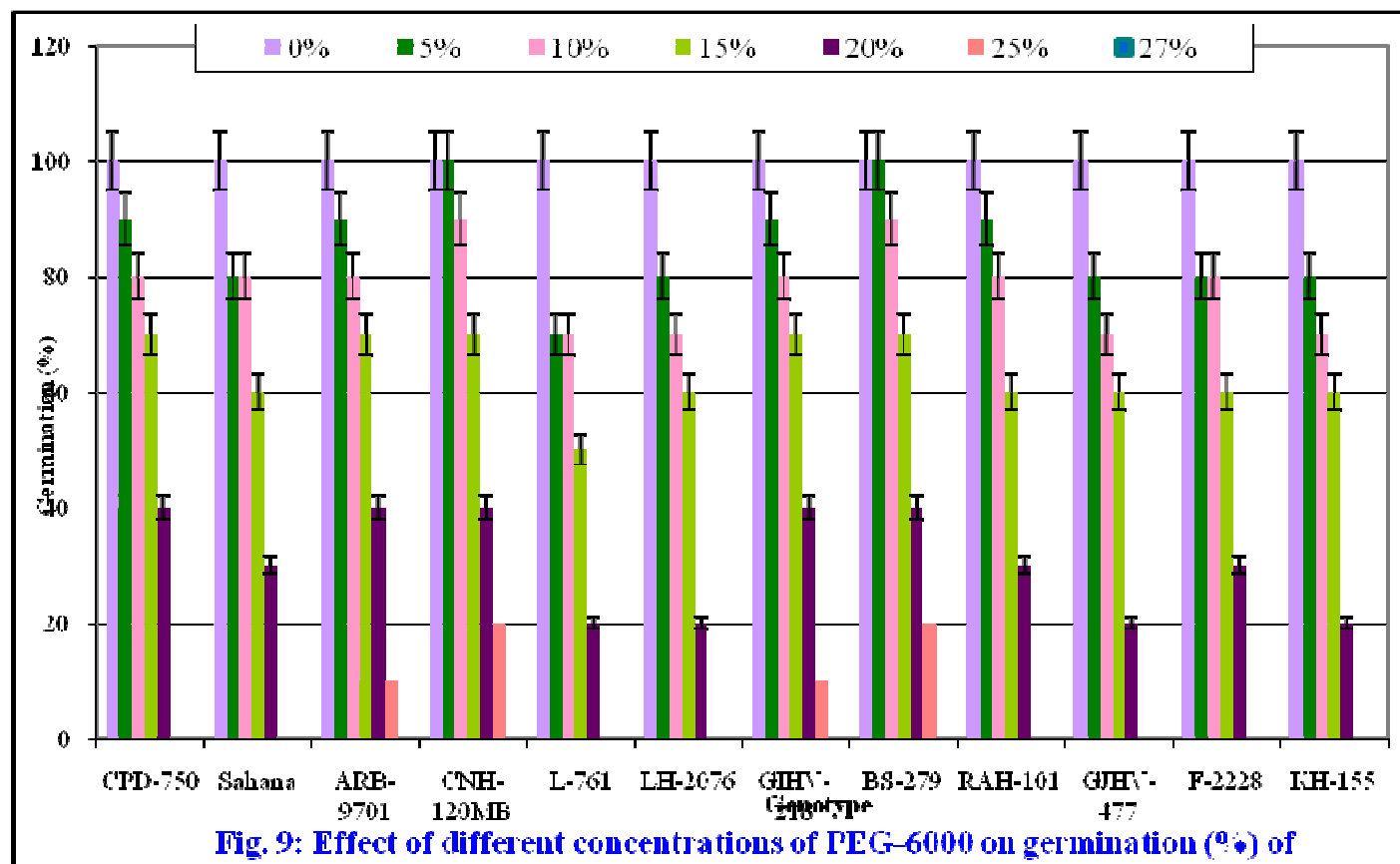


Fig.9: Effect of different concentrations of PEG-6000 on germination (%) of cotton.

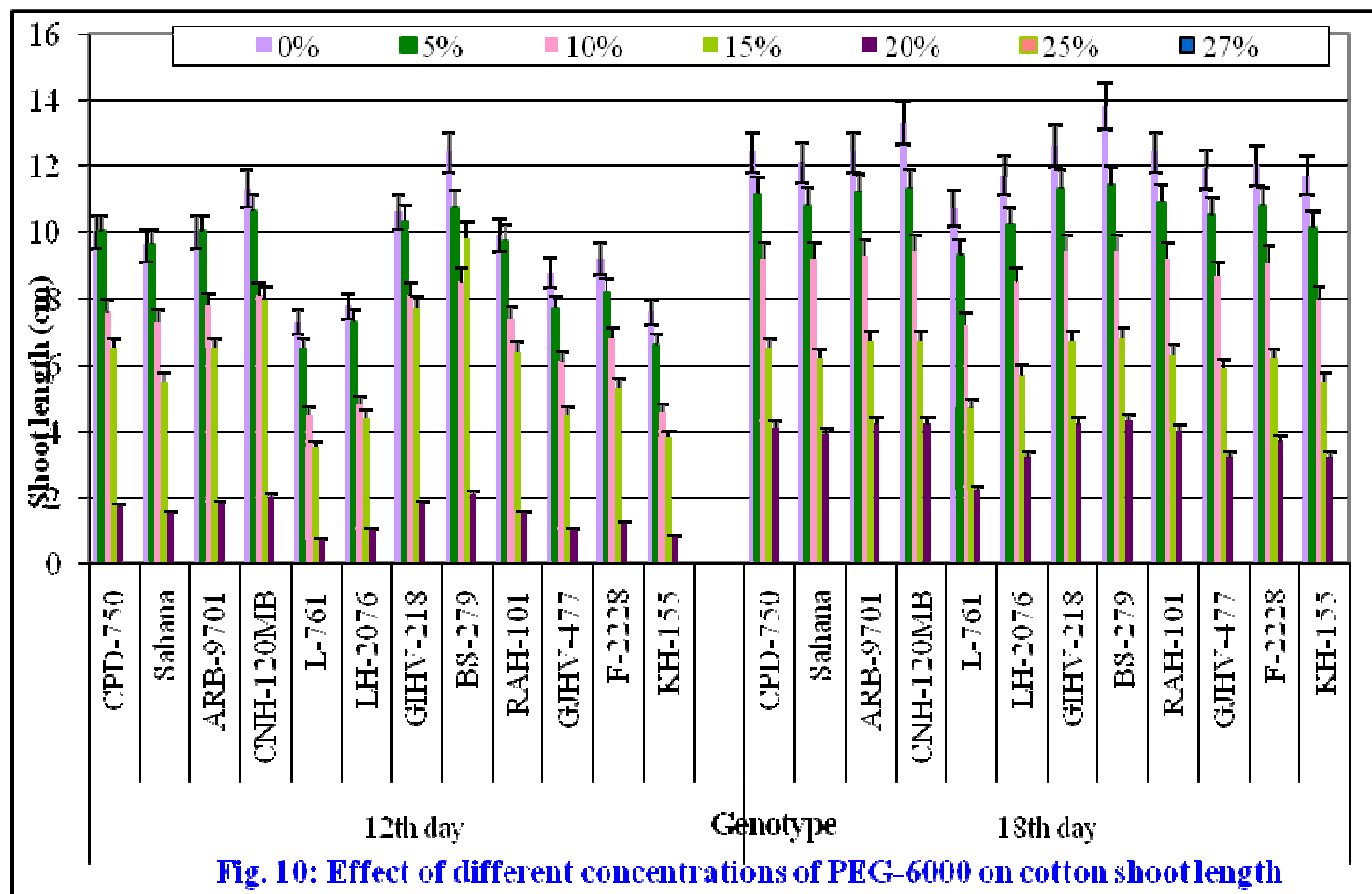


Fig.10: Effect of different concentrations of PEG-6000 on cotton shoot length (cm) at different growth stages

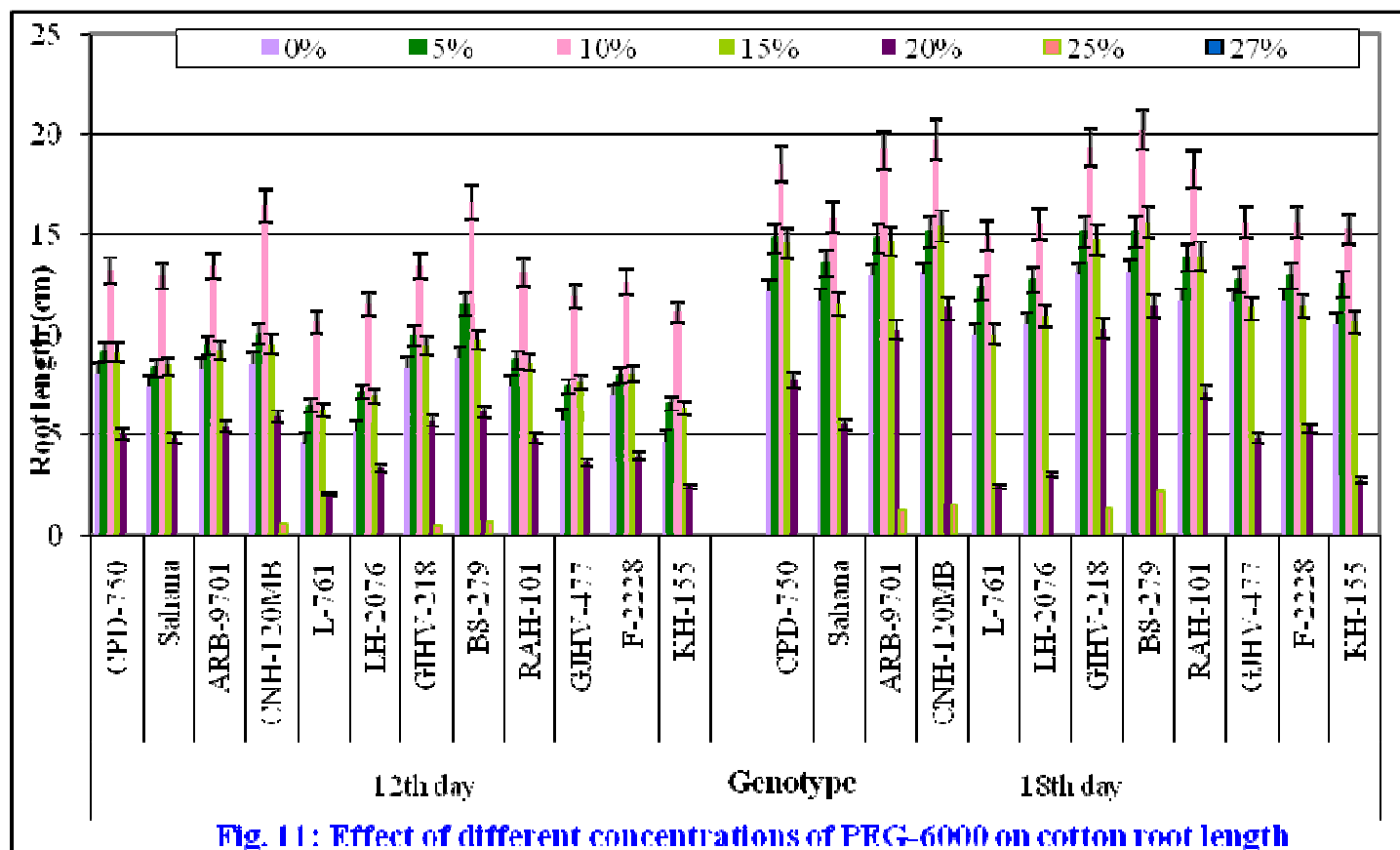


Fig.11: Effect of different concentrations of PEG-6000 on cotton root length (cm) at different growth stages

