EVALUATION OF CHLOROPHYLL FLUORESCENCE AS A TOOL FOR THE IDENTIFICATION OF DROUGHT TOLERANCE IN UPLAND COTTON

A Dissertation

by

POLLY SUZANNE LONGENBERGER

Submitted to the Office of Graduate Studies of
Texas A&M University
in partial fulfillment of the requirements for the degree of

DOCTOR OF PHILOSOPHY

May 2008

Major Subject: Plant Breeding

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Approved by:

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ABSTRACT

Evaluation of Chlorophyll Fluorescence as a Tool for the

Identification of Drought Tolerance in Upland Cotton. (May 2008)

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A novel bioassay for the evaluation of plant water status was developed by Burke (2007). The research reported herein was designed to evaluate this new protocol as a tool for use in cotton breeding programs for the identification of drought tolerant genotypes. Twenty genotypes were selected to represent diverse germplasm pools for a two-year field evaluation. Replicated tests were performed in Lubbock, TX and College Station, TX in 2005, 2006, and 2007. Dryland and irrigated treatments were administered in a split plot arrangement of a randomized complete block design. Fluorescence measurements were taken at mid-bloom and late bloom growth stages of growth. Source leaf tissue was harvested at predawn and subjected to high temperature incubation with fluorescence measurements subsequently taken hourly for five hours. Drought stressed plants had not mobilized their carbohydrate reserves from their source leaves overnight and thus maintained cell viability and therefore higher chlorophyll fluorescence values throughout the incubation with the opposite being true for non-stressed plants. Fiber lint yield and fiber properties were measured at the conclusion of the 2005 season in College Station and the 2006 season in College Station and Lubbock

for comparison with the fluorescence data. Five genotypes, 'Acala 1517-99', 'Deltapine 491' (PVP no. 200100159), 'Tamcot CAMD-E', 'Tamcot 22' and TAM 89E-51, an unreleased breeding line, were selected based on field evaluation results in a preliminary study in 2005 to be included in a diallel analysis to determine the heritability of fluorescence measurements. Genotype x treatment effects complicated the classification of genotypic responses to drought. Few and inconsistent correlations were found among fluorescence values and lint yield or fiber properties. The diallel analysis did not identify general combining ability or specific combining ability effects for chlorophyll fluorescence measurements. Thus this procedure provides little potential in selecting plants for drought tolerance when plants are grown under field culture. Selection among Tamcot 22 and TAM 89E-51 plants for high and low genotypes according to fluorescence values did not yield progeny different from unselected Tamcot 22 and TAM 89E-51.

To Carl

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NOMENCLATURE

ANOVA	Analysis of Variance
ARS	Agricultural Research Service
CPCSD	California Planting Cotton Seed Distributors
CS	College Station, TX
CSIRO	Commonwealth Scientific and Industrial Research Organization
CSRL	Cropping Systems Research Laboratory
DP	Delta & Pine Land
DS	Drought susceptible
DT	Drought tolerant
ELO	Elongation
FM	FiberMax
F_0	Minimal chlorophyll fluorescence; fluorescence intensity when all photosystem II (PS II) reaction centers are open and the photosynthetic membrane is non-energized (dark adapted) (Kooten and Snel, 1990)
F_i	transient inflection fluorescence level after exposure of dark-adapted leaf to actinic light (Baker and Rosenqvist, 2004)
F_m	Dark adapted maximal chlorophyll fluorescence; fluorescence intensity under exposure to a saturating light pulse with all PS II reaction centers closed and all non-photochemical quenching processes are minimized
F_m'	Light adapted maximal chlorophyll fluorescence; fluorescence intensity under exposure to saturation flash under steady state conditions with all PS II reaction centers closed
F_0'	Fluorescence under steady state conditions with all PS II reaction centers open

F_v	Maximum variable chlorophyll fluorescence when all non-photochemical processes are minimized; F_m-F_0
F_v'	Maximum variable chlorophyll fluorescence in light adapted conditions; F_m'-F_0'
F_v/F_m	Ratio of dark adapted variable fluorescence to dark adapted maximal fluorescence; potential yield of the photochemical reaction in photosystem II; $(F_m-F_0)/F_m$
F_v'/F_m'	Ratio of light adapted variable fluorescence to light adapted maximal fluorescence; yield of quantum efficiency; $(F_m'-F_0')/F_m'$
GCA	General combining ability
HVI	High volume instrument
LUB	Lubbock, TX
MIC	Micronaire
SCA	Specific combining ability
SFC	Short fiber content
STR	Strength
Stv	Stoneville
TAES	Texas Agricultural Experiment Station
TAM-MAR	Texas A&M Multi-Adversity Resistance
UHM	Upper-half mean length
UI	Uniformity index
USDA	United States Department of Agriculture

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INTRODUCTION

Plant breeders collaborate with plant physiologists to develop germplasm tolerant to abiotic stresses. However, germplasm evaluation is hindered by the difficulty to create screening methods which are both accurate and rapid. Plant breeders require the ability to evaluate large segregating populations for stress tolerance. To date, a quick and easy screen for drought tolerance in cotton that consistently ranks genotypes is yet to be developed.

Drought tolerance has come to the forefront of agronomic research in recent years due to dwindling irrigation reserves and increased costs associated with irrigation application (Gowda et al., 2007). Some level of water deficit stress is experienced by many crop plants grown without supplemental irrigation during most seasons even when meteorological drought conditions are not present. Therefore, all producers could benefit from the presence of drought tolerance in the genotypes they chose to cultivate.

Various tools have been used by physiologists to evaluate the water status of crop plants. Photosynthetic rate, relative water content, water use efficiency, root structure, detached leaf water loss, leaf water potential, stomatal characteristics, and osmotic adjustment have been explored for connections to drought tolerance. Unfortunately, many evaluations performed by physiologists are time consuming and in some cases destructive. There is a need for a protocol to determine the drought tolerance of cotton germplasm.

In this study, a novel chlorophyll fluorescence bioassay was evaluated for its

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This dissertation follows the style and format of Crop Science.

utility in cotton breeding programs. Twenty genotypes from diverse germplasm pools were characterized via chlorophyll fluorescence for their level of drought tolerance when grown under field culture. The heritability of the chlorophyll fluorescence measurements was estimated in a diallel analysis using five genotypes selected from the original 20 genotypes included in the field evaluation. A progeny test was also executed after selections were made in two genotypes based on fluorescence measurements to elucidate the stability and breeding behavior of this trait.

Research Objectives

The objectives of this study were to [1] determine the feasibility of chlorophyll fluorescence as a tool for drought tolerance evaluation in cotton breeding programs, [2] use chlorophyll fluorescence to classify cotton from diverse germplasm pools according to their level of drought tolerance, and [3] to evaluate the heritability of chlorophyll fluorescence measurements.

LITERATURE CITED

Water deficits occur during each growing season. To maintain water reserves and lower costs for producers, plant breeders strive to develop genotypes that maintain yield and quality under drought conditions. Plant breeders collaborate with plant physiologists to develop assays that can be used to screen germplasm for stress tolerance.

Plant physiologists have suggested chlorophyll fluorescence as a means for understanding photosynthetic metabolism and thus identify plants, or at least genotypes, that vary in tolerance to moisture deficit. According to Maxwell and Johnson (2000), fluorescence analysis has become a powerful and widely used technique among plant physiologists and ecophysiologists. The value of fluorescence measurement lies in its relationship to photosynthesis since light absorbed by plants that does not drive the production of carbohydrates is dissipated as heat or re-emitted as light in the form of fluorescence. Physiologists and plant breeders now seek to relate fluorescence measurements and genotype specific responses to stress.

Excised barley leaves were incubated with the cut end submersed in water or a 100 Mm NaCl solution and subjected to dark or high light and monitored via chlorophyll fluorescence (Belkhodja et al., 1994). Differences in chlorophyll fluorescence were only observed under the high light treatment. Differences were larger for the salt-sensitive cultivar than the salt-tolerant cultivar, leading the authors to believe that the test could serve as a salt screen among barley genotypes.

Three barley genotypes were evaluated under control and saline conditions in the field (Belkhodja et al., 1999). One genotype was documented as salt tolerant and the other two as salt susceptible. However, attached flag leaf measurements of F_v/F_m did not differ according to salinity treatment or among genotypes. Measurements taken early morning and at midday showed similar results with respect to treatments and genotypes, but overall midday measurements were lower than early morning readings. In contrast, excised leaf samples measured 30 min after excision in a laboratory showed differences in fluorescence according to salt treatments. $(F_i-F_0)/F_v$ ratios were higher for all genotypes under salt stress compared with the non saline controls.

The presence of solute glycinebetaine has been shown to confer salt tolerance in maize (Yang et al., 1996). Glycinbetaine-deficient (bet1/bet1) and glycinbetaine-containing (Bet1/Bet1) homologous, near-isogenic lines were evaluated under high temperature stress to determine the effects of glycinebetaine on membrane stability and photochemical activity of photosystem II. Electrolyte leakage indicated that Bet1/Bet1 lines had higher membrane stability at elevated temperatures and chlorophyll fluorescence showed that Bet1/Bet1 lines had a greater thermostability of photosystem II function.

The photochemical efficiency of photosystem II (F_v/F_m) was measured to evaluate the effects of salinity on two drought tolerant sorghum cultivars (Netondo et al., 2004). The F_v/F_m value decreased with increased salinity for both cultivars. The authors compared their findings with those of other investigators and concluded that the response of photosystem II varied across genotypes and suggested that chlorophyll

fluorescence was a good indicator of salt stress when NaCl concentrations exceeded 150 mM.

Misra et al. (2001) used fast chlorophyll *a* fluorescence kinetics to monitor response to various salt/ion treatments of mung bean and Brassica. They concluded that fluorescence kinetics were affected by salt/ion treatments and therefore can be used to monitor the treatment effect on plants. The authors differentiated between susceptible and tolerant genotypes using the chlorophyll *a* technique. Chlorophyll *a* variable fluorescence yield was unaffected by salt treatment in grapevine, bean, barley, spinach, citrus, and mangrove until excessive ion accumulation caused lose of turgor pressure and a subsequent decline in fluorescence (Downton and Millhouse, 1985).

Bajji et al. (2004) used F_v/F_m along with other physiological parameters to track improvements in drought tolerance due to selection of calluses after salt and PEG treatments. F_v/F_m was measured on hydrated excised leaves (control) or non-hydrated leaves (stressed) for 10 h under greenhouse conditions. Change in F_v/F_m was found to be reduced among progeny from selected plants.

Non-photochemical quenching of chlorophyll fluorescence (qN) increased in water stressed durum wheat compared to control plants in a greenhouse experiment (Tambussi et al., 2002). F_v'/F_m' decreased in water stressed plants while F_v/F_m remained unchanged among the stressed and control treatments. Massacci and Jones (1990) found similar results in apple. qN increased in water stressed apple trees while F_v/F_m remained unchanged among stressed and well-watered controls.

Six normal leaf and two okra leaf cotton genotypes were tested under dryland and irrigated conditions by Pettigrew (2004b). No differences were found among genotypes or between treatments for F_v/F_m. The okra leaf genotypes did have 14% greater F_v'/F_m' across treatments when compared to the normal leaf cottons. Higher photosynthetic rates per unit leaf area have been observed in okra leaf genotypes (Pettigrew, 2004a).

In addition to drought and salt stress, cold tolerance and chilling stress have been assessed using chlorophyll fluorescence techniques. Two corn genotypes characterized for chilling tolerance according to electrolyte leakage from leaf discs at 5ºC were evaluated under 5ºC conditions with warm breaks of 14ºC for 1 h and 4 h (Kościelniak and Biesaga-Kościelniak, 1999). Warm breaks allowed for improved water uptake and maintenance of photosynthesis as compared to the 5ºC control that did not receive warm breaks. F_v/F_m values were maintained in both genotypes subjected to the 1 h and 4 h warm breaks. F_v/F_m values declined in the 5ºC control treatment. Andrews et al. (1995) were able to track the effects of cold temperatures and high light intensities on corn during the early part of the growing season. F_v/F_m was reduced as temperatures dropped and light intensity increased.

Excised rice leaves of 16 genotypes were chilled at 10ºC for 48 h (Sthapit et al., 1995). F_v/F_m was measured after the chilling period and was found to correlate with the altitudinal adaptation with an R^2 of 0.76.

Fluorescence measurements are not always useful for the characterization of stress tolerance among genotypes. F_v/F_m was found to remain unchanged in two

sunflower hybrids subjected to long-term drought stress under field conditions (Panković et al., 1999). CO_2 assimilation and stomatal conductance decreased with drought stress. The two genotypes had been characterized as drought tolerant (DT) and drought susceptible (DS) based on yield under water-limited conditions. The tolerant genotype was found to have higher levels of Rubisco, which the authors claim may be a factor conferring the ability to better acclimate to drought situations.

Water stress was imposed via exposure of two wheat cultivars to PEG at two levels and three durations to simulate mild (15% PEG for 6 h) and severe (25% PEG for 6 h and 15% PEG for 24 h) stress (Kicheva et al., 1994). The cultivars were classified as DT and DS based on field phenological observations made during drought conditions and grain yield. F_v/F_m ratios did not differ due to PEG treatment and did not detect genotypic differences.

Triticale and *Triticum dicoccum,* Farrum showed no changes in F_v/F_m when subjected to salt stress compared with control plants (Morant-Manceau et al., 2004). Rye showed a slight decrease in F_v/F_m at 110 mmol/L NaCl at 0.743 compared to a control value of 0.768.

Pettigrew and Meredith (1994) evaluated six normal leaf cotton genotypes under irrigated conditions by taking F_v/F_m measurements. No differences were detected, as all genotypes had values at or near 0.880. The authors did find differences in CO_2 exchange rate (CER) among the six genotypes.

The following examples illustrate the suitability of chlorophyll fluorescence evaluation as a screening tool. It allows for the discrimination between genotypes and is

sensitive enough to detect differences before symptoms are visible. Chlorophyll fluorescence results for salt tolerant and salt sensitive rice seedlings paralleled those of leaf Na^+/K^+ content, net photosynthesis, and stomatal conductance (Dionisio-Sese and Tobita, 2000). Steady-state fluorescence ratio ($\Delta F/F_m$) declined among the three salt sensitive genotypes tested but was maintained by the salt tolerant genotypes. Smillie and Nott (1982) utilized chlorophyll fluorescence to monitor response to salinity in sugar beet (salt tolerant), sunflower (moderately salt tolerant), and bean (salt intolerant). They reported that even in the absence of visual symptoms chlorophyll fluorescence provided a rapid method for the detection of salt stress in leaves.

Fluorescence parameters have been both effective and ineffective in rose studies. Jimenez et al. (1997) evaluated the F_v/F_m ratio as an indicator of salt stress in roses. Morphology, nutrient, and chlorophyll content changes occurred in response to salt stress but the F_v/F_m ratio did not change. The authors found that when plants were exposed to high irradiance, in addition to salt stress, both control and stress plant F_v/F_m values decreased but the stress plants had consistently lower values. They concluded that chlorophyll fluorescence did not serve as a useful tool to detect salt stress in roses without an additional stress factor.

In another study, physiologists evaluated chlorophyll fluorescence as a screening tool for chilling tolerance in rose (Hakam et al., 2000). They found that variable fluorescence (F_v) decreased in susceptible genotypes as temperature decreased, while less susceptible genotypes maintained a more stable F_v that decreased at a slower rate as temperature decreased. The authors concluded that chlorophyll fluorescence could be

used to assess chilling tolerance in rose genotypes. Greaves and Wilson (1987) came to the same conclusion when they explored the possibility of using chlorophyll fluorescence as a screening tool for frost sensitivity among wild and cultivated potato species. Their results correlated well with visual assessment of frost injury and the authors concluded that chlorophyll fluorescence should be considered by breeders as a tool for ranking potato genotypes according to their susceptibility to low temperature injury.