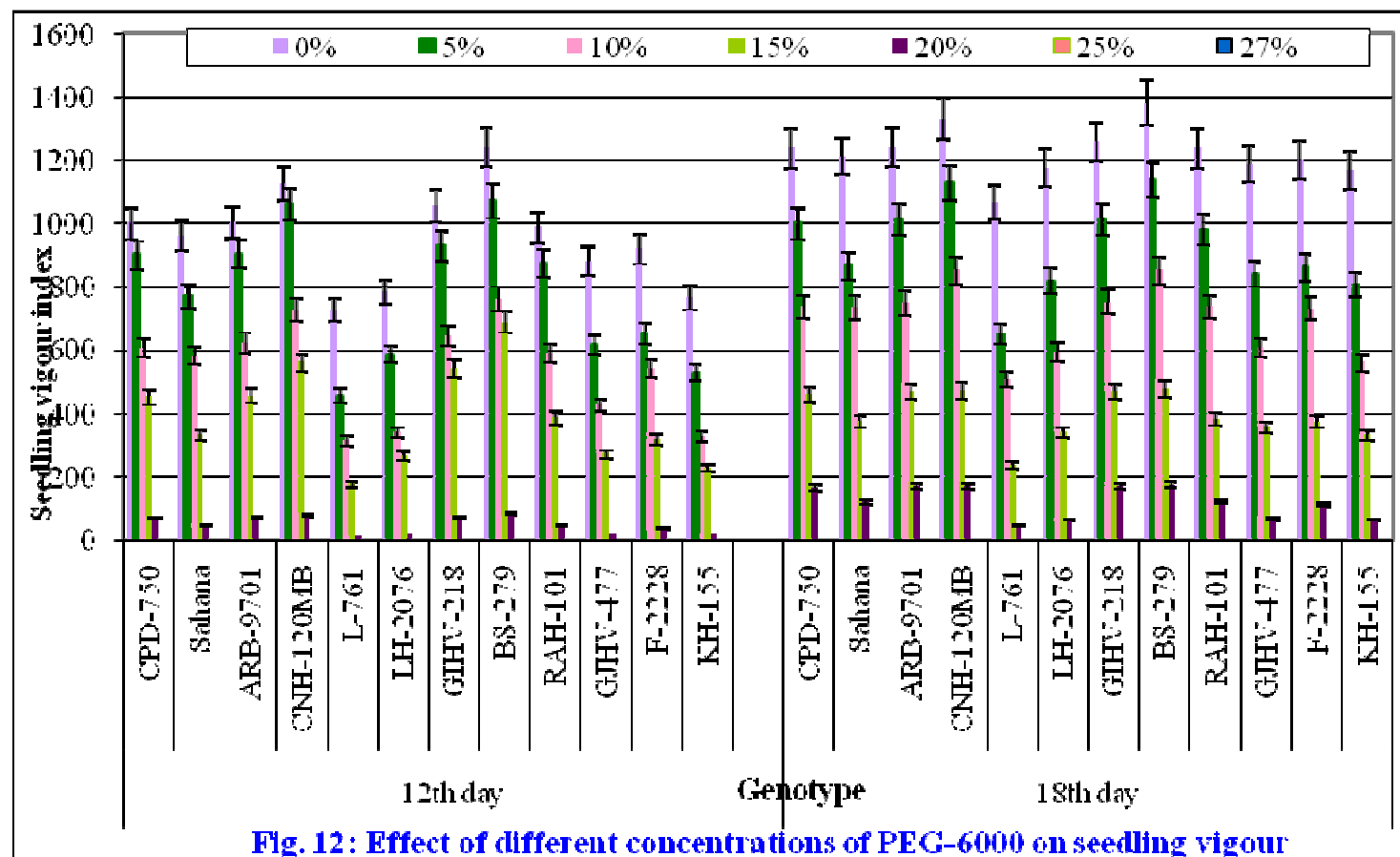


Fig. 12: Effect of different concentrations of PEG-6000 on seedling vigour

Fig.12: Effect of different concentrations of PEG-6000 on seedling vigour index of cotton at different growth stages

5.4.3.3 SPAD values and LAI (cf. Fig. 14)

Different crops possess optimum LAI conducive to maximum dry matter production. While emphasizing the importance of leaf area, previous study revealed varietal differences in LAI (Bhat, 1974).

The mean SPAD values were 41.4, 45.0 and 41.5 at 60 DAS, 90 DAS and 120 DAS respectively. The mean LAI was 1.4, 2.8 and 2.4 at 60 DAS, 90 DAS and 120 DAS respectively. The SPAD and LAI were significantly reduced with the increase in moisture stress levels in all the genotypes at all stages. Higher SPAD and LAI was maintained by the genotypes GIHV-218, BS-279, CNH-120MB, ARB-9701 and CPD-750 under moderate and severe water stresses. The SPAD and LAI were positively correlated with yield.

These results are in agreement with the findings of Patil (2011). Some of the genotypes under water stress showed higher SPAD (Chlorophyll content) values. This could be due to higher chlorophyll content which helps the plant to maintain more photosynthesis and conductance to withstand water stress and thereby maintenance of leaf area.

Patil (2011) reported that, water stress reduced cotton plant height, SLW, LAI, SPAD, number of leaves, leaf area, total dry matter, RGR in genotypes under water stressed condition compared with well watered control.

Similarly, Yi *et al.* (2000) noticed that under different intensities of water stress, the chlorophyll content in cotton in all cultivars decreased with increased water stress. Kar *et al.* (2001) reported that moisture deficit affected the total chlorophyll as well as proline content in cotton leaves irrespective of varieties.

In a similar study by Channaveeraiah (1983) reported that for selection of high yielding genotypes under rainfed condition, the cultivars having moderate duration, moderate LAI, LAD and with medium size of monopodial branches are more preferred. Puech-Swanzes *et al.* (1989) noticed that net canopy photosynthetic rate per unit ground area increased up to a LAI 3.5-4.0 in all the three cotton (*G. hirsutum* L.) genotypes studied.

5.4.3.4 Net assimilation rate (NAR)

In the present study, as the water stress increased the NAR decreased. Among the moisture stress treatments, control (0.041 g/dm²/day) and moderate moisture stress (0.041 g/dm²/day) recorded significantly more NAR followed by and severe moisture stress (0.037 g/dm²/day). Among the genotypes, GIHV-218, CNH-120MB and ARB-9701 found better performers for NAR trait, whereas KH-155, LH-2076 and L-761 performed least.

Similarly Patterson (1988) noticed that water stress reduced plant height, leaf number, leaf area, total DM, stomatal conductance, transpiration, NAR and leaf area duration in all species, in comparison with well watered controls. Water stress decreased partitioning of plant biomass into leaves and increased partitioning into roots.

5.4.3.5 Relative growth rate (RGR)

RGR in cotton was more closely associated with vegetative growth than seed cotton yield (Coy, 1976). In the present study, as the water stress increased the RGR decreased. At 0-90 DAS among the different moisture stress treatments, control (0.0182 g/g/day) recorded significantly more RGR followed by moderate moisture stress (0.0167 g/g/day) and severe moisture stress (0.0160 g/g/day). Among the genotypes, GIHV-218, CNH-120MB and ARB-970 was found significantly better performers, while, L-761 and LH-2076 performed least. At 90-120 DAS there was a significant difference among the moisture stress treatments, whereas genotypes and their interaction effect was non-significant. At 90-120 DAS control recorded significantly more RGR (0.0195 g/dm²/day) than severe moisture stress (0.0190 g/dm²/day).

The decreased RGR under moisture stress could be due to partitioning of more photosynthates for the growth of roots than shoot, which helps absorption of water.

Channaveeraiah (1983) assessed the performance of cotton (*G. hirsutum* L.) genotypes under rainfed condition and found that high yielding cotton genotypes (cv. Sharada) had moderate value of RGR (0.71 g/g/day). In a study with seven elite cotton (*G. hirsutum* L.) genotypes it was found that RGR showed positive correlation with LA and SLA. Patil (1993) reported that crosses with both high RGR parents produce high yields. In four upland cotton varieties and their hybrids observed 5.9 per cent greater RGR in hybrids over their parents during seedling stages.

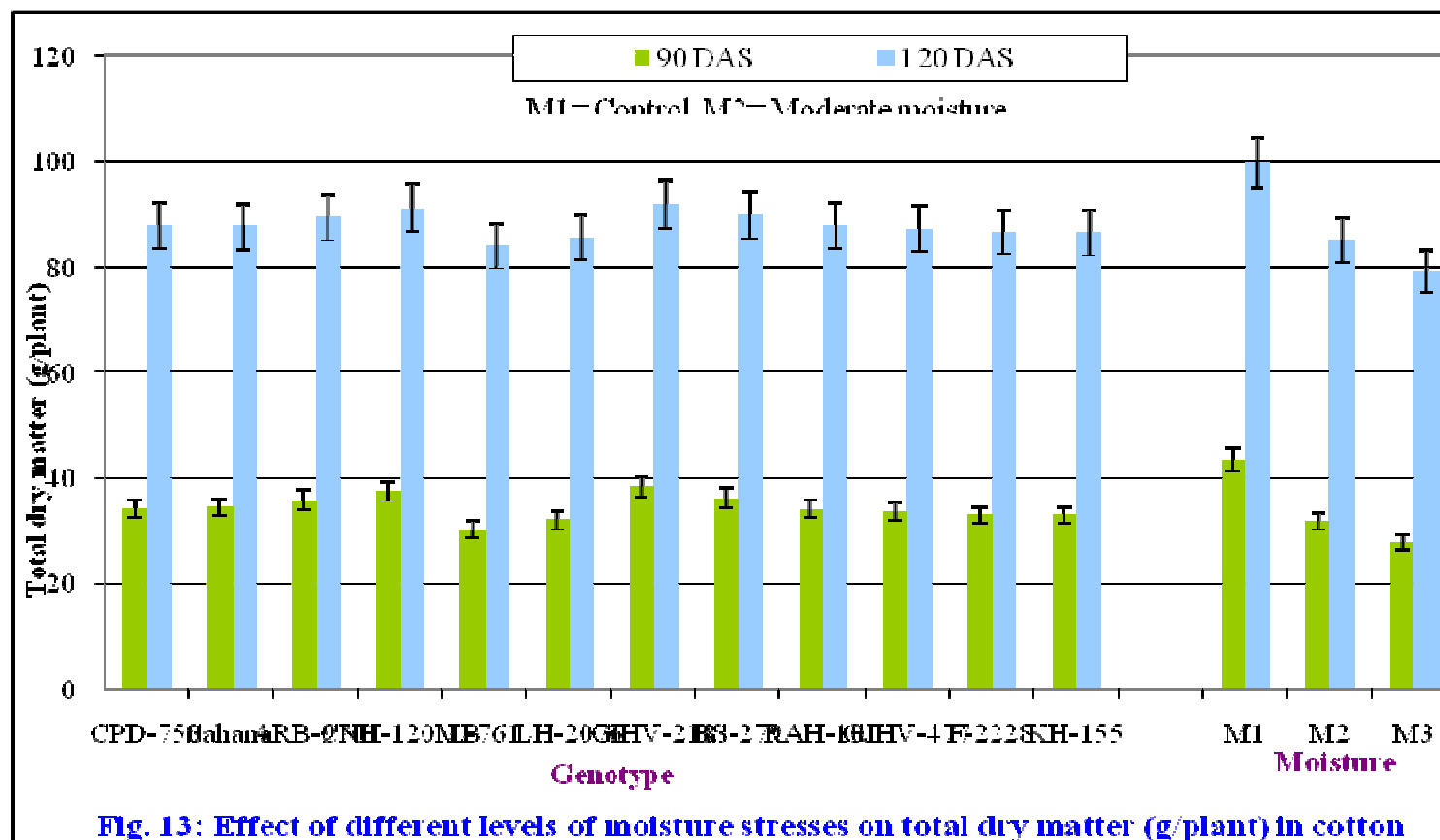


Fig.13: Effect of different levels of moisture stresses on total dry matter (g/plant) in cotton genotypes at different growth stages

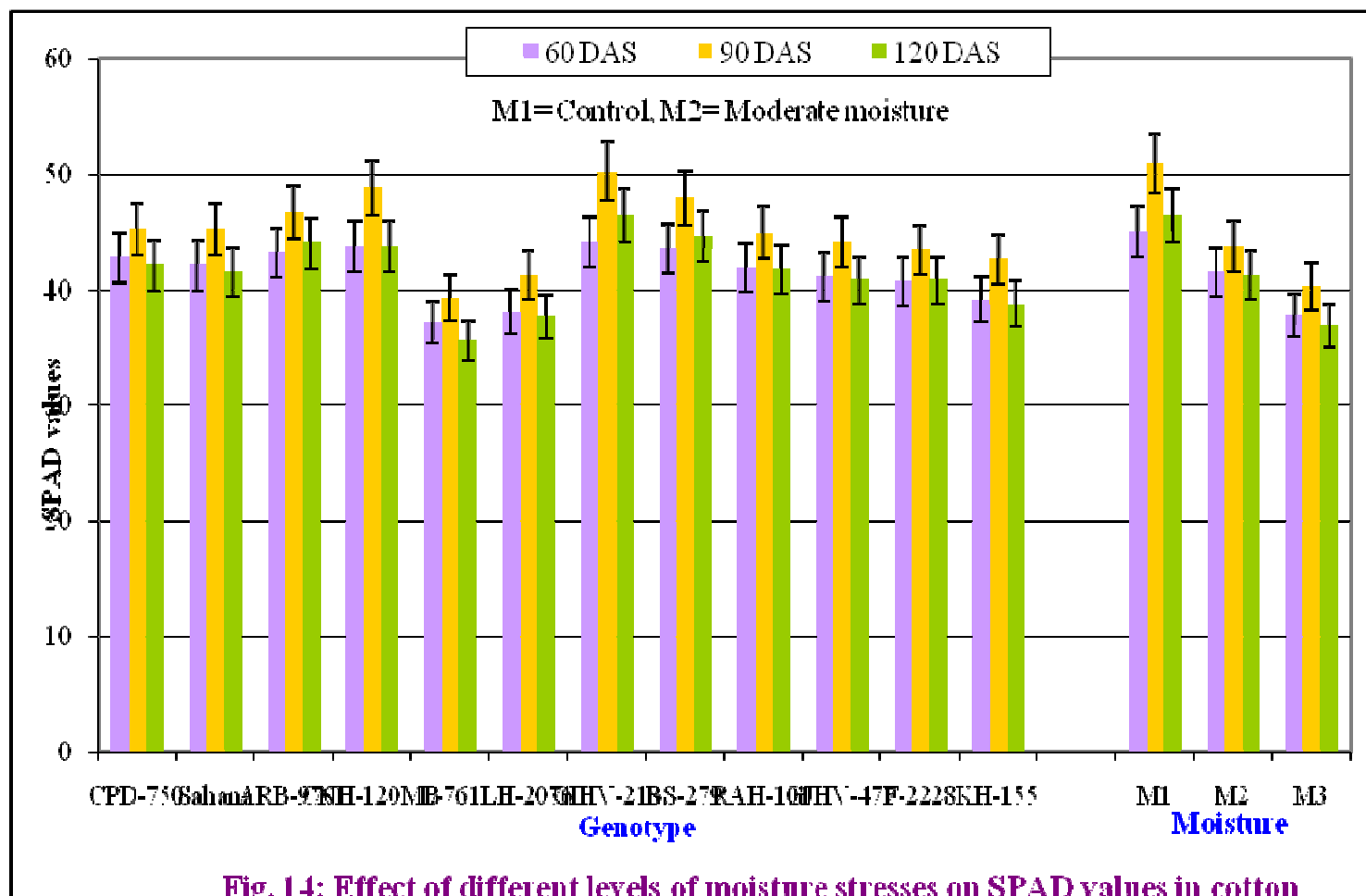


Fig.14: Effect of different levels of moisture stresses on SPAD values in cotton genotypes at different growth stages.

5.4.3.6 Gas exchange parameters

Photosynthesis plays a major role in determining crop productivity in all species and is directly affected by water stress. Photosynthetic rates of the cotton leaves decrease as the relative water content and leaf water potential decrease (Lawlor and Cornic, 2002). The effects of water stress on photosynthesis are complex and may include a combination of stomatal closure (Sharkey *et al.*, 1990) and the inhibition of metabolic processes, including ribulose biphosphate synthesis and adenosine triphosphate synthesis. In cotton, several reports have indicated that water stress causes a reduction in photosynthesis rates due to a combination of stomatal and non-stomatal limitations (Lacape *et al.*, 1998; Leidi *et al.*, 1999). Genotypic variation for physiological attributes had been reported in cotton. Inhibition of photosynthesis and stomatal conductance due to water stress is well documented (Pettigrew, 2004; Athar and Ashraf, 2005). Although photosynthesis rate have been used to distinguish water deficit tolerant and sensitive genotypes in various species, including cotton (Levi *et al.*, 2009; Saranga *et al.*, 2004) procedures for measuring gas exchanges in photosynthetic analysis are laborious and impractical for use in a breeding program (Earl and Tollenaar, 1999).

Patil (2011) reported that, water stress reduces photosynthetic rate, stomatal conductance, transpiration, NAR and leaf area duration in all the cotton genotypes under water stressed condition compared with well watered control.

In the present study the performance of cotton genotypes under different moisture stress levels were evaluated for rate of photosynthesis, rate of transpiration and stomatal conductance. The photosynthesis, transpiration and stomatal conductance was significantly reduced with the increase in moisture stress levels in all the cotton genotypes at all stages.

Water stress reduced the rate of photosynthesis from 30.2 and 26.8 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ at 90 DAS and 120 DAS in control to 21.8 and 18.4 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ at 90 DAS and 120 DAS in severe moisture stress. Similar trend (decreasing the values with increased moisture stress) was followed for rate of transpiration, stomatal conductance. The control maintained significantly less leaf temperature (33.7 $^{\circ}\text{C}$), compared to severe moisture stress (35.1 $^{\circ}\text{C}$). Similar trend was followed at 120 DAS. However, the water use efficiency increased with the increase in water stress levels among genotypes at all stages.

The genotypes which recorded higher values of gas exchange parameters under moderate and severe water stresses were GIHV-218, BS-279, ARB-9701 and CNH-120MB. While, L-761, LH-2076 and KH-155 performed least. This study reveals that these genotypes were adversely affected by water deficit for gas exchange traits. These gas exchange parameters were positively correlated with yield. These results are in agreement with the findings of Patil (2011).

The decrease in the rate of photosynthesis and stomatal conductance might be due to the damage of chlorophyll under stress condition and decrease in turgor pressure causes closure of stomata under water stress to avoid transpiration water loss. Kreig (1983) reported that both leaf area and photosynthetic rate are reduced by stress resulting in large reduction in total dry matter accumulation rates and final yield.

5.4.3.7 Leaf temperature and WUE (cf. Fig. 15)

Roark and Quisenberry (1977) found significant variability among exotic strains of *Gossypium hirsutum*, indicating possible improvements in growth stress characteristics. Chaves *et al* (2003) pointed out that it is important to understand the mechanism of drought tolerance, since different genotypes adapt to water deficit in different ways. Breeding crop varieties for higher WUE is a solution for improving water use in both rainfed and irrigated crop production.

The present study revealed that, as the water stress increased the leaf temperature and WUE increased significantly. The mean leaf temperature was 34.4 $^{\circ}\text{C}$ and 37.2 $^{\circ}\text{C}$ at 90 DAS and 120 DAS respectively. While the mean WUE was 0.201 $\mu\text{mol CO}_2/\text{m mol H}_2\text{O}$ and 0.345 $\mu\text{mol CO}_2/\text{m mol H}_2\text{O}$ at 90 DAS and 120 DAS respectively. The genotypes possessing lower leaf temperature with higher WUE were GIHV-218 followed by BS-279, ARB-9701 and CNH-120MB. These genotypes are appeared to be desirable to grow under drought conditions. While, the genotype L-761 followed by LH-2076 and KH-155 performed least which reveals that these genotypes were adversely affected by water deficit for these traits. These results are in agreement with the findings of Patil (2011). The WUE was not correlated with yield.

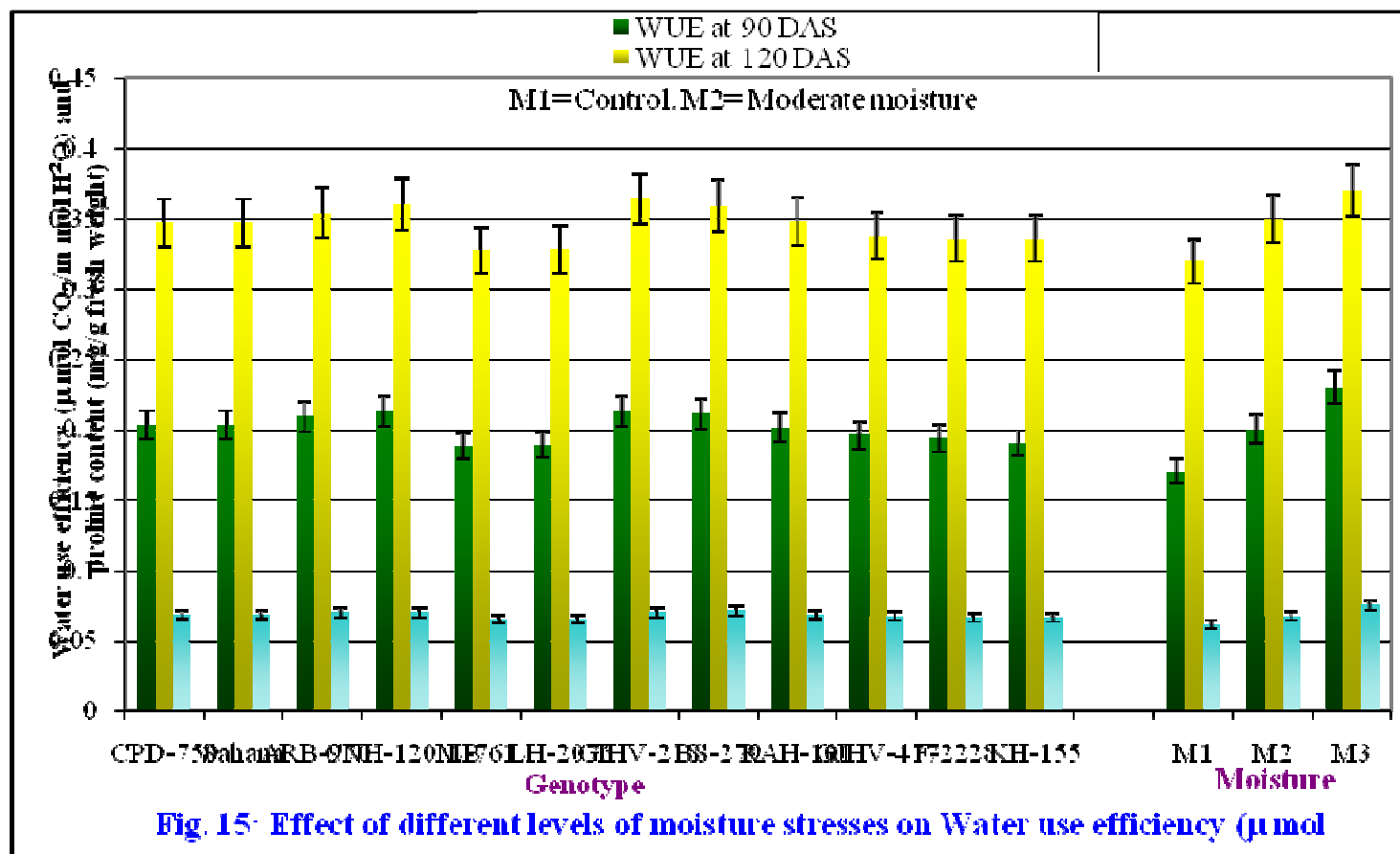


Fig.15: Effect of different levels of moisture stresses on Water use efficiency ($\mu\text{mol CO}_2/\text{m mol H}_2\text{O}$) and Proline content (mg/g fresh weight) in cotton genotypes at different growth stages