F_v was used by Binder and Fielder (1996) to identify freezing-induced changes to the photosynthetic apparatus prior to signs of needle damage in white spruce seedlings, suggesting that F_v could be used in screening experiments to find freeze tolerant genotypes among white spruce and other conifer species. Fisker et al. (1995) also tried to find a link between chlorophyll fluorescence and the frost hardiness of tree seedlings. Needle freeze damage and seedling survival had a significant linear relationship with chlorophyll fluorescence but there was no relationship between fluorescence of control seedlings and frost hardiness in Douglas fir.

F_v/F_m was used as an early indicator of photosynthetic damage caused by chilling stress in rice (Kuk et al., 2003). The authors differentiated between cold-acclimated and non-acclimated plants via chlorophyll fluorescence. Non-acclimated plants exhibited reductions in F_v/F_m while acclimated plants maintained their F_v/F_m ratio throughout chilling and recovery periods.

Chlorophyll fluorescence was measured on control and drought stressed oak trees to determine the effect of drought on the photochemical efficiency of photosystem II

(Epron et al., 1992). Control trees maintained a fairly constant ratio of variable to maximal fluorescence (F_v/F_m) throughout the day while stressed trees showed a diurnal decline in F_v/F_m. The decrease was fully recovered by the end of the afternoon. The authors believe that this temporary reduction in the efficiency of photosystem II prevented the photosynthetic apparatus from permanent damage.

Colom and Vazzana (2003) used chlorophyll fluorescence to clarify the ability of weeping lovegrass to grow and produce under drought stress. Two cultivars, one noted as being DT and the other DS, were subjected to water stress and allowed to recover. F_v/F_m decreased among both cultivars during drought stress, but in the susceptible cultivar the reduction was much greater. After irrigation was applied, both cultivars recovered within the same amount of time.

Chlorophyll fluorescence has been used by researchers interested in screening potato germplasm for drought tolerance. It was used to evaluate a potato cultivar and five breeding clones for drought tolerance (Ranalli et al., 1997). The genotypes varied in their fluorescence response to drought stress, and the authors found a highly significant correlation between fluorescence emission and tuber yield. Two genotypes selected from a group of 16 sweet potato genotypes after screening with a detached leaf water loss protocol were assessed using chlorophyll fluorescence (Newell, 1994). One of the two genotypes, previously designated as tolerant, exhibited lower leaf water loss and maintained higher variable fluorescence when compared to the other genotype. The authors concluded that chlorophyll fluorescence parameters could be used to separate genotypes according to their tolerance to water deficit.

Chlorophyll fluorescence was found to be significantly and negatively correlated with a drought susceptibility index that was calculated based on yield from irrigated and dryland treatments with wheat (Ali Dib, 1994). The authors reported that fluorescence explained 62.4% of the drought susceptibility index of grain yield, thus supporting its use as a rapid tool for the identification of drought tolerant genotypes. Havaux and Lannoye (1985) studied fluorescence responses of DT and DS hard wheat cultivars when leaf disks were subjected to rapid desiccation. Tolerant cultivars showed only minor changes in chlorophyll fluorescence while it decreased in susceptible cultivars. The authors supported for the use of chlorophyll fluorescence as a screening tool in plant stress research.

Two DT and two DS corn hybrids were evaluated under drought stressed and well watered conditions in the field with chlorophyll fluorescence (O'Neill et al., 2006). Both F_v/F_m and electron transport rate (ETR) were measured on three sampling dates between 1100 and 1300 h. On the second sampling date drought stress was most pronounced and allowed for differentiation of genotypes. Under drought stress, both F_v/F_m and ETR were lower among the two DS lines compared with the DT lines. Under well watered conditions, the four lines could not be distinguished with F_v/F_m or ETR. The authors conclude that under water limited conditions chlorophyll fluorescence measurements can be used to classify corn hybrids according to their level of drought tolerance.

This abundance of literature concerning the use of chlorophyll fluorescence in stress physiology is promising, but attention of fluorescence research must be turned to

focus on procedures that can be used to evaluate large amounts of plant material accurately and in a short time period. If such protocols can be developed with this physiological tool, then the measurement of chlorophyll fluorescence has the potential to become an important methodology for the evaluation of drought tolerance among cotton genotypes.

Burke (2007) developed a novel bioassay for the identification of drought stress in cotton that utilizes chlorophyll fluorescence to monitor cell viability under high temperature dark incubation. Differences between well watered and drought stressed plants can be established since, under stress, plants will not mobilize carbohydrate reserves overnight and will therefore maintain higher fluorescence values during high temperature dark incubation, with the opposite being true for well watered plants. Normal metabolic processes have been shown to be disrupted by drought leading to a reduction in the translocation of photosynthate from leaves to other plant tissues (Wilson et al., 1987).

Carbohydrate metabolism during water stress was monitored in lupin, sunflower, eucalyptus, and grapevine (Quick et al., 1992). A depletion of starch due to water stress was found in all four species. This reflected the two- to seven-fold inhibition of photosynthesis. Sucrose levels remained high during water stress in lupin and grapevine and increased in eucalyptus and sunflower compared to well-watered controls. Photosynthate export was decreased by 10-80% during the day. Though the leaves had similar or higher levels of soluble sugars as compared with control plants there was effectively no export during the night. The authors speculated that accumulation is due

to compartmentalization of the sugar away from the site of loading as opposed to inhibition of phloem transport since new photosynthate was readily exported during morning hours.

Although sucrose and starch levels in dryland and irrigated tissue samples support the hypothesis behind the procedure, Burke (2007) notes that other factors contribute to the overall viability of plant tissues. These factors may include membrane composition, organic acid content, osmolyte accumulation, and stress protection protein synthesis.

Unlike the papers mentioned earlier in this review, for Burke's protocol, chlorophyll fluorescence is not being used to monitor water stress responses on photosynthetic capacity but to monitor cell viability as it relates to carbohydrate concentration in source leaves. Timpa et al., (1986) found that four photoperiodic cottons could be characterized according to drought tolerance through organic acid and carbohydrate analysis. The four genotypes had been selected due to their response to water deficit. Two readily wilted, while the other two remain turgid during water deficit. Accumulation of carbohydrates under drought stress correlated with the visual observations. The wilt prone genotypes accumulated more carbohydrates in their leaf tissue that the turgid genotypes.

Carbohydrate utilization by cotton plants under drought conditions is depressed to a greater extent than photosynthesis (Eaton and Ergle, 1948). This should allow Burke's protocol to detect irrigation treatments more readily than those protocols using chlorophyll fluorescence to monitor photosynthesis changes due to water deficit.

In addition to Eaton and Ergle's (1948) findings, there is further support for the theory that translocation is more sensitive than photosynthesis to water deficit stress. Carbon-14 was fed to leaves of control and water stressed corn plants (Brevedan and Hodges, 1978). The fed and non-fed portions of the leaf on stressed plants retained more radioactive carbon than their non-stressed counterparts. Comparing Carbon-14 uptake and its retention in the leaf and other plant parts, the authors concluded that translocation appeared to be more sensitive to water stress than photosynthesis. Similarly, Hartt (1967) found that water stressed sugarcane had an 18% reduction in total carbon fixation and a 93% reduction in translocation.

Photosynthesis and translocation of labeled assimilates were monitored in wheat subjected to water stress 15-20 days post anthesis (Wardlaw, 1967). Grain fill continued during the stress treatment indicating that assimilate distribution in the plant was altered to compensate for assimilate deficiencies in the leaf caused by reduced photosynthesis. A larger proportion of labeled assimilates were found in the wilted leaves of the stressed plants. Wardlaw concluded that flag leaf photosynthesis reduction was due to direct effects on the leaf itself and not a failure to utilize assimilate or to move assimilate through conducting tissues. There was a delay and reduction in the transfer of sugars from assimilating tissue to conducting tissue but translocation within conducting vessels was not inhibited by water stress.

Darnel ryegrass (*Lolium temulentum* L.) was exposed to water stress during leaf development (Wardlaw, 1969). Leaf photosynthesis was affected only after reductions in leaf elongation were evident. A reduction in assimilate loss from leaves occurred

during stress. Slower growth resulted in reduced velocity of ^{14}C-assimilate in stressed plants. Wardlaw concluded that a balance between sugar retention by the chloroplast and sugar transfer into conducting tissue determines a plant's response to water stress.

Ackerson and Hebert (1981) subjected cotton plants to five drought cycles to develop adapted plants and compared their reaction with non-adapted control plants to five additional cycles of stress. The authors found that photosynthate export continued in drought adapted cotton plants as leaf water potentials declined. Conversely, translocation of assimilates decreased in non-adapted plants. Adapted and non-adapted plants accumulated sucrose in older leaves (node 5) as water stress occurred during the day (Akerson, 1981). Young leaves (node 8) of control plants also accumulated sucrose while young leaves of adapted plants saw declining levels of sucrose until about 20 h. The author suggested that accumulation of starch and glucose in adapted leaves at node 5 was associated with osmoregulation. Growth reduction and lowered "sink capacity" leads to the accumulation of solutes.

Unfortunately, a debate exists since research findings that water availability alters photosynthesis more readily than it alters carbohydrate translocation have been reported also. Sung and Krieg (1979) found that photosynthesis rates decline in sorghum and cotton prior to changes in translocation rates during water stress (-18 to -20 bars). Under intensified stress (-24 to -30 bars) reduction in the rate of translocation exceeded the decline in photosynthetic rate.

Starch, sucrose levels, and photosynthate export were lowered during water deficit in soybean (Huber et al., 1984). The authors found that photosynthesis was more

sensitive to water stress than photosynthate export. Photosynthesis was reduced in sweet sorghum while sucrose accumulation in the stem was maintained during drought stress (Massacci et al., 1996). Early sampling dates showed that stressed plants accumulated sugar in their stems earlier than control plants, but at the final sampling date there was no difference between treatments. Growth was only moderately affected by the drought treatment and it is believed that the water stress caused sugar to accumulate earlier in the stressed plants perhaps due to a shortening of the vegetative cycle and early senescence. The authors also found that F_v/F_m was lower in drought stressed plants.

Corn subjected to water deficit during grain fill showed cessation in apparent photosynthesis but continued photosynthate translocation (McPherson and Boyer, 1977). Despite the lack of photosynthesis, grain fill continued during the water deficit treatment due to the mobilization of stored photosynthate accumulated prior to stress induction. The authors believe that carbohydrates from the stem are mobilized in stressed corn when sink demand exceeds source capacity. It was noted that had the conditions prior to flowering been less optimal it would have been likely that grain fill would not have been maintained due to a lack of reserves.

Photosynthesis and translocation were measured in potato plants with tubers (old) and without (young) subjected to drought stress (Munns and Pearson, 1974). A 20% reduction in photosynthesis was found in older stressed plants and a 48% reduction in younger stressed plants when compared with their respective controls. The percentage loss of photosynthate was th same among stressed and control leaves. Percentage photosynthate loss from older plant leaves was double that of younger plants

regardless of the water treatment. Absolute translocation rate in stressed leaves of older plants was 80% of the controls and in younger plants it was 50% of the controls. There was a higher sugar:polysaccharide ratio in drought stressed plants. Wardlaw (1967) found a continual supply of photosynthate to the sink in wheat. There was a rapid cessation of leaf expansion and unfolding of new leaves in old plants under drought stress. The authors conclude that direct effects on photosynthesis and not vein loading or photosynthate transport within conducting tissue was responsible for the changes in photosynthate distribution in potato.

In a review of the literature, Lawlor and Cornic (2002) found that there is not a simple association between photosynthetic assimilation and carbohydrate content. When studying these aspects of plant physiology under stress, the observations are no doubt confounded by the type and degree of stress imposed and varying responses that may be species specific. Additionally, growth stage of the plant may affect photosynthesis and carbon translocation in water stressed plants.

Burke's procedure allowed for the detection of treatment differences within 24 h of the termination of irrigation and 200 to 300 samples can be evaluated per day (Burke, 2007). The author does cite concern for special variability issues when using the technique in the field. Samples taken 5 m apart on the same day differed but the sampling locations were consistent over two days of sampling. Burke noted the effect of leaf morphology when he compared four cotton genotypes. Three broad leaf cotton cultivars ('FM 989' (PVP no. 200500107), 'SG 215' (PVP no. 200100155), and 'DP 444' (200300134)) and one okra leaf cultivar ('FM 800' (PVP no. 200500110)) were

each measured under dryland and irrigated conditions. Burke's procedure differentiated the four genotypes and highlighted potential differences between broad leaf and okra leaf response to drought stress. FM 800 showed the highest level of stress in the irrigation treatment and the lowest level of stress in the dryland treatment.

MATERIALS AND METHODS

Fluorescence Bioassay

At predawn, a single paper punch was used to harvest leaf tissue samples from the fifth main stem leaf (source leaf). Leaf punches were placed in a 24-well plate half-filled with distilled water. Punches were transported to the lab and transferred to moistened filter paper lining a Pyrex dish and covered with Glad Clingwrap®. A speedball roller for Microseal® film was used to remove air bubbles and to ensure contact between the punches and the filter paper. An initial F_v'/F_m' (yield of quantum efficiency) measurement was taken with an OS1-FL modulated chlorophyll fluorometer (Opti-Sciences, Hudson, NH). The punches were incubated at 40°C in the dark and additional measurements were taken hourly for 5 hours. The procedure generates F_v'/F_m' decline curves. Preliminary experiments (data not shown) found that if differentiation between genotypes and/or treatments is to occur it will have done so by the hour 5 measurement. Therefore, the final F_v'/F_m' measurement will be used for data analysis.

Field Evaluation

Experimental Material

Twenty cotton genotypes were included in the field evaluation to be discussed in the next section. Eighteen of the 20 were upland genotypes (*Gossypium hirsutum* L.) with two additional species represented by 'Pima S-6' (*Gossypium barbadense*) and *Gossypium arboreum*. The upland genotypes were chosen to represent diverse germplasm pools of the U.S. and regions of adaptability (Table 1).

Table 1. Year of release, region of adaptation, and developer for cotton genotypes planted in 2005, 2006, and 2007.

Genotype	Year of release	Region of adaptation in USA	Developer
Acala 1517-99	1999	Western	New Mexico Agricultural Experiment Station
Acala Maxxa	1990	Western	CPCSD
All-Tex Atlas	1993	High Plains	All-Tex Seed Company
DP 14	1941	Delta	Delta & Pine Land Company
DP 491	2001	Delta	Delta & Pine Land Company
DP 50	1984	Delta	Delta & Pine Land Company
DP Acala 90	1981	Western	Delta & Pine Land Company
FM 832	1998	High Plains, Delta	CSIRO
Gossypium arboreum	NA†	NA	Accession of unknown origin acquired and maintain by Cotton Improvement Laboratory, TAES.
MD51ne	1991	Delta	USDA-ARS
Pima S-6	1984	Western	USDA-ARS
PM HS 26	1983	High Plains	Paymaster Technologies
PSC 355	2000	Mid South, Southeast	Phytogen Seed Company
Sure-Grow 747	1998	Mid South, Southeast	Sure-Grow Seed, Inc.
Stv 213	1962	Delta	Stoneville Pedigreed Seed Company
TAM 89E-51	NA	NA	Univ. of Arkansas Cotton Branch Experiment Station
TAM 94L-25	2003	Texas	Cotton Improvement Laboratory, TAES
TAM 96WD-69s	2005	Texas	Cotton Improvement Laboratory, TAES
Tamcot 22	2005	Texas	Cotton Improvement Laboratory, TAES
Tamcot CAMD-E	1977	Texas	TAM-MAR program, TAES

† NA denotes information not available.