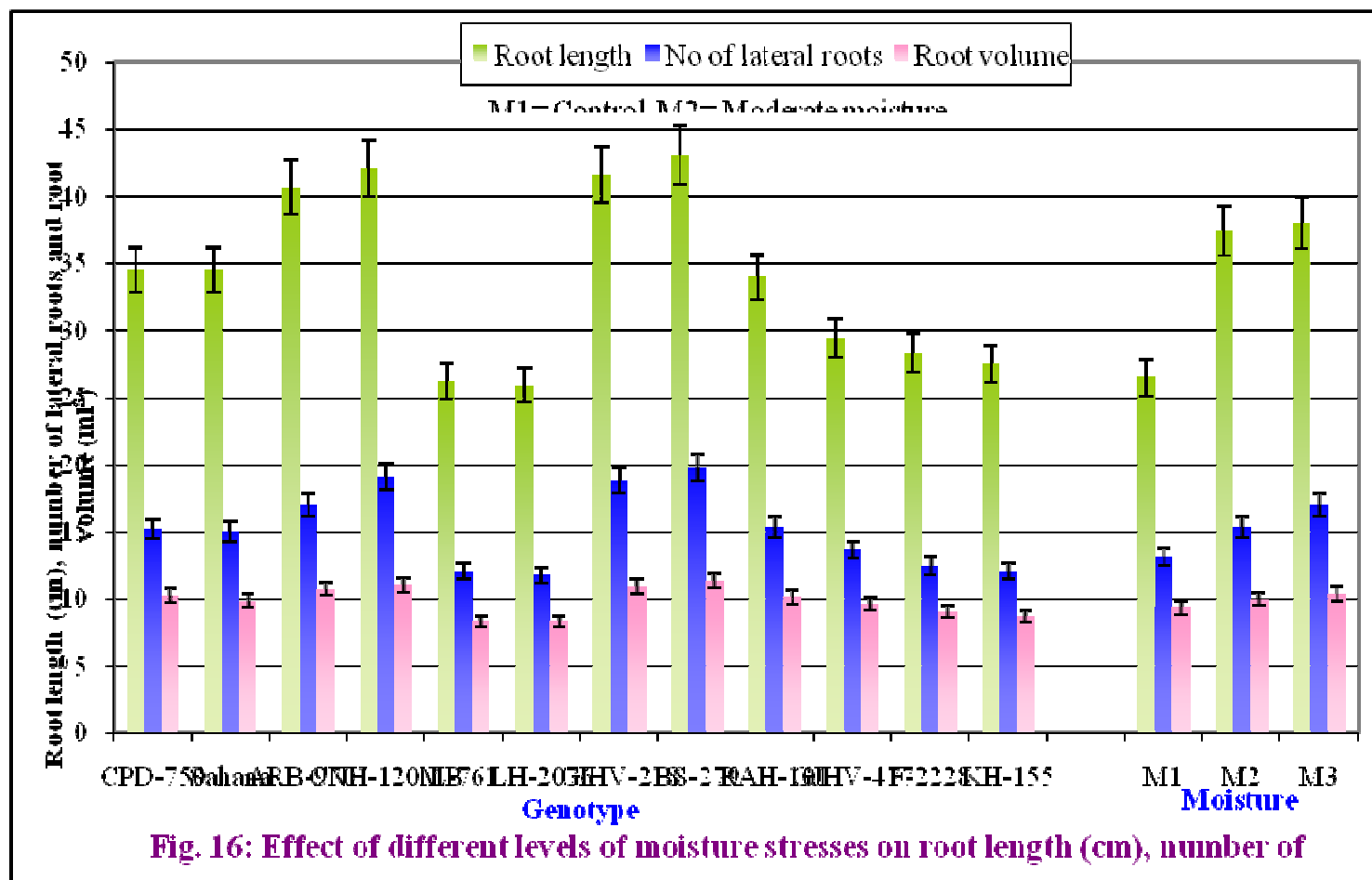


Fig.16: Effect of different levels of moisture stresses on root volume (ml³), root length (cm), and number of lateral roots in cotton genotypes at 80DAS.

5.4.3.8 Proline content (cf. Fig. 15)

Water stress increases proline accumulation in plants. Decreasing water contents resulted in progressive increase in free proline in cotton cultivars (DeRonde *et al.*, 2000; Kar *et al.*, 2005). Increases in leaf proline contents were revealed to be positively associated with biomass recovery and negatively with reduction in yield. Tolerant genotypes accumulated more proline under water stress than susceptible ones resulting in high biomass recovery and stability of seed cotton yield (Singh and Sahay, 1990).

In the present study, as the water stress increased the proline content increased significantly. The treatment control recorded significantly less proline (0.061 mg/g fresh weight) over other stress treatments, followed by moderate moisture stress (0.067 mg/g fresh weight) and severe moisture stress (0.075 mg/g fresh weight). Among the genotypes, BS-279, GIHV-218, ARB-9701 and CNH-120MB recorded significantly highest proline content and biomass and were drought tolerant than other genotypes.

Similarly the genotypes viz., BS-279, SCS-793, BGDS-802 and QJHV-500 with high nitrate reductase, peroxidase and proline content (which acts as osmoprotectant) were found as drought tolerant genotypes (Anon., 2012).

5.4.3.9 Root studies (cf. Fig. 16)

McMichael and Quisenberry (1991) observed decreased shoot-to-root ratios of plants grown under conditions of severe water stress. Malik *et al.* (1979) reported that root growth appears to be less affected by drought than shoot growth. Several researchers observed that seedlings of water stressed cotton showed increased root elongation (Pace *et al.*, 1999).

In the present study, there was significant increase in number of lateral roots, root length and root volume in all the genotypes under moisture stress. This increased root length, numbers and volume under moisture stress condition helps the plants to absorb the soil moisture from deeper soil and increased lateral roots helps in spreading roots and to absorb more water in horizontal spaces. The increased root volume helps in more availability of root surfaces to soil for water absorption.

Among the genotypes, the number of lateral roots increased from 13.0 in control to 17.0 in severe moisture stress. Similarly, the root length increased from 26.5cm in control to 38.0cm in severe moisture stress. The root volume increased from 9.3 ml³ in control and 10.4 ml³ in severe moisture stress.

This attributed to partitioning of more photosynthates for the growth of roots rather than shoots, which helps in absorbing more water from deeper surfaces. This caused increase in root:shoot ratio. Under moisture stress the decreased shoot organs growth helps in reducing transpiration water loss from shoot surfaces.

Similarly, Taylor and Klepper (1971) observed that water extraction per unit length of root was greater in wet soil and decreased exponentially with soil water potential. In general they found that deep roots were effective in extracting water from soil.

The genotypes BS-279 followed by GIHV-218, CNH-120MB and ARB-9701 due to higher value of root traits can be considered as desirable to grow under severe moisture stress and rain fed conditions. However the number of lateral roots, root length and root volume were not correlated with yield. This might have been modified under moisture stress as a survival mechanism rather than contributing to yield. Therefore these may not be any correlation between yield and root traits in this study.

Similarly Pace *et al.* (1999) found that the increased taproot length at the expense of thickening, in response to drought may be a common response in cotton. This response may permit cotton plants to survive drought by accessing water from deeper in the soil profile than the soil horizons tapped during periods of adequate water supply.

5.4.3.10 Yield and yield components (cf. Fig. 17 and Fig. 18)

Among the different moisture stress treatments, control recorded significantly more number of bolls (25.3) followed by moderate moisture stress (21.8) and severe moisture stress (17.6). Similarly the treatment control recorded more mean boll weight (4.5g/boll) than severe stress (3.0 g/boll). Similarly the treatment control recorded significantly more seed cotton yield (2343 kg/ha) followed by moderate moisture stress (1693 kg/ha) and severe moisture stress (1424 kg/ha). The seed boll weight and number of bolls were positively correlated with yield.

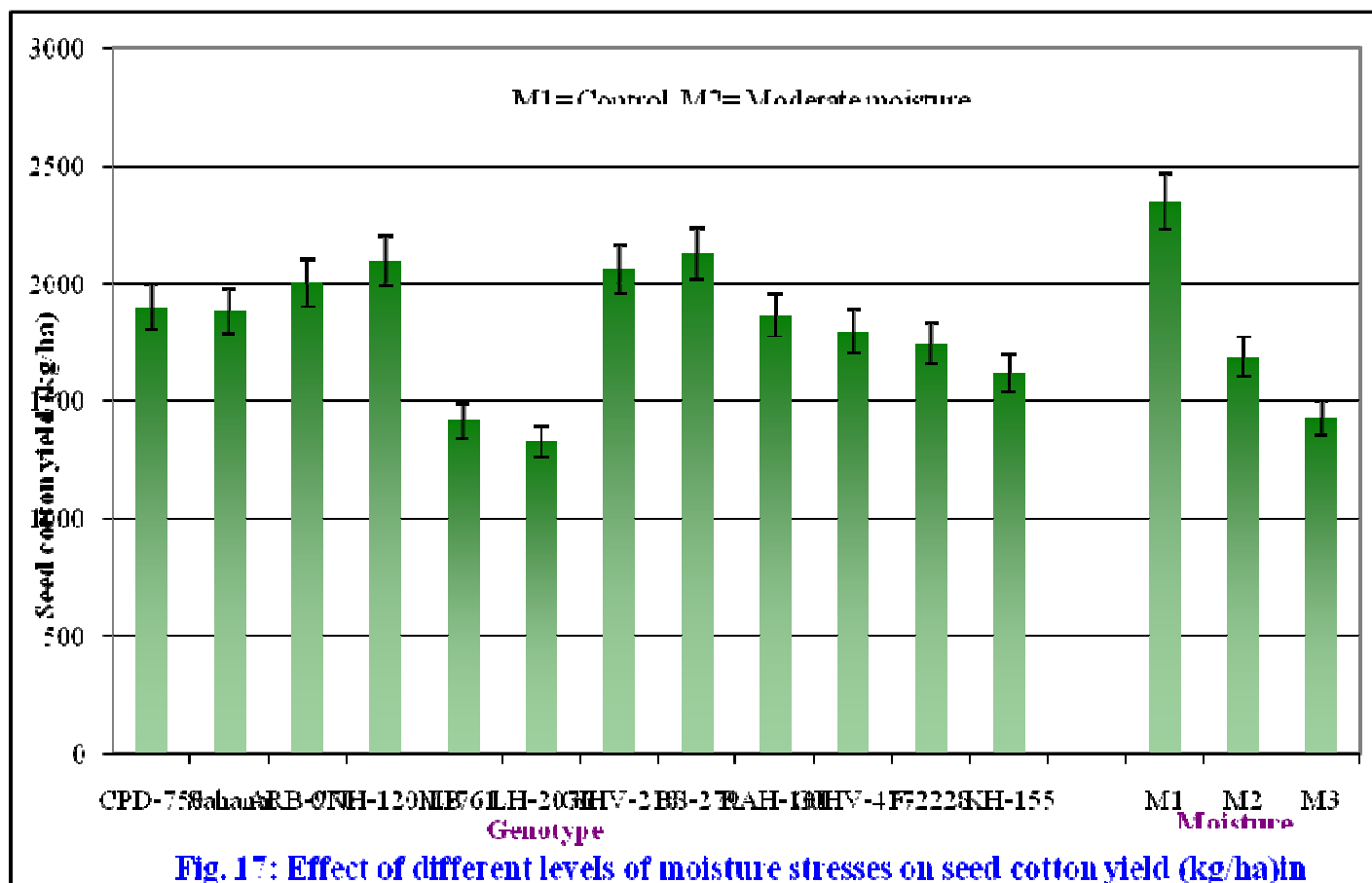


Fig.17: Effect of different levels of moisture stresses on Seed cotton yield (kg/ha) in cotton genotypes

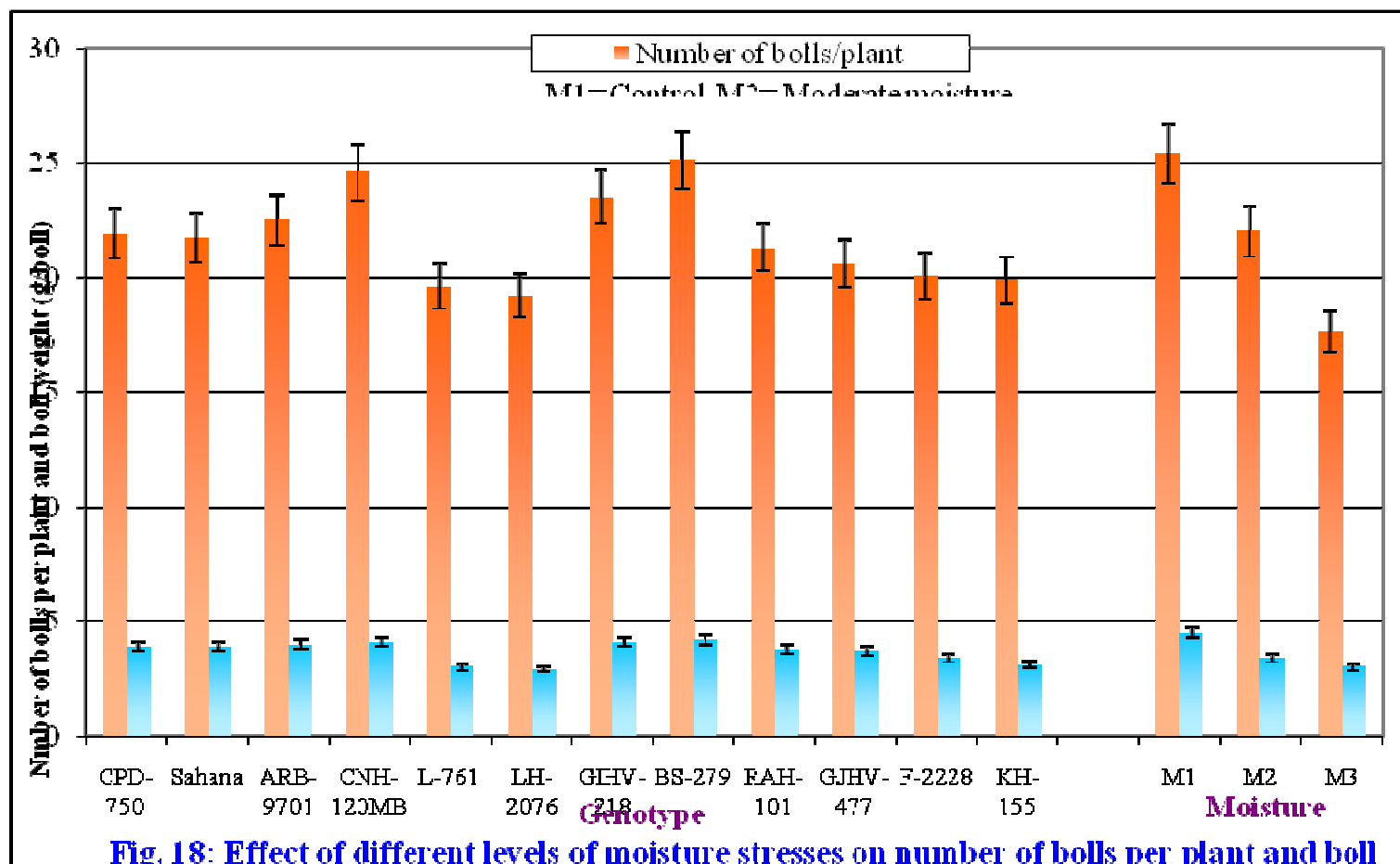


Fig.18: Effect of different levels of moisture stresses on Number of bolls per plant and Boll weight (g/boll) in cotton genotypes

Grimes *et al.* (1982) and Patil (2011) found that there is a positive correlation between yield and the number of bolls produced.

The genotypes which found drought tolerant and gave higher seed cotton yield, boll weight and boll numbers in all moisture regimes were BS-279 followed by GIHV-218, CNH-120MB and ARB-9701. The higher yield in these genotypes is due to efficient physiological traits viz. SPAD, LAI, TDM, SLW, gas exchange parameters, better root architecture, proline content, boll numbers and boll weight *etc.* These genotypes are suitable to grow under severe moisture stress and rainfed conditions. These genotypes are drought tolerant ones and can be used further for breeding programme. While, the genotype L-761 followed by LH-2076 and KH-155 performed least and were adversely affected by water deficit for yield and other traits.

Similarly Karademir *et al.* (2011) evaluated the effect of water stress and non-stress conditions on cotton yield and fibre quality properties. By evaluating twelve cotton genotypes for yield and fibre quality properties they found significant differences among genotypes and water treatments and decreased seed cotton yield, fibre yield, ginning percentage and all fibre quality properties except fibre uniformity under water stress.

Muhammad *et al.* (2011) evaluated 31 cotton genotypes under two irrigation regimes *i.e.*, seven irrigations (Control) and two irrigations (Stress). They recorded significantly decreased seed cotton yield, number of bolls, boll weight and chlorophyll content under water stressed condition compared to well watered condition.

5.4.3.11 Fibre properties and Ginning out turn (GOT)

The study was to determine the effect of water stress and non-stress conditions on cotton fibre quality properties is discussed as follows.

Among the different moisture stress treatments, as the water stress increased the fibre length and strength decreased significantly. In fibre length trait, the treatment control (29.9 mm) recorded significantly more staple length followed by moderate moisture stress (29.3 mm) and severe moisture stress (28.5 mm). Similarly control recorded significantly more fibre strength (22.2 g/tex), than severe moisture stress (19.8 g/tex). The genotypes which had higher staple length in all moisture regimes were CPD-750 followed by ARB-9701 and RAH-101. These genotypes are relatively less affected by moisture stress regimes. Whereas least ones were L-761 and GJHV-477.

The genotypes which had higher fibre strength were GIHV-218 followed by Sahana and RAH-101. These genotypes are relatively less affected by moisture stress regimes. Whereas least ones were L-761, LH-2076 and F-2228. But there was a no significant difference among the moisture stress treatments for micronaire. However there was significant difference found among genotypes. But the interaction was non-significant. The genotypes which showed significantly best fibre fineness were and GIHV-218, Sahana and CPD-750. The fibre length, fibre strength were positively correlated with yield but fibre fineness was not correlated.

Fibre length was affected by irrigation levels and fertilizer was earlier reported. Micronaire were not significantly influenced by nutrient, moisture and their interaction. Similar observations were also made by Polychronides *et al.* (1998).

As the water stress increased the GOT decreased significantly. The treatment control recorded significantly more GOT (38.2%), followed by moderate moisture stress (36.4%) and severe moisture stress (35.9%). These results are in agreement with the findings of Patil (2011).

5.5 Genetic polymorphism/diversity study among genotypes using Random Amplified Polymorphic DNA molecular markers

Drought tolerance is a quantitative trait and is known to be controlled by more than one gene and has a complex inheritance. Since cotton originates from areas that are often exposed to water-deficit stress, considerable genetic variability in drought tolerance exists (Saranga *et al.*, 1998; Pettigrew and Meredith, 1994).

For the success of any crop improvement programme genetic diversity is a pre-requisite. Traditionally, genetic diversity is assessed based on a number of morphological features such as plant height, sympodial branches, reproductive features, day length sensitivity, local adaptation *etc.* Though such characters exhibit enormous variability for the particular use of the crop, only a part of the total genetic variability is considered when assessing these characters. Classifying germplasm

accessions solely based on a few discrete morphological characteristics may not provide an accurate indication of the genetic divergence among cultivars, species and other study groups. Nowadays there are many DNA based molecular markers such as RAPD, RFLP, AFLP, SSR, SNP's, etc. are available which can detect polymorphism at the DNA level. In the present study, RAPD markers were employed to assess DNA polymorphism to assess the molecular diversity of the twelve cotton genotypes used in the investigation.

In RAPD technique, a single short oligonucleotide sequence is used for cyclic amplification of DNA, which exposes the polymorphism distributed throughout the genome. These amplified fragments were called as random amplified polymorphic DNAs. This technique has been used in genetic polymorphism study, genome mapping and gene tagging in several crop plants.

The major advantage of the RAPD technique is that, it does not need sequence information to start with and there is virtually no limit to the number of primers that can be designed for use in RAPD reaction. The polymorphism among the genotypes can be detected by using random primers. Variation in the banding pattern of the amplification products occur because of variation in the length of DNA sequences flanked by the primer. In the present study twelve cotton genotypes were used for RAPD analysis with 79 random primers. The greater genetic polymorphism (79.56%) among cotton genotypes was revealed by the primers used in the study, out of the 274 amplification products detected in the twelve genotypes, 218 were polymorphic.

Similar studies by Iqbal *et al.* (1997) found 89.1 per cent polymorphism among 23 *G. hirsutum* cultivars, wherein one cultivar was of the species *G. arboreum*. Rahman *et al.* (2002) observed 66.2 per cent polymorphism in 27 cotton varieties. Rana and Bhat (2005) studied with RAPD markers for genetic diversity estimation in 59 cotton cultivars belonging to four cultivated species of cotton. The selected eighteen RAPD primers produced a total of 251 amplicons, which generated 97.21 per cent polymorphism.

In the present study the amount of genetic similarity or diversity observed in molecular studies is dependent on the number and type of primers used and the amount of diversity among the genotypes used in the investigation. In the present study among all the twelve genotypes from the pooled data, the genetic similarity obtained was ranged from 63.8 per cent to 82.1 per cent. Similar studies by Rana and Bhat (2005) observed the number of amplification products ranged from 7 to 24 for different primers, whereas per cent genetic similarity for the studied primers ranged from 42 to 79%.