Acala 1517-99 was released in 1999 by the New Mexico Agricultural Experiment Station (Cantrell et al., 2000). The line originated from a single plant selection from experimental B2541, which was derived from the B742/E1141 cross. Acala 9136/250 is the pedigree of B742 and Acala 9136 is noted to have considerable introgression from G. barbadense L. cv. Tanguis. Acala 1517-99 was selected for fiber quality, lint yield, and bacterial blight resistance under irrigated culture in New Mexico. Its area of adaptation is the western United States.

'Acala Maxxa' was released in 1990 by CPCSD. CPCSD considered Acala Maxxa a consistent and high-yielding cultivar for California. It has good early season vigor and rapid emergence along with easy defoliation and superior lint quality. Only 1 % of the cotton hectareage in the San Joaquin Valley was planted to Acala Maxxa in 1991. By 1995 the figure had jumped to 76 %. The cultivar was accepted widely due to its seedling vigor, early fruiting habit, verticillium wilt tolerance, and high yield (Smith et al., 1999). Acala Maxxa's area of adaptation is California.

A Plant Variety Protection certificate was issued to Buz Poage in 1994 for 'All-Tex Atlas,' (PVP no. 9200188). The cultivar was released by All-Tex Seed Company in 1993. All-Tex Atlas was adapted to the High Plains of Texas.

Four cultivars developed by Delta & Pine Land Company were included in this research. 'Deltapine 14,' 'Deltapine 50,' and 'Deltapine 491' are adapted to the Mississippi Delta region of the United States. 'Deltapine Acala 90' was developed for the Western U. S. acala market but is well adapted for many regions of the United States. Development of these cultivars under rainfed conditions of the Mississippi Delta versus

irrigated conditions of the Western United States may cause differences to exist among the cultivars for drought tolerance.

CSIRO was issued a Plant Variety Protection certificate in 2004 for 'FM 832' (PVP no. 9800258) and was released by FiberMax in 1998. FM 832 is an okra-leaf cultivar that was marketed by FiberMax in East Texas, Louisiana, and Southern Mississippi. It is said to be adapted to drought conditions in heavy soils.

Gossypium arboreum L. is one of two old world diploid cotton species, the other being *G. herbaceum* L. (Lee, 1984). The *G. arboreum* used in the experiments contained in this dissertation is an accession of unknown origin acquired and maintained by the Cotton Improvement Laboratory, TAES.

'MD51ne' was developed by the USDA-ARS, Cotton Physiology and Genetics Research Unit in Stoneville, MS and released in 1991 (Meredith, 1993). MD51ne is noted to have a combination of insect resistance, high fiber strength, and lint yield. MD51ne was selected from a BC_2F_2 population originated from a cross of MD65-11ne and DP 90.

USDA-ARS in cooperation with the State Agricultural Experiment Stations of Arizona, New Mexico, and Texas developed 'Pima S-6' (Feaster and Turcotte, 1984). Pima S-6 had earlier maturity and higher yield than the line it replaced, 'Pima S-5.' The greatest yield advantage over Pima S-5 was obtained at high elevations in New Mexico and Texas.

'Paymaster HS 26' was released in 1983 by R. H. Sheetz of Paymaster Technologies (PVP no. 8600087). PM HS 26 was developed for the High Plains of

Texas. ‘SG 747’ (PVP no. 9800118) was released in 1998 by Sure-Grow Seed, Inc. Phytogen Seed Company released PSC355 in 2000. The Plant Variety Protection certificate application filed in 2000 for ‘PSC355’ was abandoned as of April 2006. ‘Stoneville 213’ was released by Stoneville Pedigreed Seed Company in 1962.

TAM 89E-51 is an unreleased breeding line of the TAES Cotton Improvement Lab (Smith, 2007). Three of the 20 genotypes in this study are recognized as germplasm lines or cultivar releases from the Cotton Improvement Laboratory, TAES. ‘TAM 94L-25’ was released in 2003 as a germplasm line with improved fiber length (Smith, 2003). ‘TAM 96WD-69s’ was released as a glabrous germplasm line in 2005 (Thaxton et al., 2005). Selection for this line was conducted at Weslaco, TX. Glabrous lines have been developed by the Cotton Improvement Laboratory in an effort to combine high yield and superior fiber quality with resistance to fleahopper and silverleaf whitefly. ‘Tamcot 22’ was released as a cultivar in 2005 (Thaxton et al., 2005). Hybridization and pedigree selection of Tamcot 22 occurred at Weslaco, TX. Tamcot 22 was shown to have high yield and gin turnout during its evaluation across central and south Texas.

‘Tamcot CAMD-E’ was released by the TAES and developed in the TAM-MAR program (Bird, 1979). The TAM-MAR program specialized in the development of cotton cultivars and germplasm lines resistant to multiple biotic and abiotic stressors. Resistance of Tamcot CAMD-E to various insects and pathogens is reported but there is no mention of tolerance or susceptibility to drought.

Experimental Design

In 2006 and 2007, the 20 genotypes described in the previous section were planted in split plot arrangement of a randomized complete block design with irrigation treatment as main plots and genotypes as subplots. Plots were sampled at early bloom and late bloom. Five plants were sampled per plot at each sampling. The experiment was planted at the TAES Research Farm near CS and at the USDA-ARS CSRL in LUB. Genotypes were planted on 28 April 2006 and 7 May 2007 in CS and on 15 May 2006 and 22 May 2007 in LUB. Precipitation at both locations delayed planting in 2007. Plots were 12.2 m x 102 cm with four replications at CS while LUB plots were 6 m x 102 cm with four replications. The seeding rates and subsequent thinning wer designed to establish 1 plant per 30 cm.

The same experiment was planted in 2005 but irrigation treatments were applied in blocks producing two experiments, a randomized complete block with irrigation and one without. The experiment consisted of only 19 genotypes, lacking DP 491 that was included in the 2006-2007 experiment; otherwise, the research protocol in 2005 was the same as 2006 and 2007. The planting date for CS was 21 April 2005 and LUB was planted on 12 May 2005. Chlorophyll fluorescence was measured on five plants per plot at mid-bloom (MB) and late bloom (LB) growth stages in 2005, 2006, and 2007. Four replications were measured per treatment and location combination at each sampling time with the exception of MB in LUB in 2007 where only two replications were measured. DL and IRR treatments were measured at each sampling time with the

exception of MB and LB at CS in 2007 when only DL plots were measured. Adequate rainfall did not allow for the establishment of an irrigation treatment.

Furrow irrigation was used in CS, while a drip irrigation system based on leaf canopy temperature termed BIOTIC was employed for establishment of the irrigated treatments in LUB. CS was irrigated on 21 Jun 2005, 15 Jun 2006, and 22 Jul 2006. LUB was irrigated 0.6 cm daily as required by the BIOTIC irrigation system. Daily climatological data were recorded at both locations using automated weather stations located at the research sites (Figs. 1-6). MB and LB sampling times are noted on each graph.

CS plots were harvested with a one-row plot picker modified for plot harvest on 10 Nov 2005, 2 Oct. 2006, and 14 Nov. 2007. Plots at LUB were not harvested for yield determination in 2005 nor were samples taken for fiber analyses LUB plots were harvested with a two-row plot stripper on 6 Nov 2006 and 22 Oct. 2007.

Sub samples of harvested yields, referred to as grab samples, were taken from two replications and ginned on a laboratory saw gin to determine gin turnout and HVI fiber properties. Lint yields ha^{-1} were calculated as ((plot seedcotton yield * gin turnout) * area conversion factor). HVI measurements were determined from the lint from each grab sample at Cotton Incorporated in Cary, NC.

Statistical Analysis

Analyses of 2005 data and 2006-2007 data were performed by location and by growth stage. Treatment structure was different at CS in 2007 than other year/location

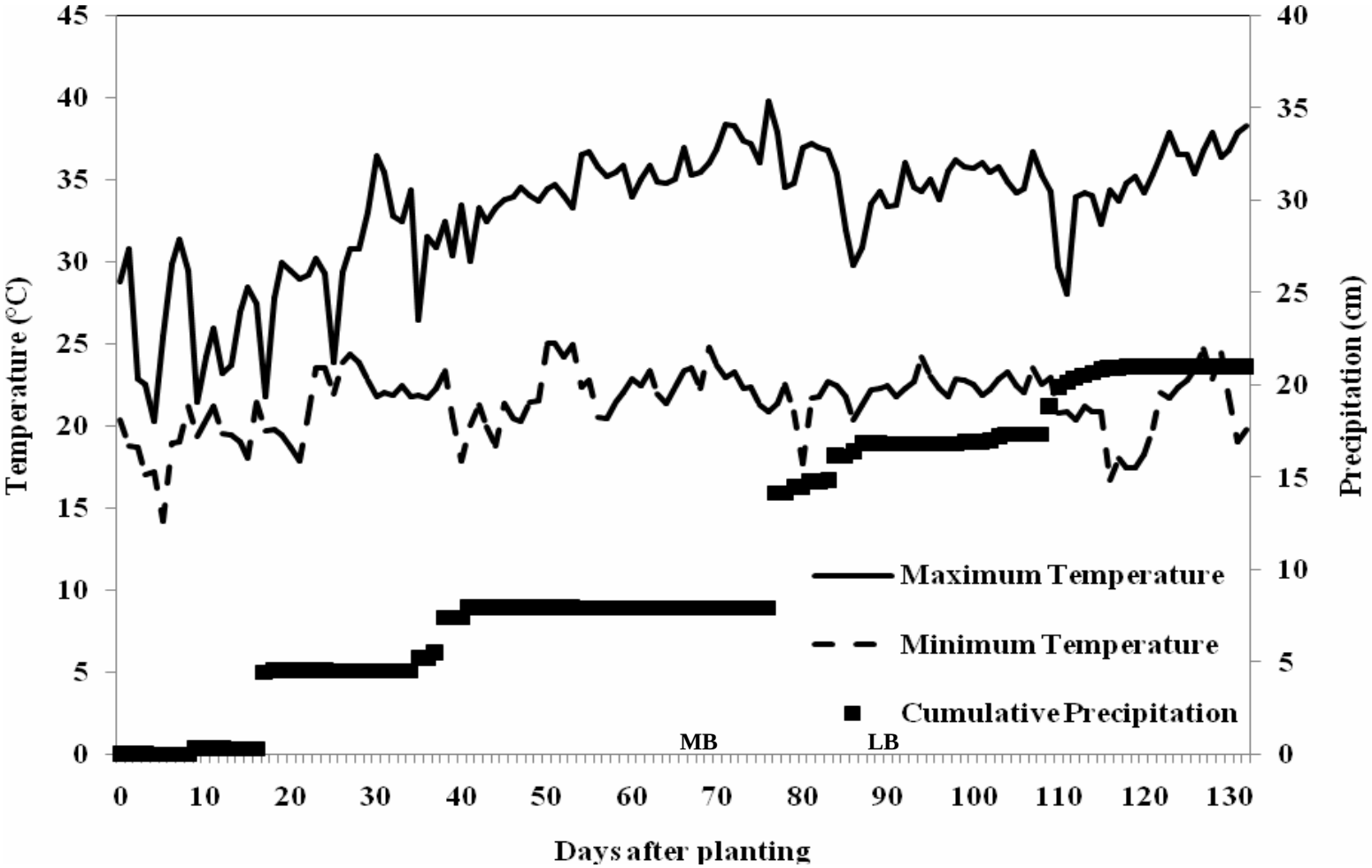

Figure 1. Daily maximum and minimum temperatures along with cumulative precipitation vs. days after planting for the 2005 growing season at College Station, TX. Mid-bloom (MB) and late bloom (LB) sampling times are depicted near the botton portion of the graph.

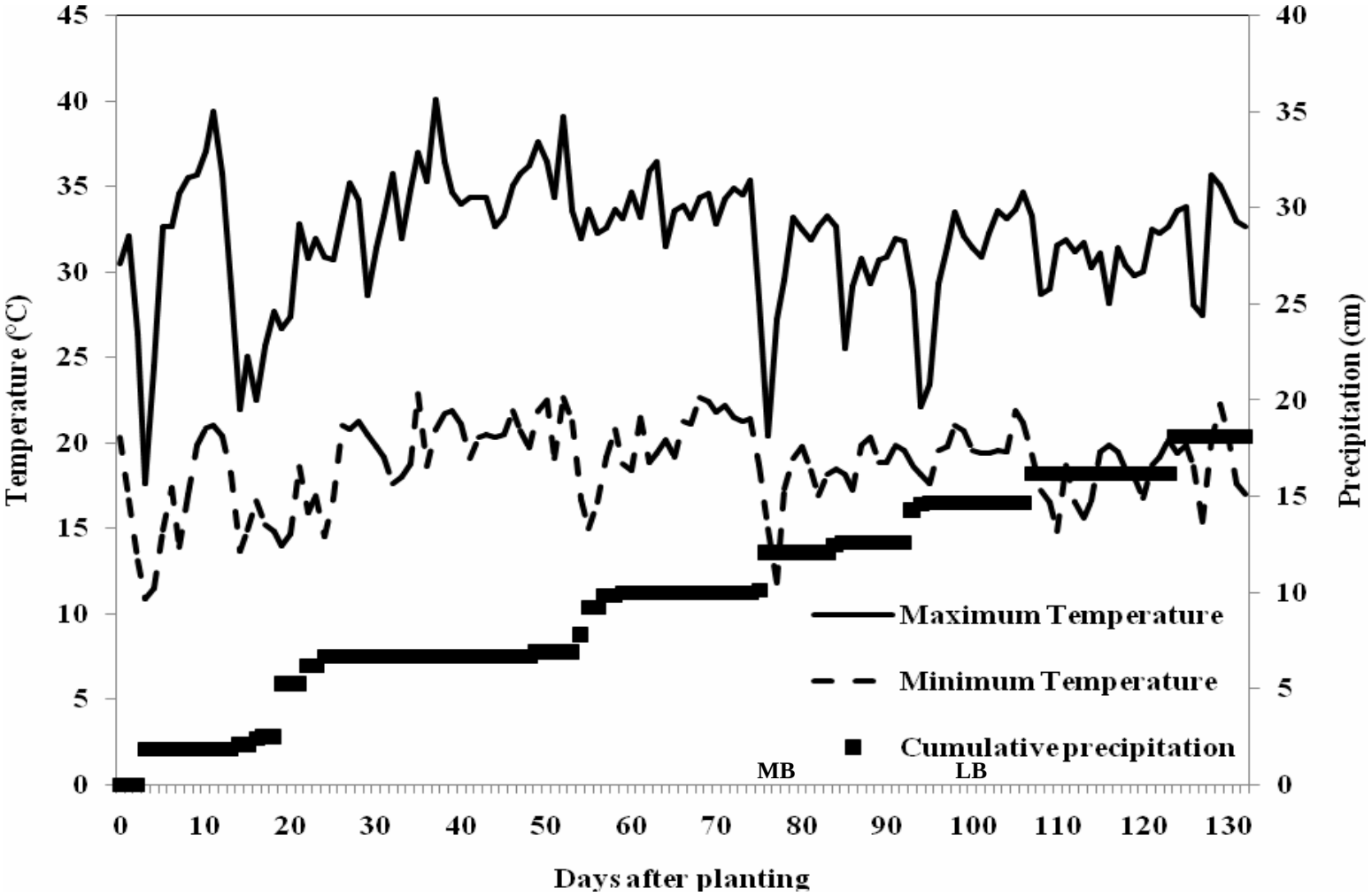

Figure 2. Daily maximum and minimum temperatures along with cumulative precipitation vs. days after planting for the 2005 growing season at Lubbock, TX. Mid-bloom (MB) and late bloom (LB) sampling times are depicted near the botton portion of the graph.