In the present study genetic diversity observed was enormous with high level of polymorphism among genotypes. Drought tolerance is a highly complex trait. It is the combination of several morphological and physiological components contributing for drought tolerance. Each genotype could tolerate to drought through different combinations of component traits. Therefore, although, the selected genotypes are uniformly drought tolerant, there could be lot of variation among the genotypes for component traits and their combination, which could be the reason for high level of polymorphism observed for the selected genotypes. The primer OPI 4 and OLIGO 652 amplified 800 bp and 400 bp respectively were specific to drought tolerant genotypes viz. CPD-750, Sahana, ARB-9701, CNH-120MB, GIHV-218, BS-279 and RAH-101 specific bands. These primers could be cotton drought specific RAPD makers, since they amplified only in drought tolerant genotypes. The primer OPE3 amplified at 400bp which was specific to only to the genotypes CPD-750, Sahana and ARB-9701. While, the primer OPI 16 produced band 450bp this was specific to the genotypes RAH-101, GJHV-477 and KH-155.

Dendrogram revealed that, set of primers chosen for study were able to group the genotypes. The dendrogram clearly indicated that there were three major clusters. In first major cluster consists of the genotypes CPD-750 and GIHV-218. The second cluster consists of Sahana, CNH-120MB, L-761, LH-2076, ARB-9701, RAH-101 and GJHV-477. Whereas in third cluster consists of the genotypes BS-279, F-2228 and KH-155.

5.6 Results of practical utility

- The genotypes CPD-750, Sahana, ARB-9701, CNH-120MB, GIHV-218, BS-279 and RAH-101 found drought tolerant from this study, can be used cultivate in moisture stressed and rain fed regions.

- The identified drought tolerance genotypes are the good source of drought tolerant traits (SLW, water potential, root traits, proline content etc.), hence these are the potential genotypes for breeding programme to develop drought tolerant varieties.
- The study of drought tolerance using slanting glass plate technique using PEG water stress to screen drought tolerance genotypes at seedling stage is simple, low cost, fast and easily operated, could be used to evaluate the drought tolerance of cotton in principle and will establish initial foundations for study on cotton drought tolerance and molecular biology.
- The identified cotton drought specific RAPD primers/markers (OPI 4 and OLIGO 652 markers) can be used in cotton drought tolerant genotypes screening studies and they can be used to develop SCAR markers.

5.7 Future line of work

- The identified drought tolerant lines can be used in breeding programme to develop drought tolerant varieties.
- Best performers 200 germplasm lines can be further fine tuned to smaller numbers by extensive study of physiological and biochemical attributes.
- The selected twelve genotypes could be studied extensively for biochemical and other drought tolerance traits (^{13}C , Florescence etc.) and proteomics study.
- The genotypes can be further studied in large scale field trials and multi location study to elucidate their performance and stability.
- The identified probable drought specific RAPD primers/markers can be further analysed extensively to develop certain drought specific markers in cotton.
- Use of drought specific RAPD markers, other co-dominant markers for precise identification of drought tolerant genotypes is needed.

SUMMARY AND CONCLUSIONS

Environmental stresses are among the most limiting factors to plant productivity. Drought is an important abiotic stress affecting the productivity of all rainfed crops. Moisture stress potentially limits the future of agriculture in most productive areas of world. The productivity of cotton in India is very low as compared to world average due to many reasons such as less area under irrigation and around 70 per cent of cotton cultivated area under rainfed condition, which is characterized by scarcity of soil moisture. Taking these facts into consideration, experiments in field and laboratory was conducted to find out the genotypes which perform better under these moisture stress conditions.

The initial research work was carried out in *kharif* season during 2011-2012 at two locations viz. ARS Dharwad and ARS Annigeri to assess the genetic variability of cotton genotypes for drought tolerance by biophysical and physiological traits. Simultaneously 600 cotton germplasm lines were evaluated under rain fed condition at ARS Dharwad. Finally 12 genotypes were selected based on performance of the genotypes in the first year field experiment.

The selected genotypes were evaluated for tolerance to osmotic stress conditions by slanting glass plate technique. Here genotypes were grown in the different concentrations of PEG during germination stage and early seedling stage.

During second year (2012-13) *kharif* season, the selected twelve genotypes were grown in rain out shelter and were evaluated for drought tolerance by biophysical, root architecture, yield and fibre properties. During 2012-13 the selected twelve genotypes were studied for genetic polymorphism using cotton specific RAPD molecular markers.

6.1 Field experiment at ARS Dharwad and ARS Annigeri

- At all the growth stages the lower moisture level in ARS Annigeri resulted in poor performance of the genotypes for physiological traits viz. SLW, SPAD values, leaf water potential, photosynthesis, stomatal conductance, transpiration, leaf temperature and seed cotton yield compared to ARS Dharwad.
- Less SPAD, SLW and water potential was recorded in the cotton genotypes grown in ARS Annigeri (water stressed) compared to ARS Dharwad (assured rainfall area). The mean SLW values was reduced from 8.5 mg/cm², 8.8 mg/cm², 9.9 mg/cm² at 60 DAS, 90 DAS and 125 DAS respectively at ARS Dharwad to 7.7 mg/cm², 8.4 mg/cm², 8.9 mg/cm² respectively in ARS Annigeri. Similar trend was observed for SPAD values.
- Higher mean photosynthesis rate (31.4 μ mol CO₂/m²/s), stomatal conductance (0.30 μ mol CO₂/m²/s) and transpiration rate (4.4 m mol H₂O/m²/s) recorded at ARS Dharwad compared to ARS Annigeri at 90DAS. Whereas lower mean leaf temperature of 29.6°C recorded in ARS Dharwad genotypes compared to ARS Annigeri (31.0°C).
- The mean seed cotton yield at ARS Dharwad was 25 per cent higher (2155 kg/ha), than ARS Annigeri (1616 kg/ha).
- At ARS Dharwad, out of 30 genotypes better performed genotypes for physiological traits (viz. SLW, SPAD, leaf water potential and gas exchange parameters) were GIHV-218, CNH-120MB, BS-30, KH-155, ARB-9701, CPD-168, GSHV-01/26, and Sahana. While, the genotypes L-761, H-1353, LH-2076, KH-138, F-186, GSHV-97/13 and L-763 performed least.
- At ARS Annigeri, the genotypes which performed best for physiological traits were GIHV-218, CNH-120MB, KH-155, ARB-9701, CPD-750, Sahana, RAH-101 and RAH-30. While, the genotypes LH-2076, L-761, H-1353 and KH-138 performed least.
- Based on the initial results of 2011-12 field experiment, out of thirty genotypes, the genotypes CPD-750, Sahana, ARB-9701, CNH-120MB, GIHV-218, BS-279, RAH-101, GJHV-477, F-2228 and KH-155 were identified as relatively drought tolerant genotypes and two genotypes (L-761 and LH-2076) as water stress sensitive lines.

6.2 Evaluation 600 cotton germplasm lines for drought tolerance

- The ANOVA for augmented analysis revealed that, there was highly significant genotypic difference observed for all the physiological traits.

- Among the germplasms GPDWD 613, GPDWD 606, GPDWD 622, GPDWD 608, GPDWD 501, GPDWD 520, GPDWD 484, GPDWD 561, GPDWD 607, GPDWD 592, GPDWD 596, GPDWD 610, GPDWD 614, GPDWD 611, GPDWD 601, GPDWD 620, GPDWD 598, GPDWD 602, GPDWD 620, GPDWD 616, GPDWD 600, GPDWD 624, GPDWD 590 and GPDWD 618 which were having statistically significant higher values for most of the recorded physiological traits hence these are the superior genotypes which might have drought tolerance.
- While grouping the 600 genotypes for physiological traits, there were 200 best performers' germplasm lines which performed superior to other lines.
- Most of the best performer's lines for SPAD trait were also having higher values of SLW and gas exchange traits.
- Among the germplasm lines there was more genetic diversity observed for physiological traits. The SPAD values ranged from 36.3 to 43.1 at 60 DAS and 43.2 to 48.9 at 90 DAS. The highest mean SLW recorded in best performers (10.5 mg/cm^2) followed by moderate performers (9.8 mg/cm^2) and least performers (9.1 mg/cm^2).
- The best performers germplasm lines were recorded highest photosynthetic rate, stomatal conductance and transpiration rate compared to least performers.

6.3 Evaluation of cotton genotypes for drought tolerance using PEG water stress by slanting glass plate technique

- Evaluation of cotton genotypes for drought tolerance using PEG stress by slanting glass plate technique revealed that, germination percentage and shoot length were decreased as the PEG 6000 concentration increased from 0% to 27%. The mean seed germination at 0.0 MPa, -0.05 MPa, -0.148 MPa, -0.295 MPa, -0.491 MPa, -0.735 MPa and -0.846 MPa PEG -6000 osmotic concentration was 100%, 86%, 78%, 63%, 31%, 5% and 0% respectively. Hence -0.735 MPa is the maximum PEG concentration for these cotton genotypes germination.
- The root length increased with the increase in PEG concentration, whereas the shoot length decreased with increase in PEG. Root length (increased up to 10 per cent PEG concentrations and declined thereafter). Root:shoot ratio increased with the increase in PEG concentrations from 0% to 27 % at both 12th and 18th day after seed germination. Hence increasing root: shoot ratio could be one of the drought tolerant mechanism under water stress.
- Similarly the seedling vigour index and shoot vigour index decreased with the increase in PEG concentrations. At both 12th DAS and 18th DAS the root length index was maximum in 10 per cent PEG followed by 05% PEG, where as it was least in 27 per cent PEG followed by 25% PEG.
- At all the PEG concentrations at both 12th and 18th DAS stages the genotypes BS-279, followed by CNH-120MB, GIHV-218 and ARB-9701 found better tolerant to increased PEG solutions, Whereas, the sensitive genotypes were L-761, KH-155 and LH-2076.

6.4 Studies on drought tolerance under Rain out shelter

- In ROS, the increased level of water stress reduced the plant height and number of leaves in all the twelve genotypes at all growth stages in comparison with control. The mean plant height was 43.2cm, 69.6cm and 85.8cm at 60 DAS, 90 DAS and 120 DAS respectively. The mean number of leaves per plant was 43.7, 101.7 and 95.5 at 60 DAS, 90 DAS and 120 DAS respectively.
- The genotypes which had higher plant height and number of leaves under moderate (70% field capacity) and severe water stresses (50% field capacity) at all growth stages were RAH-101 followed by GIHV-218, ARB-9701, CNH-120MB and BS-279. While, L-761, LH-2076 and KH-155 found adversely affected by water deficit moisture regimes.
- Moisture stress significantly reduced the genotypes TDM, relative growth rate, net assimilation rate, specific leaf weight, leaf area index and SPAD values at all growth stages.

- Among the different moisture stress treatments, the fourth fully expanded leaf from the apex genotypes in control recorded more SPAD values (45.0), followed by moderate moisture stress (41.5) and severe moisture stress (37.8).
- Water stress reduced the net assimilation rate from 0.041 g/dm²/day in control to 0.037 g/dm²/day in severe moisture stress. The treatment control recorded significantly more relative growth rate (0.0182 g/g/day) followed by moderate moisture stress (0.0167 g/g/day) and severe moisture stress (0.0160 g/g/day).
- The moisture stress reduced TDM from 43.4 g/ plant at 90 DAS and 99.8 at 120 DAS to 27.8 g/plant at 90 DAS and 79.1 g/ plant at 120 DAS. The genotypes, GIHV-218, CNH-120MB, BS-279 and ARB-9701 recorded more TDM over all other genotypes.
- The genotypes in the treatment control (9.3 mg/cm²) recorded more SLW, followed by moderate moisture stress (8.4 mg/cm²) and severe moisture stress (7.3 mg/cm²). The mean SLW was 8.4 mg/cm² and 8.8 mg/cm² at 90 DAS and 120 DAS respectively. Among the different moisture stress treatments, the treatment control recorded more LAI (1.6), followed by moderate moisture stress (1.4) and severe moisture stress (1.2).
- The genotypes which performed well for physiological traits viz., gas exchange traits, LAI, SLW, SPAD, RGR, NAR, TDM, root length, root volume, and WUE over all other genotypes were GIHV-218, BS-279, ARB-9701 and CNH-120MB. While, the genotype LH-2076, L-761 and KH-155 performed least for above traits.
- The genotypes GIHV-218, BS-279, ARB-9701, CPD-750 and CNH-120MB were found promising under severe moisture stress because of higher gas exchange traits, LAI, SLW, SPAD, TDM, root length, root volume, proline and WUE.
- The rate of photosynthesis, stomatal conductance and rate of transpiration was reduced as the water stress increased. However, the WUE and leaf temperature were increased with the increase in water stress levels among the genotypes.
- Water stress reduces the rate of photosynthesis from 30.2 and 26.8 μ mol CO₂/ m²/s at 90 DAS and 120 DAS in control to 21.8 and 18.4 μ mol CO₂/ m²/s at 90 DAS and 120 DAS in severe moisture stress respectively.
- Water stress reduces rate of transpiration of the genotypes from 58% at 90 DAS and 62% at 120 DAS in control compared to in severe moisture stress condition. Similar trend was observed for stomatal conductance. Whereas leaf temperature increased from 33.7°C in control to 35.1 °C in severe moisture stress at 90 DAS. Similar trend was observed at 120 DAS. The genotypes GIHV-218, BS-279, ARB-9701 and CNH-120MB performed well for gas exchange parameters. While, the genotype L-761, LH-2076 and KH-155 performed the least.
- As the water stress increased the proline content increased significantly. The treatment control recorded significantly less proline (0.061 mg/g fresh weight) while severe moisture stress recorded least (0.075 mg/g fresh weight). Among the genotypes, BS-279, GIHV-218, ARB-9701 and CNH-120MB recorded significantly high proline content. While, L-761 followed by LH-2076 and KH-155 recorded least.
- As the water stress increased at 80DAS there was significant increase in root length, number of lateral roots and root volume was noticed among all the genotypes at 80DAS. Among the genotypes, the number of lateral roots increased from 13.0 in control to 17.0 in severe moisture stress. The root length increased from 26.5cm in control to 38.0cm in severe moisture stress. Similarly among the genotypes, the root volume increased from 9.3 ml³ in control and 10.4 ml³ in severe moisture stress. The genotypes which performed under root traits under increased moisture stress were BS-279, GIHV-218, CNH-120MB and ARB-9701 While, L-761, LH-2076 and KH-155 performed least.
- Among the genotypes, the water stress reduced the boll weight from 4.5 g/boll in control to 3.0g/boll in severe moisture stress. The number of bolls per plant was reduced from 25.3 in control to 17.6 in severe moisture stress. Similarly seed cotton yield was reduced from 2543Kg in control to 1424Kg per ha in severe moisture stress. The genotypes which had drought tolerance with highest seed cotton yield, boll weight and boll numbers were BS-279 followed by GIHV-218, CNH-120MB and ARB-9701. While, L-761, LH-2076 and KH-155 performed least and were adversely affected by water deficit for yield traits.

- Water stress reduced fibre strength from 22.2 g/tex in control to 19.8 g/tex in severe moisture stress. The treatment control recorded more staple length (29.9 mm) followed by moderate moisture stress (29.3 mm) and severe moisture stress (28.5 mm). Similarly water stress reduces the ginning out turn from 38.2 per cent in control to 35.9 per cent in severe moisture stress. But there was a no significant difference among the moisture stress treatments for micronaire. However, genotypes showed significantly difference for fibre fineness.

6.5 Genetic polymorphism/diversity study among genotypes using Random Amplified Polymorphic DNA molecular markers

- Out of 79 random RAPD primers the greater genetic similarity/diversity of 79.56 per cent among cotton genotypes. Total 274 amplification products detected in the twelve genotypes, among which 218 were polymorphic. Out of 79 RAPD primers 76 primers indicated genetic polymorphism. The genetic diversity observed was enormous with high level of polymorphism among genotypes.
- The primer OPI 4 and OLIGO 652 amplified 800 bp and 400 bp respectively were specific to relatively drought tolerant genotypes viz.CPD-750, Sahana, ARB-9701, CNH-120MB, GIHV-218, BS-279 and RAH-101 specific bands. These primers could be cotton drought specific RAPD makers, since they amplified only in drought tolerant genotypes. The primer OPE3 amplified at 400bp which was specific to the genotypes CPD-750, Sahana and ARB-9701. While, the primer OPI 16 produced band 450bp this was specific to the genotypes RAH-101, GJHV-477 and KH-155.
- Dendrogram revealed that, set of primers chosen for study were able to group the genotypes. The dendrogram clearly indicated there were three major clusters. In the first major cluster consists of the genotypes CPD-750 and GIHV-218. In second cluster consists of Sahana, CNH-120MB, L-761, LH-2076, ARB-9701, RAH-101 and GJHV-477. Whereas in third cluster consists of the genotypes BS-279, F-2228 and KH-155.

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Appendix I: List of 600 germplasm lines used in the study at ARS Dharwad

Germplasm number	Germplasm Accession No.	Germplasm number	Germplasm Accession No.	Germplasm number	Germplasm Accession No.
1	GPDWD 1	46	GPDWD 46	91	GPDWD 92
2	GPDWD2	47	GPDWD 47	92	GPDWD 93
3	GPDWD3	48	GPDWD 48	93	GPDWD 94
4	GPDWD4	49	GPDWD 49	94	GPDWD 95
5	GPDWD5	50	GPDWD 50	95	GPDWD 96
6	GPDWD6	51	GPDWD 51	96	GPDWD 97
7	GPDWD7	52	GPDWD 52	97	GPDWD 98
8	GPDWD8	53	GPDWD 53	98	GPDWD 99
9	GPDWD9	54	GPDWD 54	99	GPDWD 100
10	GPDWD10	55	GPDWD 56	100	GPDWD 101
11	GPDWD11	56	GPDWD 57	101	GPDWD 102
12	GPDWD12	57	GPDWD 58	102	GPDWD 103
13	GPDWD13	58	GPDWD 59	103	GPDWD 104
14	GPDWD14	59	GPDWD 60	104	GPDWD 105
15	GPDWD15	60	GPDWD 61	105	GPDWD 106
16	GPDWD16	61	GPDWD 62	106	GPDWD 107
17	GPDWD17	62	GPDWD 63	107	GPDWD 108
18	GPDWD18	63	GPDWD 64	108	GPDWD 109
19	GPDWD19	64	GPDWD 65	109	GPDWD 110
20	GPDWD20	65	GPDWD 66	110	GPDWD 111
21	GPDWD 21	66	GPDWD 67	111	GPDWD 112
22	GPDWD 22	67	GPDWD 68	112	GPDWD 113
23	GPDWD 23	68	GPDWD 69	113	GPDWD 114
24	GPDWD 24	69	GPDWD 70	114	GPDWD 115
25	GPDWD 25	70	GPDWD 71	115	GPDWD 116
26	GPDWD 26	71	GPDWD 72	116	GPDWD 117
27	GPDWD 27	72	GPDWD 73	117	GPDWD 118
28	GPDWD 28	73	GPDWD 74	118	GPDWD 119
29	GPDWD 29	74	GPDWD 75	119	GPDWD 120
30	GPDWD 30	75	GPDWD 76	120	GPDWD 121
31	GPDWD 31	76	GPDWD 77	121	GPDWD 122
32	GPDWD 32	77	GPDWD 78	122	GPDWD 123
33	GPDWD 33	78	GPDWD 79	123	GPDWD 124
34	GPDWD 34	79	GPDWD 80	124	GPDWD 125
35	GPDWD 35	80	GPDWD 81	125	GPDWD 126
36	GPDWD 36	81	GPDWD 82	126	GPDWD 127
37	GPDWD 37	82	GPDWD 83	127	GPDWD 128
38	GPDWD 38	83	GPDWD 84	128	GPDWD 130
39	GPDWD 39	84	GPDWD 85	129	GPDWD 132
40	GPDWD 40	85	GPDWD 86	130	GPDWD 135
41	GPDWD 41	86	GPDWD 87	131	GPDWD 136
42	GPDWD 42	87	GPDWD 88	132	GPDWD 138
43	GPDWD 43	88	GPDWD 89	133	GPDWD 139
44	GPDWD 44	89	GPDWD 90	134	GPDWD 140
45	GPDWD 45	90	GPDWD 91	135	GPDWD 141

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Germplasm number	Germplasm Accession No.	Germplasm number	Germplasm Accession No.	Germplasm number	Germplasm Accession No.
136	GPDWD 142	181	GPDWD 198	226	GPDWD 247
137	GPDWD 143	182	GPDWD 200	227	GPDWD 248
138	GPDWD 144	183	GPDWD 201	228	GPDWD 249
139	GPDWD 145	184	GPDWD 202	229	GPDWD 250
140	GPDWD 146	185	GPDWD 203	230	GPDWD 251
141	GPDWD 147	186	GPDWD 204	231	GPDWD 252
142	GPDWD 148	187	GPDWD 205	232	GPDWD 253
143	GPDWD 149	188	GPDWD 206	233	GPDWD 254
144	GPDWD 150	189	GPDWD 207	234	GPDWD 255
145	GPDWD 152	190	GPDWD 208	235	GPDWD 256
146	GPDWD 153	191	GPDWD 209	236	GPDWD 257
147	GPDWD 156	192	GPDWD 211	237	GPDWD 258
148	GPDWD 158	193	GPDWD 212	238	GPDWD 259
149	GPDWD 160	194	GPDWD 213	239	GPDWD 260
150	GPDWD 161	195	GPDWD 214	240	GPDWD 261
151	GPDWD 162	196	GPDWD 215	241	GPDWD 262
152	GPDWD 163	197	GPDWD 216	242	GPDWD 263
153	GPDWD 165	198	GPDWD 217	243	GPDWD 264
154	GPDWD 167	199	GPDWD 218	244	GPDWD 265
155	GPDWD 168	200	GPDWD 219	245	GPDWD 266
156	GPDWD 170	201	GPDWD 220	246	GPDWD 267
157	GPDWD 172	202	GPDWD 221	247	GPDWD 268
158	GPDWD 173	203	GPDWD 222	248	GPDWD 269
159	GPDWD 174	204	GPDWD 223	249	GPDWD 270
160	GPDWD 175	205	GPDWD 224	250	GPDWD 271
161	GPDWD 176	206	GPDWD 225	251	GPDWD 272
162	GPDWD 177	207	GPDWD 226	252	GPDWD 273
163	GPDWD 180	208	GPDWD 228	253	GPDWD 274
164	GPDWD 181	209	GPDWD 229	254	GPDWD 275
165	GPDWD 182	210	GPDWD 230	255	GPDWD 276
166	GPDWD 183	211	GPDWD 232	256	GPDWD 277
167	GPDWD 184	212	GPDWD 233	257	GPDWD 278
168	GPDWD 185	213	GPDWD 234	258	GPDWD 279
169	GPDWD 186	214	GPDWD 235	259	GPDWD 280
170	GPDWD 187	215	GPDWD 236	260	GPDWD 281
171	GPDWD 188	216	GPDWD 237	261	GPDWD 282
172	GPDWD 189	217	GPDWD 238	262	GPDWD 283
173	GPDWD 190	218	GPDWD 239	263	GPDWD 284
174	GPDWD 191	219	GPDWD 240	264	GPDWD 285
175	GPDWD 192	220	GPDWD 241	265	GPDWD 286
176	GPDWD 193	221	GPDWD 242	266	GPDWD 287
177	GPDWD 194	222	GPDWD 243	267	GPDWD 288
178	GPDWD 195	223	GPDWD 244	268	GPDWD 289
179	GPDWD 196	224	GPDWD 245	269	GPDWD 290
180	GPDWD 197	225	GPDWD 246	270	GPDWD 291