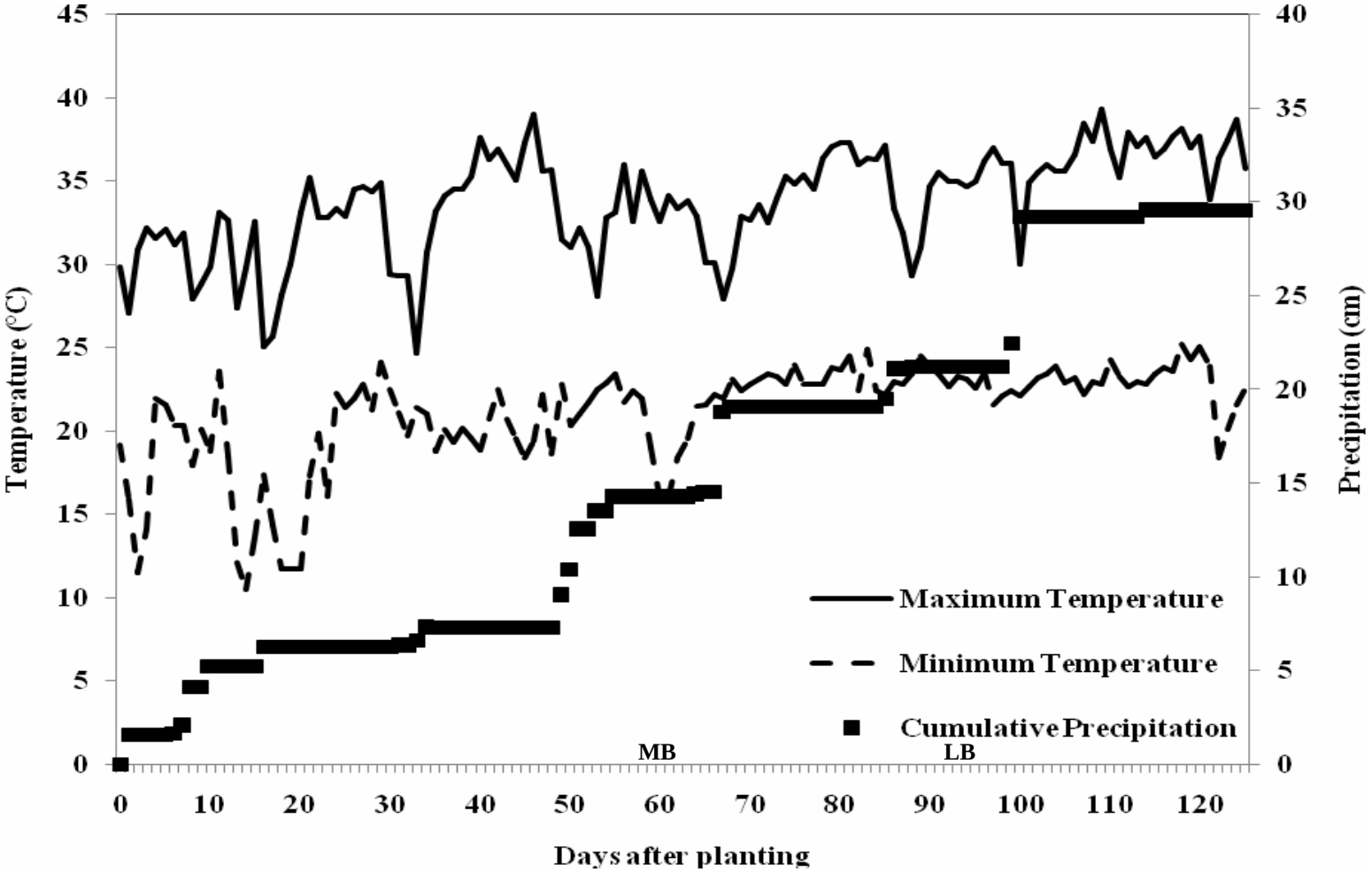

Figure 3. Daily maximum and minimum temperatures along with cumulative precipitation vs. days after planting for the 2006 growing season at College Station, TX. Mid-bloom (MB) and late bloom (LB) sampling times are depicted near the botton portion of the graph.

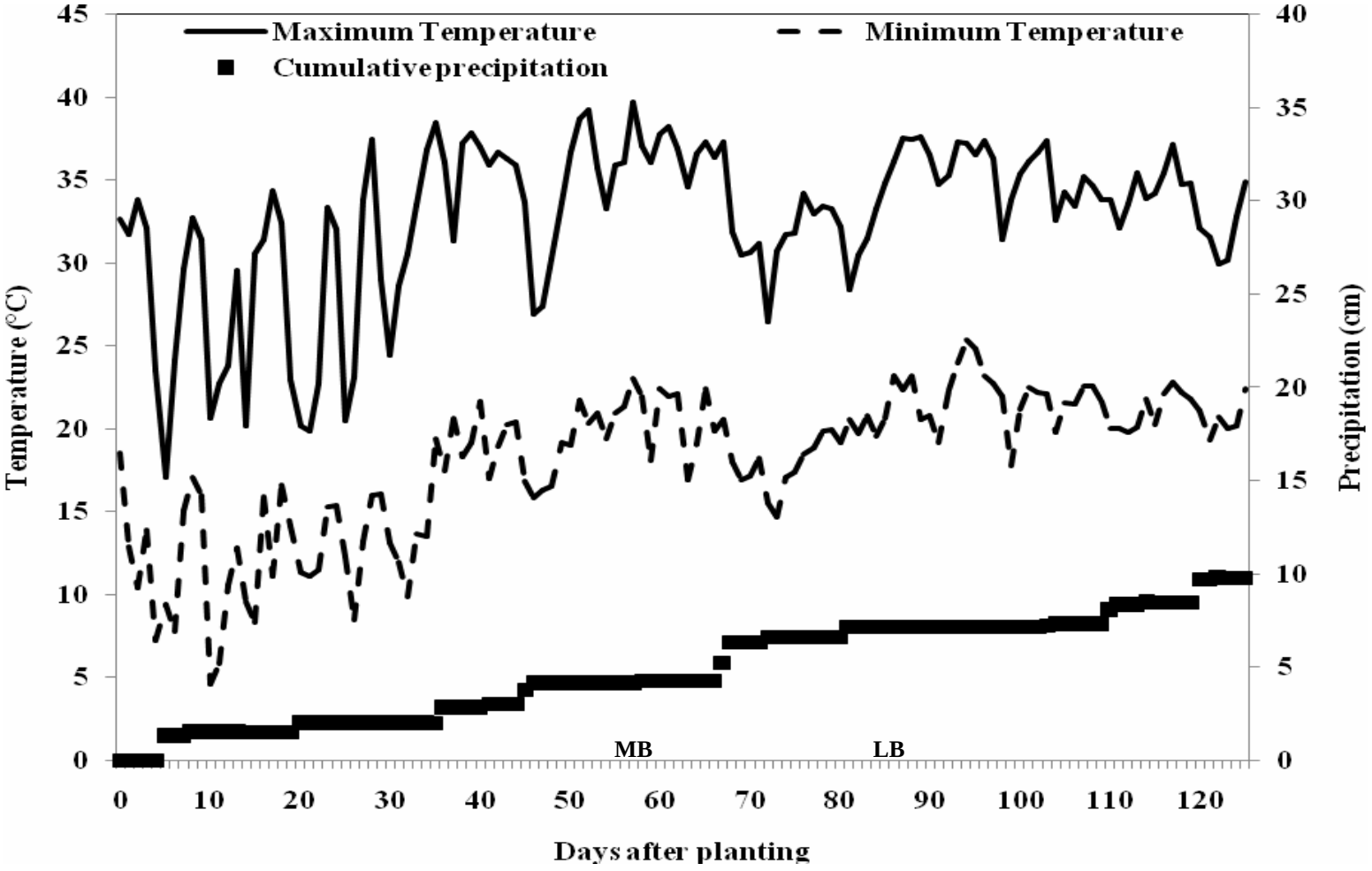

Figure 4. Daily maximum and minimum temperatures along with cumulative precipitation vs. days after planting for the 2006 growing season at Lubbock, TX. Mid-bloom (MB) and late bloom (LB) sampling times are depicted near the botton portion of the graph.

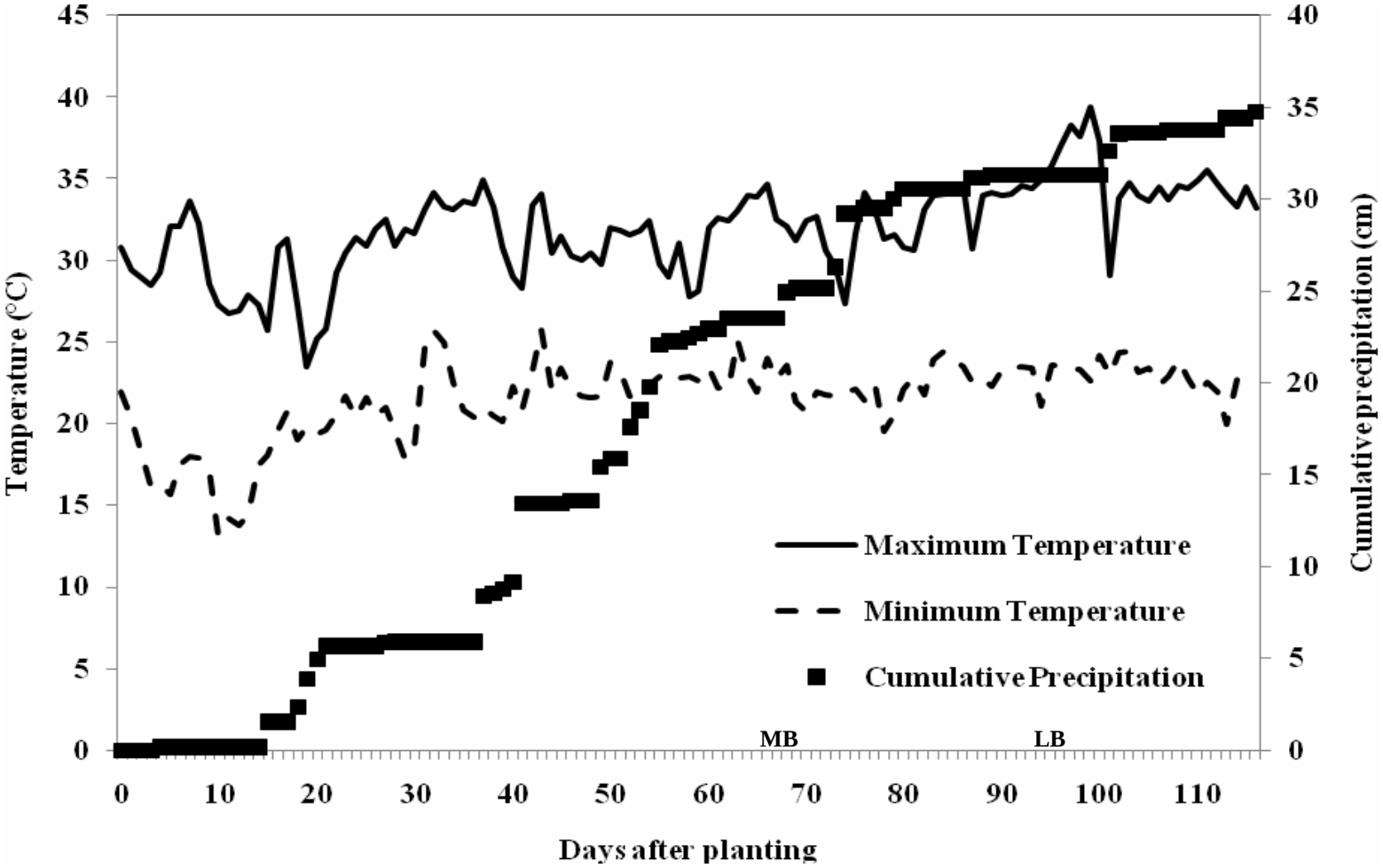

Figure 5. Daily maximum and minimum temperatures along with cumulative precipitation vs. days after planting for the 2007 growing season at College Station, TX. Mid-bloom (MB) and late bloom (LB) sampling times are depicted near the botton portion of the graph.

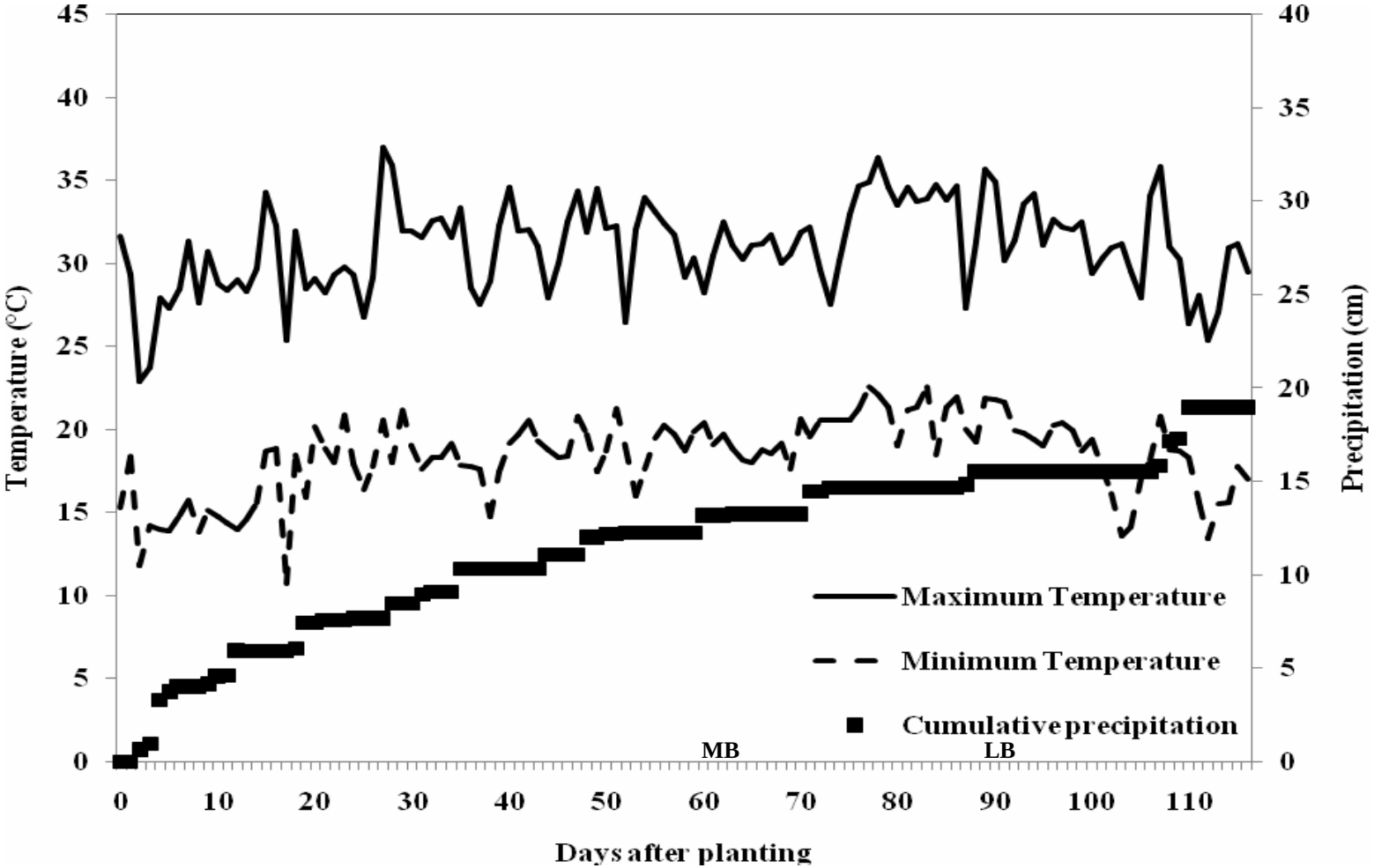

Figure 6. Daily maximum and minimum temperatures along with cumulative precipitation vs. days after planting for the 2007 growing season at Lubbock, TX. Mid-bloom (MB) and late bloom (LB) sampling times are depicted near the botton portion of the graph.

combinations since frequent rainfall events did not allow for the establishment of an irrigated treatment.