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Germplasm number	Germplasm Accession No.	Germplasm number	Germplasm Accession No.	Germplasm number	Germplasm Accession No.
271	GPDWD 292	316	GPDWD 337	361	GPDWD 383
272	GPDWD 293	317	GPDWD 338	362	GPDWD 384
273	GPDWD 294	318	GPDWD 339	363	GPDWD 385
274	GPDWD 295	319	GPDWD 340	364	GPDWD 386
275	GPDWD 296	320	GPDWD 341	365	GPDWD 387
276	GPDWD 297	321	GPDWD 342	366	GPDWD 388
277	GPDWD 298	322	GPDWD 343	367	GPDWD 389
278	GPDWD 299	323	GPDWD 344	368	GPDWD 390
279	GPDWD 300	324	GPDWD 345	369	GPDWD 391
280	GPDWD 301	325	GPDWD 346	370	GPDWD 392
281	GPDWD 302	326	GPDWD 347	371	GPDWD 393
282	GPDWD 303	327	GPDWD 348	372	GPDWD 394
283	GPDWD 304	328	GPDWD 349	373	GPDWD 395
284	GPDWD 305	329	GPDWD 350	374	GPDWD 396
285	GPDWD 306	330	GPDWD 351	375	GPDWD 397
286	GPDWD 307	331	GPDWD 352	376	GPDWD 399
287	GPDWD 308	332	GPDWD 353	377	GPDWD 400
288	GPDWD 309	333	GPDWD 354	378	GPDWD 401
289	GPDWD 310	334	GPDWD 355	379	GPDWD 402
290	GPDWD 311	335	GPDWD 356	380	GPDWD 403
291	GPDWD 312	336	GPDWD 357	381	GPDWD 404
292	GPDWD 313	337	GPDWD 358	382	GPDWD 405
293	GPDWD 314	338	GPDWD 359	383	GPDWD 406
294	GPDWD 315	339	GPDWD 360	384	GPDWD 407
295	GPDWD 316	340	GPDWD 361	385	GPDWD 408
296	GPDWD 317	341	GPDWD 362	386	GPDWD 409
297	GPDWD 318	342	GPDWD 363	387	GPDWD 410
298	GPDWD 319	343	GPDWD 364	388	GPDWD 411
299	GPDWD 320	344	GPDWD 365	389	GPDWD 412
300	GPDWD 321	345	GPDWD 366	390	GPDWD 413
301	GPDWD 322	346	GPDWD 367	391	GPDWD 414
302	GPDWD 323	347	GPDWD 368	392	GPDWD 415
303	GPDWD 324	348	GPDWD 369	393	GPDWD 416
304	GPDWD 325	349	GPDWD 370	394	GPDWD 417
305	GPDWD 326	350	GPDWD 371	395	GPDWD 418
306	GPDWD 327	351	GPDWD 373	396	GPDWD 419
307	GPDWD 328	352	GPDWD 374	397	GPDWD 420
308	GPDWD 329	353	GPDWD 375	398	GPDWD 421
309	GPDWD 330	354	GPDWD 376	399	GPDWD 422
310	GPDWD 331	355	GPDWD 377	400	GPDWD 423
311	GPDWD 332	356	GPDWD 378	401	GPDWD 424
312	GPDWD 333	357	GPDWD 379	402	GPDWD 425
313	GPDWD 334	358	GPDWD 380	403	GPDWD 426
314	GPDWD 335	359	GPDWD 381	404	GPDWD 427
315	GPDWD 336	360	GPDWD 382	405	GPDWD 428

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Germplasm number	Germplasm Accession No.	Germplasm number	Germplasm Accession No.	Germplasm number	Germplasm Accession No.
406	GPDWD 429	451	GPDWD 475	496	GPDWD 520
407	GPDWD 430	452	GPDWD 476	497	GPDWD 521
408	GPDWD 431	453	GPDWD 477	498	GPDWD 522
409	GPDWD 432	454	GPDWD 478	499	GPDWD 523
410	GPDWD 433	455	GPDWD 479	500	GPDWD 524
411	GPDWD 434	456	GPDWD 480	501	GPDWD 525
412	GPDWD 435	457	GPDWD 481	502	GPDWD 526
413	GPDWD 436	458	GPDWD 482	503	GPDWD 527
414	GPDWD 437	459	GPDWD 483	504	GPDWD 528
415	GPDWD 438	460	GPDWD 484	505	GPDWD 529
416	GPDWD 439	461	GPDWD 485	506	GPDWD 530
417	GPDWD 440	462	GPDWD 486	507	GPDWD 531
418	GPDWD 441	463	GPDWD 487	508	GPDWD 532
419	GPDWD 442	464	GPDWD 488	509	GPDWD 533
420	GPDWD 443	465	GPDWD 489	510	GPDWD 534
421	GPDWD 444	466	GPDWD 490	511	GPDWD 535
422	GPDWD 445	467	GPDWD 491	512	GPDWD 536
423	GPDWD 446	468	GPDWD 492	513	GPDWD 537
424	GPDWD 447	469	GPDWD 493	514	GPDWD 538
425	GPDWD 448	470	GPDWD 494	515	GPDWD 539
426	GPDWD 449	471	GPDWD 495	516	GPDWD 540
427	GPDWD 450	472	GPDWD 496	517	GPDWD 541
428	GPDWD 451	473	GPDWD 497	518	GPDWD 542
429	GPDWD 452	474	GPDWD 498	519	GPDWD 543
430	GPDWD 453	475	GPDWD 499	520	GPDWD 544
431	GPDWD 454	476	GPDWD 500	521	GPDWD 545
432	GPDWD 455	477	GPDWD 501	522	GPDWD 546
433	GPDWD 456	478	GPDWD 502	523	GPDWD 547
434	GPDWD 457	479	GPDWD 503	524	GPDWD 548
435	GPDWD 458	480	GPDWD 504	525	GPDWD 549
436	GPDWD 459	481	GPDWD 505	526	GPDWD 550
437	GPDWD 460	482	GPDWD 506	527	GPDWD 551
438	GPDWD 461	483	GPDWD 507	528	GPDWD 552
439	GPDWD 462	484	GPDWD 508	529	GPDWD 553
440	GPDWD 463	485	GPDWD 509	530	GPDWD 554
441	GPDWD 464	486	GPDWD 510	531	GPDWD 555
442	GPDWD 466	487	GPDWD 511	532	GPDWD 556
443	GPDWD 467	488	GPDWD 512	533	GPDWD 557
444	GPDWD 468	489	GPDWD 513	534	GPDWD 558
445	GPDWD 469	490	GPDWD 514	535	GPDWD 559
446	GPDWD 470	491	GPDWD 515	536	GPDWD 560
447	GPDWD 471	492	GPDWD 516	537	GPDWD 561
448	GPDWD 472	493	GPDWD 517	538	GPDWD 562
449	GPDWD 473	494	GPDWD 518	539	GPDWD 563
450	GPDWD 474	495	GPDWD 519	540	GPDWD 564

Contd.....

Germplasm number	Germplasm Accession No.	Germplasm number	Germplasm Accession No.	Germplasm number	Germplasm Accession No.
541	GPDWD 565	561	GPDWD 585	581	GPDWD 605
542	GPDWD 566	562	GPDWD 586	582	GPDWD 606
543	GPDWD 567	563	GPDWD 587	583	GPDWD 607
544	GPDWD 568	564	GPDWD 588	584	GPDWD 608
545	GPDWD 569	565	GPDWD 589	585	GPDWD 609
546	GPDWD 570	566	GPDWD 590	586	GPDWD 610
547	GPDWD 571	567	GPDWD 591	587	GPDWD 611
548	GPDWD 572	568	GPDWD 592	588	GPDWD 612
549	GPDWD 573	569	GPDWD 593	589	GPDWD 613
550	GPDWD 574	570	GPDWD 594	590	GPDWD 614
551	GPDWD 575	571	GPDWD 595	591	GPDWD 615
552	GPDWD 576	572	GPDWD 596	592	GPDWD 616
553	GPDWD 577	573	GPDWD 597	593	GPDWD 617
554	GPDWD 578	574	GPDWD 598	594	GPDWD 618
555	GPDWD 579	575	GPDWD 599	595	GPDWD 619
556	GPDWD 580	576	GPDWD 600	596	GPDWD 620
557	GPDWD 581	577	GPDWD 601	597	GPDWD 621
558	GPDWD 582	578	GPDWD 602	598	GPDWD 622
559	GPDWD 583	579	GPDWD 603	599	GPDWD 623
560	GPDWD 584	580	GPDWD 604	600	GPDWD 624

Appendix II. Soil moisture status of the experimental plot in rain house shelter at different days

Date of sampling	Soil moisture %		
	Control	Medium moisture stress	Severe moisture stress
31-07-2012	36.2	35.6	35.5
15/08/2012	34.1	29.5	29.2
01/09/2012	32.3	26.5	22.3
15/09/2012	30.4	24.8	20.4
01/10/2012	30.2	22.2	17.5
15/10/2012	30.1	22.9	13.6
01/11/2012	29.8	23.4	19.1
15/11/2012	29.8	23.6	18.5
01/12/2012	29.7	22.8	13.2
15/12/2012	29.5	20.3	12.1
Mean	31.2	25.2	20.1

IDENTIFYING DROUGHT TOLERANT COTTON (*Gossypium hirsutum* L.) GENOTYPES BY PHYSIOLOGICAL AND MOLECULAR APPROACHES

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2013

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Major Advisor

Abstract

A field experiment was conducted during 2011-12 for the evaluation drought tolerance using thirty *Gossypium, hirsutum* L. genotypes in RBD design at ARS Dharwad and ARS Annigeri. Ten best (CPD-750, Sahana, ARB-9701, CNH-120MB, GIHV-218, BS-279, RAH-101, GJHV-477, F-2228 and KH-155) and two least (L-761 and LH-2076) performed genotypes were selected from these experiments based on drought tolerant physiological traits viz. SLW, water potential, SPAD values, gas exchange parameters and yield.

Simultaneously 600 cotton germplasms lines were also evaluated for drought tolerance by physiological traits at ARS Dharwad. Based on the SPAD, SLW and gas exchange parameters 24 germplasm lines were showed significantly on par for the most of the physiological traits.

During 2012-13, the selected twelve genotypes were evaluated for performance under different concentrations of PEG-6000 osmotic solutions at germination stage by slanting glass plate technique. The germination %, shoot length, seedling vigour index and shoot vigour index decreased as the PEG 6000 concentration increase from 0% to 27% in all genotypes, while the root length and root: shoot ratio increased. These genotypes were further evaluated at rain out shelter for drought tolerance by morphological, physiological, biophysical, biochemical, root architecture (length, volume and lateral roots) yield, yield components and fibre properties. The genotypes viz. CPD-750, Sahana, ARB-9701, CNH-120MB, GIHV-218, and BS-279 were found relatively drought tolerant. Further these twelve genotypes were studied for genetic diversity study using 79 cotton specific RAPD molecular markers. There was 79.56 per cent genetic polymorphism/diversity. The primers OPI 4 and OLIGO 652 amplified 800 bp and 400 bp respectively were specific to relatively drought tolerant genotypes. The dendrogram revealed that the primers were able to group the genotypes in to three major clusters. From the overall present investigation, the genotypes viz. CPD-750, Sahana, ARB-9701, CNH-120MB, GIHV-218, BS-279 and RAH-101 were identified as drought tolerant lines.