Data from 2005 and 2006-2007 were analyzed with a mixed effects model in SAS software using the GLIMMIX procedure (SAS Institute, 2004). The 2005 analysis included genotype and treatment as fixed effects and replication as a random effect.

For 2006 and 2007 the analysis included year, genotype, and treatment as fixed effects and replication as a random effect. Evaluation of normal probability plots of residuals and fluorescence data did not raise concerns of non-normal data distribution. A scatter plot of residuals versus expected fluorescence values indicated equality of error variances. Therefore, a gaussian distribution and identity link function were used in the analysis.

Treatment structure was not balanced at CS in 2006-2007. An irrigated treatment was never established in 2007 due to adequate rainfall. Therefore, two interactions (treatment x year and treatment x year x genotype) could not be included in the CS analysis.

Lint yields were measured at CS in 2005 and at CS and LUB in 2006. The data were analyzed by year and location with a mixed effects model using the GLIMMIX procedure. The 2005 analysis included genotype and treatment as fixed effects and replication as a random effect. For 2006 the analysis included year, genotype, and treatment as fixed effects and replication as a random effect. Gaussian distribution and identity link function were used in the analysis. The same type of analysis was used to

evaluate fiber properties, including micronaire, length, uniformity, strength, elongation, and short fiber content.

Fluorescence, yield, and fiber property data were analyzed with SAS software using the CORR procedure (SAS Institute, 2004). Pearson correlation coefficients were calculated.

Diallel

Five genotypes were selected based on the results of the 2005 field experiments to be included in a diallel analysis to determine the heritability of fluorescence measurements. Tamcot 22 and TAM 89E-51 had consistently expressed low and high average fluorescence values, respectively. Selections based on fluorescence values were made of the highest 10 % and lowest 10 % of 100 plants of each genotype (Tamcot 22 and TAM 89E-51) grown under greenhouse conditions. These forty plants served as parents in the diallel analysis. In addition, 10 plants each of Acala 1517-99, Deltapine 491, and Tamcot CAMD-E were included as parents in the diallel and all had average fluorescence values that fell between those of Tamcot 22 and TAM 89E-51.

Parents and F_1s were hand-planted in a randomized complete block design on 9 May 2007 at the TAES research farm in CS and at the TAES research farm near LUB on 23 May 2007. At both locations, 10 seeds were sown per 1.5 m x 102 cm plot. The LUB location suffered soil-crusting following a rainfall event that occurred shortly after planting. In addition, a hail storm occurred shortly after emergence. These events led to a poor stand in LUB. On 10 Aug 2007, LUB plots were thinned uniformly to 1 or 2 plants in each plot with at least 1 m between. A single plant in each plot was sampled on

23 Aug 2007. Three plants per mini-plot were sampled in CS on 9 Aug 2007. LUB was irrigated on 20 Jul 2007 and 15 Aug 2007, while no irrigation was necessary at CS.

Statistical Analysis

Data were analyzed using Gardner and Eberhart's Analysis III (Gardener and Eberhart, 1966). Analyses of variance were computed for hour 3 and hour 5 Fv'/Fm' measurements using DIALLEL-SAS05 (Zhang et al., 2005). The means across locations for hour 3 and hour 5 measurements are shown in the results and discussion section of this dissertation.

Due to the poor stand at LUB, least square means could not be estimated for two combinations, TAM 89E-51 lo/Acala 1517-99 and TAM 89E-51 hi/Acala 1517-99. Thus, Acala 1517-99 and its F_1 combinations were dropped from the analysis.

Progeny Test

Selfed progeny of the selected Tamcot 22 and TAM 89E-51 described in the previous section were hand-planted in the same manner as the diallel along with their unselected parents in a randomized complete block design on 9 May 2007 in CS and on 23 May 2007 in LUB adjacent to the diallel tests. Three plants per plot were sampled on 8 Aug 2007 in CS and single plants were sampled on 23 Aug 2007 in LUB. Early season conditions, thinning events, and irrigation schedules described for the diallel tests also applied to the progeny test in LUB. Analysis of variance for each location was performed with the SAS PROC GLIMMIX procedure (SAS Institute, 2004).

RESULTS AND DISCUSSION

Field Evaluation

Climatological Conditions

Seasonal air temperatures during 2005-2007 (Figs. 1-6) were near long-term average for both locations. The precipitation at both locations was above the long term averages in 2005-2007. Frequent rain events during each growing season complicated the ability to establish stress conditions both in LUB and CS.

Fluorescence ANOVA

In 2005, significant genotypic effects were detected for all location, stage, and treatment combinations (Tables 2, 4). G. arboreum had the highest Fv'/Fm' value when grown at CS under DL conditions sampled at the mid-bloom growth stage but not different than Pima S-6 (Table 3). The upland type with the highest Fv'/Fm' value was PM HS 26 but it was not different than five other genotypes in the test. Tamcot 22 had the lowest Fv'/Fm' absolute value indicating it is drought tolerant along with eight other upland genotypes. While the two non-upland types appeared to be distinctly drought susceptible, there is a lot of overlap among the means for the upland types. At the late bloom growth stage of the same test, PM HS 26 again had the highest numerical Fv'/Fm' value but was not different than G. arboreum, TAM 94L-25, nor PSC 355. DP 90 had the lowest Fv'/Fm' value but it was not different than five other genotypes, including Tamcot 22. This ranking is different from the ranking found at the mid-bloom growth stage, which provided an early indication that drought classifications made with the Burke method are growth stage specific. Low Fv'/Fm' values at the late bloom growth

Table 2. Variance analysis for Fv'/Fm' measurement taken after 5 hours of incubation for 19 cotton genotypes at mid-bloom and late bloom growth stages grown under dryland field conditions at College Station, TX and Lubbock, TX in 2005.

		MB stage		LB stage	
Source	**df**	**CS**	**LUB**	**CS**	**LUB**
		———	——— *F* ———		———
Genotype	18, 54	16.50***	3.97***	3.24***	5.94***

***Significant at $P < 0.001$.

Table 3. Fv'/Fm' measurement taken after 5 hours of incubation of 19 cotton genotypes at mid-bloom and late bloom growth stages grown under dryland field conditions at College Station, TX and Lubbock, TX in 2005.

Genotype	MB stage		LB stage	
	CS	LUB	CS	LUB
	Fv'/Fm'			
Acala 1517-99	0.225 cdefghi‡	0.448 bcde	0.084 ef	0.142 i
Acala Maxxa	0.284 bc	0.388 efg	0.128 bcde	0.186 fghi
AllTex Atlas	0.278 bcde	0.412 cde	0.156 abcd	0.274 bcde
DP 14	0.221 defghi	0.394 efg	0.092 def	0.316 bc
DP 50	0.194 ghi	0.407 de	0.117 cdef	0.266 cdef
DP 90	0.218 efghi	0.297 g	0.081 ef	0.216 defghi
FM 832	0.205 fghi	0.382 efg	0.079 ef	0.246 cdef
G. arboreum	0.505 a	0.511 ab	0.206 a	0.251 cdef
MD51ne	0.217 efghi	0.410 cde	0.099 def	0.203 efghi
Pima S-6	0.467 a	0.440 bcde	0.189 ab	0.352 ab
PM HS 26	0.310 b	0.571 a	0.157 abcd	0.277 bcde
PSC355	0.256 bcdefg	0.499 abcd	0.110 def	0.229 defg
SG 747	0.185 hi	0.362 efg	0.076 ef	0.160 ghi
Stv 213	0.265 bcdef	0.431 bcde	0.061 f	0.224 defgh
TAM 89E-51	0.280 bcd	0.448 bcde	0.181 abc	0.400 a
TAM 94L-25	0.230 cdefgh	0.503 abc	0.121 cdef	0.315 bc
TAM 96WD-69s	0.191 hi	0.419 bcde	0.102 def	0.289 bcd
Tamcot 22	0.163 i	0.307 fg	0.087 ef	0.147 hi
Tamcot CAMD-E	0.246 cdefgh	0.439 bcde	0.114 def	0.283 bcd
Mean	0.260	0.425	0.118	0.251
Standard deviation	0.089	0.067	0.042	0.068

‡ Means in the same column followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 4. Variance analysis for Fv'/Fm' measurement taken after 5 hours of incubation for 19 cotton genotypes at mid-bloom and late bloom growth stages grown under irrigated field conditions at College Station, TX and Lubbock, TX in 2005.

		MB stage		LB stage	
Source	**df**	**CS**	**LUB**	**CS**	**LUB**
			F		
Genotype	18, 54	8.17***	3.53***	10.81***	5.39***

***Significant at $P < 0.001$.

stage at CS were unexpected as the soil was saturated with rainfall at the time the samples were taken. The measurements may have been compromised by lack of oxygen available to the root system or low solar radiation levels.

Fv'/Fm' measurements taken at LUB under DL conditions at the mid-bloom growth stage again indicated that *G. arboreum* and Pima S-6 are drought susceptible, having the highest ($p<.05$) Fv'/Fm' values along with 3 upland genotypes in the test, TAM 89E-51, PM HS 26, and AllTex Atlas. Stv 213 along with 13 other upland genotypes were identified as drought resistant, having the lowest Fv'/Fm' values. This same experiment measured at late bloom at LUB showed TAM 89E-51 and Pima S-6 to have the highest ($p<.05$) Fv'/Fm' values and six upland genotypes, including Tamcot 22, to be the most drought resistant, as indicated by low Fv'/Fm' values .

Under IRR conditions at CS, mid-bloom, Pima S-6 and *G. arboreum* had the highest Fv'/Fm' values ($p<.05$) while FM 832, PSC 355, and Stv 213 had the highest Fv'/Fm' value among the upland types (Table 5). Tamcot 22 had the lowest absolute Fv'/Fm' value but was not different than over half of the genotypes tested. This experiment measured at late bloom in CS indicated that TAM 94L-25, PSC 355, and TAM 89E-51 had the higher ($p<.05$) Fv'/Fm' values than Tamcot 22 or DP 90. Similar to the DL measurements made under the same conditions, the Fv'/Fm' values are higher than expected given the moist soil conditions.

The mid-bloom Fv'/Fm' value of *G. arboreum* under irrigated conditions at LUB was higher ($p<.05$) than all other genotypes while 15 of the 20 genotypes measured were not different than DP 14, which had the lowest absolute value. Acala 1517-99 had the

Table 5. Fv'/Fm' measurement taken after 5 hours of incubation of 19 cotton genotypes at mid-bloom and late bloom growth stages grown under dryland field conditions at College Station, TX and Lubbock, TX in 2005.

Genotype	MB stage		LB stage	
	CS	LUB	CS	LUB
	Fv'/Fm'			
Acala 1517-99	0.213 hi‡	0.540 abc	0.047 b	0.062 defg
Acala Maxxa	0.208 hi	0.514 abcd	0.030 bcd	0.079 cdefg
AllTex Atlas	0.285 def	0.551 abc	0.047 b	0.089 cdefg
DP 14	0.215 ghi	0.470 cd	0.010 d	0.056 efg
DP 50	0.210 hi	0.507 abcd	0.018 cd	0.099 cde
DP 90	0.268 defgh	0.349 e	0.017 cd	0.077 cdefg
FM 832	0.357 bc	0.553 abc	0.032 bcd	0.078 cdefg
G. arboreum	0.393 ab	0.481 bcd	0.155 a	0.168 ab
MD51ne	0.227 fghi	0.506 abcd	0.019 cd	0.088 cdefg
Pima S-6	0.422 a	0.531 abc	0.033 bcd	0.201 a
PM HS 26	0.252 defghi	0.559 ab	0.019 cd	0.083 cdefg
PSC355	0.301 cd	0.577 a	0.039 bc	0.110 cd
SG 747	0.257 defghi	0.528 abc	0.033 bcd	0.045 g
Stv 213	0.300 cde	0.537 abc	0.025 bcd	0.050 fg
TAM 89E-51	0.237 efghi	0.569 a	0.024 bcd	0.095 cdef
TAM 94L-25	0.232 fghi	0.591 a	0.023 bcd	0.122 bc
TAM 96WD-69s	0.229 fghi	0.472 cd	0.027 bcd	0.104 cde
Tamcot 22	0.205 i	0.429 de	0.036 bcd	0.050 fg
Tamcot CAMD-E	0.278 defg	0.511 abcd	0.012d	0.075 cdefg
Mean	0.268	0.514	0.034	0.091
Standard deviation	0.063	0.057	0.031	0.039

‡ Means in the same column followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

highest Fv'/Fm' value among the upland types but it was not different than over half of the genotypes tested. DP 14 had the lowest Fv'/Fm' numerical value but was not different than over half of the genotypes tested. The Fv'/Fm' value of *G. arboreum,* again, was higher ($p<.05$) than all genotypes except Pima S-6 when measured at late bloom in LUB. G. arboreum was not different than 94L-25, which was the upland type with the highest Fv'/Fm' value while SG 747 had the lowest Fv'/Fm' value but was not different than over half of the genotypes tested.

In general, more separation between genotypes was found under DL rather than IRR conditions during 2005. The late bloom measurements at CS were apparently compromised by some unknown stress factor other than drought stress.

In 2006 and 2007, the analysis of variance for Fv'/Fm' for the 20 genotypes evaluated indicated significant variation for genotypes, year and their interaction in CS at the mid-bloom growth stage (Table 6). In 2006, G arboreum had the highest Fv'/Fm' value indicating that it had the highest level of drought susceptibility (Table 7). TAM 89E-51 was the most susceptible upland type and was not different than Pima S-6 and four upland types. Acala Maxxa had the lowest Fv'/Fm' value but was not different than over half of the other genotypes in the test. Pima S-6 had the highest Fv'/Fm' value in 2007 at CS. It was more susceptible than all other genotypes in the test. TAM 94L-25 had the highest Fv'/Fm' value among the upland types but was not different than G. arboreum, TAM 89E-51, and PSC355. As in 2006, Acala Maxxa had the lowest Fv'/Fm' value and was not different than over half of the genotypes tested. The significant interaction was due to direction of response differences among the genotypes. Many of

Table 6. Variance analysis for Fv'/Fm' measurement taken after 5 hours of incubation of twenty cotton genotypes at mid-bloom and late bloom grown under dryland and irrigated field conditions at College Station, TX in 2006 and 2007.

		MB stage	LB stage
Source	**df**	**Fv'/Fm'**	
		F	
Genotype	19, 174	12.43***	6.12***
Year	1, 174	12.32***	165.51***
Year x Genotype	19, 174	4.70***	1.75*
Treatment	1, 6	2.21	2.78
Treatment x Genotype	19, 174	0.53	1.01

***Significant at $P < 0.001$.

the genotypes, notably TAM 96WD-69s, DP 90, PM HS 26, and MD-51ne were essentially unchanged across years. However, two genotypes, TAM 94L-25 and Pima S-6 were unique in their large increase in Fv'/Fm' value in 2007 compared with 2006 at this stage of growth.

Late bloom measurements taken at CS in 2006 indicated that Pima S-6 was the most drought susceptible genotype tested (Table 8). TAM 89E-51 had the highest Fv'/Fm' value among the upland types and was not different than G. arboreum, SG 747, nor TAM 94L-25. TAM 96WD-69s, Tamcot 22, DP 90, FM 832, and DP 491 were drought tolerant with the lowest Fv'/Fm' values in 2006. Numerically, Pima S-6 had the highest Fv'/Fm' value in 2007 but was not different than five other genotypes in the test. As in 2006, TAM 96WD-69s had the lowest Fv'/Fm' value. However, it was not different than six other genotypes who also had low Fv'/Fm' values. The significant interaction at late bloom in CS was caused by differences in magnitude and direction. DP 491 was the only genotype to have a higher Fv'/Fm' value in 2007 versus 2006, although it, along with AllTex Atlas and FM 832, was essentially unchanged across years. TAM 94L-25 and Acala Maxxa showed large decreases in their Fv'/Fm' values from 2006 to 2007.

Analysis of variance for LUB at mid-bloom in 2006 and 2007 indicated that significant variation occurred for genotypes, years, and their interaction and also for the interaction of treatments and years (Table 9). At late bloom there was significant variation for genotypes, years, and treatments. The interactions between treatment and genotypes and treatment and years were also significant.

Table 7. Difference in Fv'/Fm' of twenty cotton genotypes at mid-bloom grown under Dryland and irrigated field conditions at College Station, TX in 2006-2007.

Genotype	Fv'/Fm'		
	2006	**2007**	**difference**
Acala 1517-99	0.167 f†	0.149 ef	0.018 abc‡
Acala Maxxa	0.163 f	0.144 f	0.019 ab
AllTex Atlas	0.212 cd	0.237 cde	-0.025 bcdef
DP 14	0.211 cd	0.193 def	0.018 abc
DP 491	0.187 def	0.237 cde	-0.050 defg
DP 50	0.170 ef	0.147 ef	0.023 ab
DP 90	0.176 ef	0.188 def	-0.012 abcde
FM 832	0.176 ef	0.227 cdef	-0.051 efg
G. arboreum	0.313 a	0.344 b	-0.031 cdef
MD51ne	0.171 ef	0.181 def	-0.010 abcde
Pima S-6	0.250 b	0.538 a	-0.288 i
PM HS 26	0.180 def	0.193 def	-0.013 abcde
PSC355	0.180 def	0.269 bcd	-0.089 g
SG 747	0.211 cd	0.186 def	0.025 a
Stv 213	0.204 cde	0.213 cdef	-0.009 abcde
TAM 89E-51	0.223 bc	0.291 bc	-0.068 fg
TAM 94L-25	0.177 ef	0.345 b	-0.168 h
TAM 96WD-69s	0.179 def	0.180 def	-0.001 abcd
Tamcot 22	0.186 def	0.179 def	0.007 abc
Tamcot CAMD-E	0.188 def	0.205 cdef	-0.017 abcde
Mean	0.196	0.232	
Standard deviation	0.035	0.092	

† Means in the same column followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

‡ Means in the same column followed by the same letter are not different according to Fisher's LSD ($P < 0.05$).

Table 8. Difference in Fv'/Fm' of twenty cotton genotypes at late bloom grown under dryland and irrigated field conditions in 2006 and dryland field conditions in 2007 at College Station, TX.

Genotype	Fv'/Fm'		
	2006	**2007**	**difference**
Acala 1517-99	0.422 fghi†	0.245 ef	0.177 bcd‡
Acala Maxxa	0.467 cdefg	0.243 ef	0.224 ab
AllTex Atlas	0.421 fghi	0.369 abc	0.052 hij
DP 14	0.420 fghi	0.330 bcde	0.090 fgh
DP 491	0.396 hij	0.400 ab	-0.004 j
DP 50	0.417 ghi	0.401 ab	0.016 ij
DP 90	0.371 ij	0.246 ef	0.125 cdefg
FM 832	0.402 hij	0.344 bcde	0.058 hij
G. arboreum	0.500 bc	0.365 abcd	0.135 cdefg
MD51ne	0.415 ghi	0.255 def	0.160 bcde
Pima S-6	0.643 a	0.477 a	0.166 bcde
PM HS 26	0.435 efgh	0.353 bcde	0.082 fgh
PSC355	0.482 bcde	0.326 bcde	0.156 bcdef
SG 747	0.475 bcdef	0.299 bcde	0.176 bcd
Stv 213	0.444 defgh	0.342 bcde	0.102 efgh
TAM 89E-51	0.527 b	0.345 bcde	0.182 bc
TAM 94L-25	0.496 bcd	0.243 ef	0.253 a
TAM 96WD-69s	0.359 j	0.183 f	0.176 bcd
Tamcot 22	0.368 ij	0.260 cdef	0.108 defgh
Tamcot CAMD-E	0.439 efgh	0.370 abc	0.069 ghi
Mean	0.445	0.320	
Standard deviation	0.065	0.072	

† Means in the same column followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

‡ Means in the same column followed by the same letter are not different according to Fisher's LSD ($P < 0.05$).

Table 9. Variance analysis for Fv'/Fm' measurement taken after 5 hours of incubation of twenty cotton genotypes at mid-bloom and late bloom grown under dryland and irrigated field conditions at Lubbock, TX in 2006 and 2007.

		MB stage	LB stage
Source	**df**	**Fv'/Fm'**	
		F	
Genotype	19, 154	6.87***	12.80***
Year	1, 154	743.24***	144.94***
Year x Genotype	19, 154	2.07**	1.38
Treatment	1, 6	0.59	21.80**
Treatment x Genotype	19, 154	0.52	2.46**
Treatment x Year	1, 154	7.32**	28.63***
Treatment x Year x Genotype	19, 154	0.48	0.62

** Significant at $P < 0.01$.

*** Significant at $P<0.001$.

At LUB-mid-bloom in 2006, Pima S-6 was the most drought susceptible genotype (Table 10). It was not different than G. arboreum, which was not different than the five most susceptible upland types, including TAM 89E-51. Acala Maxxa was the most tolerant genotype but was not different than four other upland types, one of which was Tamcot 22. In 2007, G. arboreum was the most drought susceptible genotype based on its large Fv'/Fm' value, and, along with Pima S-6 was more susceptible than the 18 other genotypes in the test. PSC 355 had the highest Fv'/Fm' value among the upland types but was not different than over half of the other genotypes tested. The significant interaction of genotype and year at LUB during the mid-bloom growth stage was due to changes in magnitude of Fv'/Fm' values across years. All Fv'/Fm' values in 2006 at LUB were larger than those measured in 2007. Eight genotypes were not different than the genotype with the largest change across years, Tamcot CAMD-E at 0.293. G. arboreum changed the least across years and its change was not different than Acala Maxxa and TAM 96WD-69s. More rainfall occurred in 2007 in LUB causing Fv'/Fm' values to be lower and similar across treatments at compared to 2006 (Table 11).

Pima S-6 and G. arboreum were more drought susceptible than all other genotypes tested at LUB in 2006 at the late bloom growth stage (Table 12). TAM 89E-51 was the most susceptible among the upland types but was not different than PSC 355 or DP 50. MD51ne was the most drought tolerant genotype but was not different than over half of the genotypes in the test. In 2007, Pima S-6 and G. arboreum were the most drought susceptible, and not different than TAM 89E-51, the most susceptible upland type. DP 50 and PSC 355 were not different than TAM 89E-51. Acala Maxxa was the

Table 10. Difference in Fv'/Fm' of twenty cotton genotypes at mid-bloom grown at Lubbock, TX in 2006-2007.

Genotype	Fv'/Fm'		
	2006	**2007**	**difference**
Acala 1517-99	0.331 bcde†	0.078 cd	0.253 abcde‡
Acala Maxxa	0.245 h	0.063 d	0.181 ghi
AllTex Atlas	0.367 bc	0.094 cd	0.273 abc
DP 14	0.298 efg	0.061 d	0.237 bcdef
DP 491	0.292 efgh	0.080 cd	0.212 efgh
DP 50	0.280 fgh	0.070 cd	0.209 efgh
DP 90	0.296 efg	0.081 cd	0.214 defgh
FM 832	0.365 bc	0.081 cd	0.284 ab
G. arboreum	0.375 ab	0.237 a	0.138 i
MD51ne	0.320 cdef	0.072 cd	0.248 abcde
Pima S-6	0.419 a	0.156 b	0.263 abcd
PM HS 26	0.309 defg	0.093 cd	0.216 defgh
PSC 355	0.333 bcde	0.107 c	0.226 cdefg
SG 747	0.263 gh	0.071 cd	0.192 fgh
Stv 213	0.325 cdef	0.079 cd	0.246 abcde
TAM 89E-51	0.361 bc	0.073 cd	0.287 a
TAM 94L-25	0.309 defg	0.074 cd	0.235 bcdef
TAM 96WD-69s	0.266 fg	0.096 cd	0.170 hi
Tamcot 22	0.291 efgh	0.065 d	0.226 cdefg
Tamcot CAMD-E	0.351 bcd	0.058 d	0.293 a
Mean	0.320	0.089	
Standard deviation	0.044	0.041	

† Means in the same column followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

‡ Means in the same column followed by the same letter are not different according to Fisher's LSD ($P < 0.05$).

Table 11. Difference in Fv'/Fm' of dryland and irrigated treatments across twenty cotton genotypes at mid-bloom grown at Lubbock, TX in 2006-2007.

Genotype	Fv'/Fm'		
	Dryland	**Irrigated**	**difference**
2006	0.341 a‡	0.299 a	0.042 a
2007	0.124 b	0.121 b	0.003 a
Mean	0.232	0.210	
Standard deviation	0.153	0.126	

‡ Means in the same column followed by the same letter are not different according to Fisher's LSD ($P < 0.05$).

Table 12. Difference in Fv'/Fm' of twenty cotton genotypes at late bloom grown at Lubbock, TX in 2006-2007.

Genotype	Fv'/Fm'		
	Dryland	**Irrigated**	**difference**
Acala 1517-99	0.290 f†	0.195 efghi	0.095 bcd‡
Acala Maxxa	0.284 f	0.163 i	0.121 ab
AllTex Atlas	0.323 def	0.232 cdef	0.092 bcd
DP 14	0.328 def	0.222 cdefgh	0.106 abcd
DP 491	0.295 ef	0.213 defgh	0.082 bcd
DP 50	0.328 cd	0.258 bc	0.070 cde
DP 90	0.277 f	0.191 fghi	0.086 bcd
FM 832	0.277 f	0.186 ghi	0.091 bcd
G. arboreum	0.333 b	0.302 a	0.031 e
MD51ne	0.272 f	0.184 hi	0.088 bcd
Pima S-6	0.466 a	0.319 a	0.147 a
PM HS 26	0.319 def	0.211 defgh	0.109 abcd
PSC 355	0.331 cde	0.248 bcd	0.084 bcd
SG 747	0.341 def	0.223 cdefgh	0.118 abc
Stv 213	0.326 def	0.226 cdefg	0.099 abcd
TAM 89E-51	0.390 c	0.286 ab	0.103 abcd
TAM 94L-25	0.299 ef	0.233 cde	0.066 de
TAM 96WD-69s	0.324 def	0.236 cde	0.088 bcd
Tamcot 22	0.280 ef	0.183 hi	0.097 bcd
Tamcot CAMD-E	0.339 def	0.230 cdef	0.109 abcd
Mean	0.320	0.227	
Standard deviation	0.044	0.041	

† Means in the same column followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

‡ Means in the same column followed by the same letter are not different according to Fisher's LSD ($P < 0.05$).

most tolerant genotype but was not different than five others in the test, including Tamcot 22. The genotype by treatment interaction is due to the magnitude of differences in Fv'/Fm' values across years. The genotype with the largest treatment response was SG 747, but it was not different than nine other genotypes. DL treatment samples had larger values than irrigated samples as expected. As with the mid-bloom treatment x year interaction, the LSD did not distinguish differences among years (Table 13).

Some consistency of ranking was seen in 2006 and 2007. Pima S-6, G. arboreum, and TAM 89E-51 are consistently found to be drought susceptible. While Acala Maxxa and Tamcot 22 have reliably low Fv'/Fm' values and thus would be considered drought tolerant.

Lint Yield ANOVA

Analysis of variance for lint yield in CS in 2005 indicated that genotypes differed in lint yield (Table 14). DP 90 was the highest yielding ($p<.05$) genotype but was not different from 8 other genotypes (Table 15). G. arboreum had lower lint yield than all other genotypes tested. Acala Maxxa and Acala 1517-99 had the lowest lint yields of the upland types but were not different than five other genotypes. This was not unexpected since these lines are adapted to California and New Mexico, respectively, and not to the humid east, central region of Texas. The 2006 analysis of variance for lint yield at CS and LUB indicated differences for genotypes, irrigation treatments, and their interaction (Table 16). TAM 96WD-69s had the highest lint yield ($p<.05$) under DL conditions but was not different than five other upland types, Tamcot 22 among them (Table 17). G. arboreum was the lowest yielding genotype, followed by Pima S-6

Table 13. Difference in Fv'/Fm' of dryland and irrigated treatments across twenty cotton genotypes at late bloom grown at Lubbock, TX in 2006-2007.

Genotype	Fv'/Fm'		
	Dryland	**Irrigated**	**difference**
2006	0.373 a‡	0.225 a	0.148 a
2007	0.269 b	0.185 b	0.084 a
Mean	0.321	0.205	
Standard deviation	0.073	0.028	

‡ Means in the same column followed by the same letter are not different according to Fisher's LSD ($P < 0.05$).

which was not different than Acala Maxxa. Under IRR conditions, G. arboreum again had the lowest yield followed by Pima S-6. Pima S-6 was not different than Acala Maxxa and DP 14. The highest yielding genotype under irrigation was Tamcot 22, which was not different than DP 491, PSC355, and FM 832. The significant genotype by treatment interaction was due to differences in magnitude of yield change across irrigation treatments. All differences indicated higher lint yields under irrigated conditions, as expected. G. arboreum, PSC355, and DP 14 showed the least change in yield due to irrigation regime, while Tamcot 22 and DP 491 had the largest yield response to irrigation.

Under DL conditions at LUB in 2006, G. arboreum had the lowest lint yield (Table 18). Over half of the genotypes in the test did not differ from the genotype with the next lowest lint yield, PM HS 26, while FM 832 had the highest DL yield and was not different than DP 491 or Tamcot 22. Under irrigation, G. arboreum again had the lowest lint yield. The next lowest yielding genotype was Tamcot CAMD-E, which was not different than Pima S-6 or Acala 1517-99. Tamcot 22 had the highest yield under IRR conditions and was not different than 10 other genotypes in the test. Among the high yielding genotypes were DP 491 and FM 832. As with the CS data, genotypes responded positively to supplemental irrigation at LUB, with Tamcot 22 being the most responsive genotype to irrigation treatment as it was at CS in 2006. However, the magnitude of its response was not different than eight other genotypes in the test. G. arboreum was again the least response genotype and was different than all other genotypes.

Table 14. Variance analysis for lint yield (kg ha^{-1}) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Source	df	Lint yield
		F
Genotype	18, 108	4.63***
Treatment	1, 6	0.65
Treatment x Genotype	18, 108	0.92

***Significant at $P < 0.001$.

Table 15. Lint yield (kg ha^{-1}) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Genotype	Lint yield
DP 90	1432 a‡
PSC 355	1394 ab
TAM 94L-25	1290 abc
Tamcot 22	1288 abc
DP 50	1258 abc
MD51ne	1230 abc
DP 14	1166 abc
FM 832	1152 abc
SG 747	1143 abc
Tamcot CAMD-E	1119 bc
PM HS 26	1096 bcd
AllTex Atlas	1066 dc
Pima S-6	1043 dc
TAM 96WD-69s	1038 dc
TAM 89E-51	1026 dc
Stv 213	1017 dc
Acala 1517-99	1002 dc
Acala Maxxa	810 d
G. arboreum	379 e
Mean	1103
Standard deviation	230

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 16. Variance analysis for lint yield (kg ha^{-1}) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX and Lubbock, TX in 2006.

Source	df	CS	LUB
		Lint yield	
		F	
Genotype	19, 114	24.31***	12.49***
Treatment	1, 6	53.89***	242.01**
Treatment x Genotype	19, 114	3.55***	3.88***

***Significant at $P < 0.001$.

Table 17. Difference in lint yield (kg ha^{-1}) of twenty cotton genotypes grown at College Station, TX in 2006.

Genotype	Lint yield (kg ha^{-1})		
	Dryland	**Irrigated**	**difference**
Acala 1517-99	622 bcdef†	1031 cde	-409 cdef‡
Acala Maxxa	363 hi	695 fg	-332 cd
AllTex Atlas	620 bcdef	1053 cde	-433 defg
DP 14	563 defg	679 fg	-116 a
DP 491	717 abc	1363 a	-646 jk
DP 50	563 defg	854 ef	-291 bc
DP 90	640 abcde	1035 cde	-395 cde
FM 832	719 abc	1237 abc	-518 efghij
G. arboreum	17 j	113 h	-96 a‡
MD51ne	576 defg	1117 bcd	-542 fghij
Pima S-6	332 i	494 g	-162 ab
PM HS 26	561 defg	717 fg	-157 ij
PSC 355	745 ab	1340 ab	-595 ab
SG 747	499 fgh	1069 cde	-570 hij
Stv 213	543 efg	1028 cde	-485 efghi
TAM 89E-51	582 cdefg	1104 cd	-522 efghij
TAM 94L-25	489 fgh	1058 cde	-568 ghij
TAM 96WD-69s	775 a	1228 abc	-453 defgh
Tamcot 22	685 abcd	1432 a	-747 k
Tamcot CAMD-E	475 gh	890 def	-414 cdef
Mean	554	977	
Standard deviation	174	308	

† Means in the same column followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

‡ Means in the same column followed by the same letter are not different according to Fisher's LSD ($P < 0.05$).

G. arboreum had the lowest lint yields across all experiments and also has consistently high Fv'/Fm' values indicating that it is not drought tolerant. G. arboreum's low yields and high Fv'/Fm' values under irrigated conditions may indicate a general lack of adaptation to Texas and therefore disrupt our ability to characterize its drought tolerance with the Burke method. Tamcot 22's low Fv'/Fm' values and drought tolerance classification are confirmed by high lint yields under DL and IRR conditions at CS and LUB in 2006.

Fluorescence and Lint Yield Correlations

Significant correlations between lint yield and Fv'/Fm' values were found with 5 of the 18 year, location, treatment, growth stage combinations (Table 19). A correlation does not appear to be more likely to be found under DL or IRR conditions nor at mid-bloom or late bloom.

Table 18. Difference in lint yield (kg ha^{-1}) of twenty cotton genotypes grown at Lubbock, TX in 2006.

Genotype	Lint yield (kg ha^{-1})		
	Dryland	**Irrigated**	**difference**
Acala 1517-99	907 def†	2461 def	-1554 c‡
Acala Maxxa	755 f	2758 cde	-2003 def
AllTex Atlas	937 cdef	2931 abcd	-1994 de
DP 14	837 def	2749 cde	-1912 d
DP 491	1202 ab	3405 ab	-2202 defgh
DP 50	829 ef	2746 cde	-1917 d
DP 90	944 cdef	3096 abc	-2151 defgh
FM 832	1288 a	3277 abc	-1989 de
G. arboreum	160 g	787 g	-627 a
MD51ne	1001 bcde	3079 abc	-2078 defgh
Pima S-6	745 f	2217 ef	-1472 efgh
PM HS 26	732 f	3032 abcd	-2300 gh
PSC 355	1007 bcde	3328 abc	-2321 c
SG 747	990 bcde	3122 abc	-2132 defgh
Stv 213	906 def	2914 bcd	-2009 defg
TAM 89E-51	1136 def	3529 abc	-2393 defgh
TAM 94L-25	874 def	3062 abc	-2188 fgh
TAM 96WD-69s	855 cdef	3165 bcd	-2311 d
Tamcot 22	945 abc	2925 a	-1980 h
Tamcot CAMD-E	1059 bcd	2095 f	-1036 b
Mean	905	2834	
Standard deviation	232	596	

† Means in the same column followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

‡ Means in the same column followed by the same letter are not different according to Fisher's LSD ($P < 0.05$).

Table 19. Pearson correlation coefficients for lint yield (kg ha^{-1}) versus Fv'/Fm' for 19 cotton genotypes grown under irrigated (IRR) and dryland (DL) conditions at College Station, TX (CS) in 2005 and twenty cotton genotypes grown under irrigated and dryland conditions at College Station, TX and Lubbock, TX (LUB) in 2006 and 2007.

Year	Location	Treatment	Stage	N	Lint yield:Fv'/Fm' r
2005	CS	DL	Mid-bloom	19	-0.6941***
2005	CS	DL	Late bloom	19	-0.4005
2005	CS	IRR	Mid-bloom	19	-0.2128
2005	CS	IRR	Late bloom	19	-0.0072
2006	CS	DL	Mid-bloom	20	-0.6598**
2006	CS	DL	Late bloom	20	-0.6424**
2006	CS	IRR	Mid-bloom	20	-0.6436**
2006	CS	IRR	Late bloom	20	-0.3711
2006	LUB	DL	Mid-bloom	20	-0.1584
2006	LUB	DL	Late bloom	20	-0.2903
2006	LUB	IRR	Mid-bloom	20	-0.4206
2006	LUB	IRR	Late bloom	20	-0.6253**

**Significant at $P < 0.01$.

*** Significant at $P < 0.001$.

Fiber Properties ANOVA

The variance analysis for micronaire at CS in 2005 indicated significant genotypic effects (Table 20). G. arboreum had a higher ($p<.05$) micronaire value than all other genotypes in the test as expected, while Pima S-6 had the lowest micronaire, although not different than DP 14 and Acala Maxxa (Table 21). Genotypes averaged 4.4 mic, even with *G. arboreum's* 5.6 included in the average and all upland genotypes produced micronaires within the base range of 3.5 to 4.9 units. This is not unexpected, since breeders strive to select genotypes, discounting *G. arboreum,* with micronaire with a range of 3.5 to 4.9 units for marketing purposes. Since breeders test progeny rows and strains over multiple locations and multiple years prior to the decision to release, one would expect somewhat random reaction to irrigation across a number of genotypes.

Genotypes varied in micronaire values when grown at College Station in 2006 and the AOV indicated a significant treatment x genotype interaction although irrigation treatment did not impact micronaire when genotypes were pooled (Table 22). *G. arboreum* again was well outside the base range of 3.5 – 4.9 but most other genotypes were within the base range (Table 23). Under dryland conditions, DP 90, SG 747, PM HS 26, and DP 50 were slightly high mic while SG 747, DP 50, MD51ne, and Pima S-6 were displayed slightly high values under irrigated conditions at College Station this year. Seven genotypes, including TAM 94L-25 and Tamcot CAMD-E, had numerically higher micronaire values when irrigated which was different ($p<0.05$) in direction of response than seven genotypes, including Tamcot 22 and three Deltapine genotypes. The micronaire values of FM 832 and TAM 96WD-69s were not affected by irrigation

Table 20. Variance analysis for micronaire (units) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Source	df	Miconaire
		F
Genotype	18, 36	32.66***
Treatment	1, 2	1.98
Treatment x Genotype	18, 36	1.85

***Significant at $P < 0.001$.

Table 21. Micronaire (units) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Genotype	Micronaire
G. arboreum	5.3 a‡
PSC 355	4.9 b
AllTex Atlas	4.8 bc
SG 747	4.8 bc
DP 90	4.7 cd
MD51ne	4.7 cd
PM HS 26	4.5 de
TAM 89E-51	4.5 de
TAM 96WD-69s	4.5 de
FM 832	4.5 de
TAM 94L-25	4.4 ef
DP 50	4.3 ef
Tamcot 22	4.3 ef
Stv 213	4.3 f
Acala 1517-99	4.2 f
Tamcot CAMD-E	4.2 f
Acala Maxxa	3.9 g
DP 14	3.8 g
Pima S-6	3.7 g
Mean	4.4
Standard deviation	0.4

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 22. Variance analysis for micronaire (units) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX and Lubbock, TX in 2006.

		CS	LUB
Source	**df**	**Micronaire**	
		F	
Genotype	19, 38	25.51***	15.38***
Treatment	1, 2	2.73	1.00
Treatment x Genotype	19, 38	2.35*	4.21***

*Significant at $P < 0.05$.
***Significant at $P < 0.001$.

along with eight other genotypes. While separating the interaction elements revealed which genotypes responded the same to irrigation relative to micronaire values, no trends such as germplasm pool origin could be determined.

Similar results were obtained at the LUB location in 2006, with significant effects due to genotype and a significant treatment x genotype interaction (Table 22). Again, most genotypes exhibited mic values within the 3.5 – 4.9 base range under both irrigation regimes (Table 24). Exceptions were SG 747, PM HS 26, DP 50 under irrigated conditions, and Pima S-6 and *G. arboreum.* The significant interaction was again a direction of response differential among the genotypes. The majority of the genotypes responded the same to irrigation as indicated by the separation of the interaction elements indicated as the difference in Table 24. SG 747 displayed the same micronaire value under irrigated and dryland conditions and thus a difference of 0.0. Fourteen other genotypes were not different ($p<.05$) in response. PSC 355 responded differently with a difference of 0.6 units when grown dryland, while DP 50, DP 90, TAM 96WD-69s, and arboreum expressed lower micronaire when grown dryland.

The analysis of variance for UHM at CS in 2005 showed genotypes differed in fiber length but irrigation treatments did not affect length (Table 25). Pima S-6 had the longest UHM at 33.0 mm and was different than all other genotypes in the test (Table 26). TAM 94L-25 had numerically the longest UHM at 30.9 mm among the upland types but was not different than FM 832 and Acala 1517-99. G. arboreum had the shortest UHM but surprisingly was not different ($p<.05$) than AllTex Atlas, Stv 213, or PM HS 26.

Table 23. Difference in micronaire (units) of twenty cotton genotypes grown at College Station, TX in 2006.

Genotype	Micronaire (units)		
	Dryland	**Irrigated**	**difference**
Acala 1517-99	4.3 hi†	4.2 ghi	0.2bc‡
Acala Maxxa	4.3 ij	4.1 hi	0.2bc
AllTex Atlas	4.7 efg	4.8 bcde	-0.1de
DP 14	4.6 fgh	4.3 fghi	0.3ab
DP 491	4.9 def	4.5 cdefgh	0.3ab
DP 50	5.2 bcd	5.0 bc	0.2bc
DP 90	5.3 bc	4.8 bcd	0.5a
FM 832	4.4 hi	4.4 efghi	0.0cd
G. arboreum	5.7 a	6.0 a	-0.3ef
MD51ne	4.8 efg	5.0 bc	-0.2de
Pima S-6	4.7 efg	5.0 bc	-0.3ef
PM HS 26	5.0 cde	4.7 bcdef	0.3ab
PSC 355	3.5 k	3.5 j	0.0cd
SG 747	5.4 ab	5.0 bc	0.4ab
Stv 213	4.7 def	4.4 efghi	0.4ab
TAM 89E-51	4.4 hi	4.4 defghi	0.0cd
TAM 94L-25	4.3 hi	4.6 bcdef	-0.3ef
TAM 96WD-69s	4.6 fgh	4.6 bcdefg	0.0cd
Tamcot 22	4.5 ghi	4.1 i	0.5a
Tamcot CAMD-E	4.0 j	4.5 defghi	-0.5f
Mean	4.7	4.6	
Standard deviation	0.5	0.5	

† Means in the same column followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

‡ Means in the same column followed by the same letter are not different according to Fisher's LSD ($P < 0.05$).

Table 24. Difference in micronaire (units) of twenty cotton genotypes grown at Lubbock, TX in 2006.

Genotype	Micronaire (units)		
	Dryland	**Irrigated**	**difference**
Acala 1517-99	4.7 cdef	4.4 ef	0.3 b
Acala Maxxa	4.6 efg	4.5 def	0.1 bcd
AllTex Atlas	4.8 bcdef	4.9 bcde	0.0 cde
DP 14	4.5 fg	4.6 cdef	-0.1 def
DP 491	4.7 cdefg	4.6 cdef	0.1 bcd
DP 50	4.9 bcde	5.2 b	-0.3 fgh
DP 90	4.5 fg	4.8 bcde	-0.4 gh
FM 832	4.6 efg	4.4 ef	0.1 bcd
G. arboreum	5.4 a	7.0 a	-1.7 i
MD51ne	4.7 cdefg	4.6 def	0.1 bcd
Pima S-6	5.0 g	5.1 g	-0.1 def
PM HS 26	5.1 abcd	5.3 bc	-0.3 fgh
PSC 355	4.3 abc	3.7 b	0.6 a
SG 747	5.2 ab	5.2 b	0.0 cde
Stv 213	4.8 bcdef	4.6 cdef	0.2 bc
TAM 89E-51	4.8 bcdef	4.6 def	0.3 b
TAM 94L-25	4.7 cdef	4.9 bcde	-0.2 efg
TAM 96WD-69s	4.5 fg	4.9 bcd	-0.5 h
Tamcot 22	4.6 efg	4.6 cdef	0.0 cde
Tamcot CAMD-E	4.6 defg	4.3 f	0.3 b
Mean	4.7	4.8	
Standard deviation	0.2	0.4	

† Means in the same column followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

‡ Means in the same column followed by the same letter are not different according to Fisher's LSD ($P < 0.05$).

Table 25. Variance analysis for upper half mean length (mm) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Source	df	UHM
		F
Genotype	18, 36	8.19***
Treatment	1, 2	0.25
Treatment x Genotype	18, 36	0.56

***Significant at $P < 0.001$.

Genotype and treatments varied ($p<.001$ and .05, respectively) for UHM length at CS in 2006 (Table 27). Again, Pima S-6 had the longest UHM at 33.2 mm, and was different than all other genotypes, while PM HS 26 averaged only 25.7 mm and was not different than four other genotypes, which included *G. arboreum* and three uplands (Table 28). Among the upland genotypes, FM 832, TAM 94L-25, and Acala 1517-99 had the longest UHM lengths with Acala 1517-99 being not longer than DP 491 ($p<.05$). Average UHM length under irrigated conditions was longer ($p<.05$) at 28.4 mm than when grown without supplemental irrigation (27.1 mm) at College Station in 2006.

The variance analysis of UHM at LUB in 2006 revealed significant genotype and treatment effects (Table 27). Once again, Pima S-6 had the largest UHM and TAM 94L-25 had numerically the longest fibers among the upland types and not different than FM 832 and Acala 1517-99 (Table 29). G. arboreum had the lowest UHM and was shorter than all other genotypes. AllTex Atlas had the lowest UHM among the upland types and was not different than TAM 96WD-69s, DP 14, and Stv 213.

Analysis of variance for UI at CS in 2005 showed differences existed among genotypes (Table 30). FM 832 had the highest UI but was not different than three other upland genotypes and Pima S-6 (Table 31). G. arboreum had the lowest UI and was lower than all other genotypes. Stv 213 had the lowest UI among the upland types but was not different than the majority of genotypes tested. Uniformity of fiber lengths has not been a selection criterion among breeders of upland cotton. It has received considerable verbal attention in recent years since U.S. cotton now competes for market share on the world market and some proponents believe that improving the uniformity of

Table 26. Upper half mean length (mm) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Genotype	UHM
Pima S-6	33.0 a‡
TAM 94L-25	30.9 b
FM 832	30.8 b
Acala 1517-99	30.1 bc
Acala Maxxa	28.8 cd
MD51ne	28.5 cd
DP 50	28.4 cd
SG 747	28.4 d
Tamcot 22	28.4 d
DP 14	28.3 d
PSC 355	27.9 de
TAM 89E-51	27.9 de
DP 90	27.9 de
Tamcot CAMD-E	27.8 de
TAM 96WD-69s	27.7 de
AllTex Atlas	27.4 def
Stv 213	27.2 def
PM HS 26	26.5 ef
G. arboreum	25.8 f
Mean	28.5
Standard deviation	1.7

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 27. Variance analysis for upper half mean length (mm) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX and Lubbock, TX in 2006.

Source	df	CS UHM	LUB
		F	
Genotype	19, 38	22.66***	18.58***
Treatment	1, 2	56.54*	87.02*
Treatment x Genotype	19, 38	0.74	1.17

*Significant at $P < 0.05$.
***Significant at $P < 0.001$.

Table 28. Upper half mean length (mm) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2006.

Genotype	UHM
Pima S-6	33.2 a‡
FM 832	29.8 b
TAM 94L-25	29.7 b
Acala 1517-99	29.3 bc
DP 491	28.3 cd
Acala Maxxa	28.2 d
TAM 89E-51	27.9 de
Tamcot 22	27.7 def
DP 50	27.5 defg
DP 14	27.3 defgh
SG 747	27.3 defgh
PSC 355	27.0 efghi
MD51ne	26.9 efghi
DP 90	26.8 fghi
TAM 96WD-69s	26.6 ghij
Tamcot CAMD-E	26.5 ghij
AllTex Atlas	26.4 hij
G. arboreum	26.4 hij
Stv 213	26.2 ij
PM HS 26	25.7 j
Mean	27.7
Standard deviation	1.7

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 29. Upper half mean length (mm) of twenty cotton genotypes grown under dryland and irrigated conditions at Lubbock, TX in 2006.

Genotype	UHM
Pima S-6	34.1 a‡
TAM 94L-25	30.7 b
Acala 1517-99	30.4 bc
FM 832	29.7 bcd
DP 491	29.4 cde
MD51ne	29.0 def
PM HS 26	28.7 defg
Tamcot 22	28.6 defg
Acala Maxxa	28.3 efgh
DP 50	28.3 efgh
Tamcot CAMD-E	28.3 efgh
DP 90	28.1 fgh
SG 747	27.9 fghi
TAM 89E-51	27.7 ghi
PSC 355	27.7 ghi
Stv 213	27.3 hij
DP 14	27.2 hij
TAM 96WD-69s	26.9 ij
AllTex Atlas	26.4 j
G. arboreum	25.0 k
Mean	28.5
Standard deviation	1.9

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 30. Variance analysis for uniformity index (%) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Source	df	UI
		F
Genotype	18, 36	7.95***
Treatment	1, 2	0.37
Treatment x Genotype	18, 36	0.79

***Significant at $P < 0.001$.

Table 31. Uniformity index (%) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Genotype	UI
FM 832	84.8 a‡
Pima S-6	84.7 a
Acala 1517-99	83.5 ab
PSC 355	83.3 abc
Acala Maxxa	83.3 abcd
SG 747	83.1 bcde
AllTex Atlas	82.9 bcdef
PM HS 26	82.8 bcdef
DP 90	82.7 bcdef
TAM 94L-25	82.6 bcdef
Tamcot 22	82.6 bcdef
DP 50	82.2 bcdef
MD51ne	81.9 cdef
Tamcot CAMD-E	81.8 cdef
DP 14	81.8 cdef
TAM 96WD-69s	81.7 def
TAM 89E-51	81.6 ef
Stv 213	81.4 f
G. arboreum	77.3 g
Mean	82.4
Standard deviation	1.6

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

fiber length would positively impact spinning performance and reduce wastage of fibers during processing.

Uniformity of fiber lengths, UI, varied across genotypes when grown at CS in 2006 (Table 32). Irrigation treatment did not affect UI and genotypes responded similarly across the two irrigation treatments. Genotype means for UI were similar in 2006 as in 2005 at CS and it is interesting to note that in both years that three of the longest fibered genotypes, Pima S-6, FM 832, and Acala 1517-99, also had high UI values and were not different (Tables 31 and 33). G. arboreum again had a significantly lower UI than all other genotypes. Tamcot CAMD-E had the lowest UI among the upland types but was not different than the majority of genotypes tested.

Genotypes were different for UI at LUB in 2006 while treatments and their interaction were non significant (Table 32). As in CS, Pima S-6 had the highest numerical UI and G. arboreum had the lowest numerical UI but both were than most other genotypes (Table 34).

Genotypic differences in HVI STR were indicated by the variance analysis at CS in 2005 and 2006, and in LUB in 2006 (Tables 35 and 37). Irrigation treatment did not affect STR across this set of genotypes and genotypes responded the same to irrigation. While there were differences in rank across the experiments, genotypes generally performed as expected for this fiber trait (Tables 36, 38, and 39). Pima S-6 was the strongest genotype in all tests. Among the strongest upland genotypes were Acala 1517-99, FM 832 Acala Maxxa, and MD51ne. The genotypes with the weakest fibers included

Table 32. Variance analysis for uniformity index (%) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX and Lubbock, TX in 2006.

Source	df	CS UI	LUB
		F	
Genotype	19, 38	27.50***	4.52***
Treatment	1, 2	16.40	18.46
Treatment x Genotype	19, 38	1.19	1.37

***Significant at $P < 0.001$.

Table 33. Uniformity index (%) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2006.

Genotype	UI
Pima S-6	84.0 a‡
FM 832	83.4 ab
Acala 1517-99	82.8 abc
Acala Maxxa	82.7 bcd
PSC 355	82.5 bcde
AllTex Atlas	82.4 bcdef
TAM 94L-25	82.1 bcdefg
TAM 89E-51	82.1 bcdefg
DP 50	81.9 cdefgh
SG 747	81.7 cdefgh
PM HS 26	81.7 cdefgh
Tamcot 22	81.5 defgh
TAM 96WD-69s	81.3 efgh
DP 14	81.1 fgh
MD51ne	81.1 gh
DP 491	81.0 gh
DP 90	80.9 gh
Stv 213	80.8 gh
Tamcot CAMD-E	80.6 h
G. arboreum	71.9 i
Mean	81.4
Standard deviation	2.4

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 34. Uniformity index (%) of twenty cotton genotypes grown under dryland and irrigated conditions at Lubbock, TX in 2006.

Genotype	UI
Pima S-6	83.7 a‡
Acala 1517-99	83.4 ab
PSC 355	83.2 abc
TAM 94L-25	83.0 abcd
MD51ne	82.8 abcd
FM 832	82.7 abcd
SG 747	82.6 abcde
DP 50	82.5 abcde
DP 90	82.4 abcde
Acala Maxxa	82.3 abcde
TAM 89E-51	82.3 abcde
PM HS 26	82.1 abcde
Stv 213	82.0 abcde
Tamcot 22	81.9 bcde
DP 491	81.8 bcde
TAM 96WD-69s	81.8 bcde
AllTex Atlas	81.5 cde
Tamcot CAMD-E	81.2 de
DP 14	80.9 e
G. arboreum	77.4 f
Mean	82.1
Standard deviation	1.3

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 35. Variance analysis for strength (kN·m kg^{-1}) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Source	df	STR
		F
Genotype	18, 36	19.12***
Treatment	1, 2	0.55
Treatment x Genotype	18, 36	0.46

***Significant at $P < 0.001$.

Table 36. Strength (kN·m kg^{-1}) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Genotype	STR
Pima S-6	353 a‡
Acala Maxxa	300 b
Acala 1517-99	293 bc
FM 832	292 bc
MD51ne	291 bc
TAM 94L-25	290 bc
DP 90	281 cd
AllTex Atlas	279 cd
TAM 89E-51	276 cd
TAM 96WD-69s	271 de
PM HS 26	269 de
PSC 355	265 def
DP 50	256 efg
Tamcot CAMD-E	256 efg
SG 747	251 fg
DP 14	248 fg
G. arboreum	246 g
Stv 213	244 g
Tamcot 22	243 g
Mean	274
Standard deviation	27

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 37. Variance analysis for strength (kN·m kg^{-1}) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX and Lubbock, TX in 2006.

Source	df	CS STR	LUB
		F	
Genotype	19, 38	37.67***	18.22***
Treatment	1, 2	2.74	0.14
Treatment x Genotype	19, 38	1.00	1.16

***Significant at $P < 0.001$.

Table 38. Strength (kN·m kg^{-1}) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2006.

Genotype	STR
Pima S-6	385 a‡
Acala 1517-99	325 b
FM 832	321 b
Acala Maxxa	312 bc
TAM 89E-51	297 cd
DP 491	295 de
TAM 94L-25	295 de
MD51ne	290 de
AllTex Atlas	289 de
DP 90	286 de
PM HS 26	284 de
PSC 355	281 def
TAM 96WD-69s	280 efg
Tamcot 22	268 fgh
SG 747	265 gh
DP 14	259 h
Tamcot CAMD-E	254 h
DP 50	254 h
Stv 213	252 h
G. arboreum	223 i
Mean	286
Standard deviation	34

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 39. Strength (kN·m kg^{-1}) of twenty cotton genotypes grown under dryland and irrigated conditions at Lubbock, TX in 2006.

Genotype	STR
Pima S-6	382 a‡
Acala 1517-99	339 b
FM 832	322 bc
PM HS 26	316 cd
MD51ne	309 cde
DP 90	304 cdef
TAM 89E-51	301 defg
TAM 94L-25	300 defg
DP 491	295 efgh
Acala Maxxa	294 efgh
AllTex Atlas	285 fghi
TAM 96WD-69s	283 ghi
PSC 355	283 ghi
Tamcot CAMD-E	280 hij
DP 14	275 hij
Tamcot 22	272 ijk
DP 50	272 ijk
G. arboreum	260 jk
Stv 213	260 jk
SG 747	253 k
Mean	294
Standard deviation	30

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

G. arboreum, DP 50, Tamcot 22, Tamcot CAMD-E, and Stv 213. Again, these rankings were expected since many fiber properties are stable across an array of environments.

ELO is another HVI fiber measurement for which breeders have exacted little if any selection pressure. ELO measurements varied among genotypes at CS in 2005 and 2006, and LUB in 2006 (Tables 40 and 42). As expected, irrigation treatment did not affect ELO among nor across these genotypes. PSC 355, SG 747, and G. arboreum consistently elongated more before fiber breakage occurred than most genotypes and TAM 94L-25 was consistently expressed the lowest numerical value for ELO across these environments (Tables 41, 43, and 44). Several of the high strength genotypes were similar to TAM 94L-25.

SFC is a recent and welcomed addition to HVI data provided to plant breeders and selection for this trait is expected to improve UI. However, since it is another fiber trait for which breeders have not directly selected, one would expect the results to be species related or appear random.

Genotypic differences for SFC occurred at CS in 2005 and 2006, and at LUB in 2006 (Tables 45 and 47). While G. arboreum, the genotype with the shortest UHM, exhibited the largest SFC and Pima S-6, the longest fiber genotype, always exhibited at least the numerically lowest SFC, the upland genotypes appear to be less predictable (Tables 46, 48, and 49). Tamcot CAMD-E, short UHM, exhibited high SCF as predicted by some literature, so did DP 491, long UHM, in 2006 at both CS and LUB. These values are informative and interesting but little variation was exhibited across the upland genotypes with the ranges within environment generally within 2 or 3 percentage points.

Table 40. Variance analysis for elongation (%) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Source	df	ELO
		F
Genotype	18, 36	13.90***
Treatment	1, 2	2.83
Treatment x Genotype	18, 36	1.24

***Significant at $P < 0.001$.

Table 41. Elongation (%) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Genotype	ELO
PSC 355	6.90 a‡
PM HS 26	6.85 ab
G. arboreum	6.68 abc
SG 747	6.65 abcd
DP 50	6.45 abcde
AllTex Atlas	6.30 bcdef
TAM 96WD-69s	6.15 cdefg
DP 14	6.08 defg
Tamcot 22	6.05 efg
MD51ne	5.85 fg
Stv 213	5.63 gh
Pima S-6	5.58 gh
Acala 1517-99	5.23 hi
TAM 89E-51	5.08 hi
Tamcot CAMD-E	5.05 hi
Acala Maxxa	4.98 i
FM 832	4.80 i
DP 90	4.68 i
TAM 94L-25	4.65 i
Mean	5.77
Standard deviation	0.76

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 42. Variance analysis for elongation (%) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX and Lubbock, TX in 2006.

Source	df	CS ELO	LUB
		F	
Genotype	19, 38	15.49***	25.59***
Treatment	1, 2	0.00	3.36
Treatment x Genotype	19, 38	0.66	1.40

***Significant at $P < 0.001$.

Table 43. Elongation (%) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2006.

Genotype	ELO
PSC 355	6.35 a‡
TAM 96WD-69s	6.10 ab
PM HS 26	6.03 ab
G. arboreum	6.00 ab
SG 747	5.95 ab
AllTex Atlas	5.83 bc
Tamcot 22	5.40 cd
DP 50	5.38 cd
DP 14	5.20 de
Stv 213	5.13 def
MD51ne	5.03 defg
TAM 89E-51	4.95 defg
Acala 1517-99	4.88 efgh
Pima S-6	4.78 efgh
Tamcot CAMD-E	4.73 fgh
Acala Maxxa	4.68 fghi
DP 491	4.58 ghi
DP 90	4.45 hi
FM 832	4.43 hi
TAM 94L-25	4.23 i
Mean	5.20
Standard deviation	0.64

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 44. Elongation (%) of twenty cotton genotypes grown under dryland and irrigated conditions at Lubbock, TX in 2006.

Genotype	ELO
TAM 96WD-69s	7.80 a‡
PSC 355	7.75 a
SG 747	7.73 a
G. arboreum	7.20 b
Tamcot 22	7.18 bc
AllTex Atlas	7.00 bc
PM HS 26	6.83 bc
DP 14	6.78 bc
DP 50	6.73 c
Stv 213	6.25 d
DP 90	6.23 d
MD51ne	6.18 d
FM 832	5.95 de
TAM 89E-51	5.95 de
Acala 1517-99	5.93 de
DP 491	5.88 de
Pima S-6	5.83 de
Tamcot CAMD-E	5.63 e
Acala Maxxa	5.50 e
TAM 94L-25	4.98 f
Mean	6.46
Standard deviation	0.80

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 45. Variance analysis for short fiber content (%) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Source	df	SFC
		F
Genotype	18, 36	4.61***
Treatment	1, 2	0.21
Treatment x Genotype	18, 36	0.66

***Significant at $P < 0.001$.

Table 46. Short fiber content (%) of 19 cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2005.

Genotype	SFC
G. arboreum	14.63 a‡
Stv 213	10.20 b
DP 14	10.05 bc
TAM 96WD-69s	9.45 bcd
DP 50	9.30 bcde
TAM 89E-51	8.80 bcdef
Tamcot 22	8.10 bcdef
PSC 355	7.90 bcdefg
SG 747	7.83 bcdefg
AllTex Atlas	7.80 bcdefg
Tamcot CAMD-E	7.43 bcdefg
MD51ne	7.40 bcdefg
DP 90	7.33 bcdefg
Acala Maxxa	7.05 cdefg
TAM 94L-25	6.48 defg
PM HS 26	6.25 efgh
Acala 1517-99	6.13 fgh
FM 832	4.93 gh
Pima S-6	3.30 h
Mean	7.91
Standard deviation	2.35

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 47. Variance analysis for short fiber content (%) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX and Lubbock, TX in 2006.

Source	df	CS	LUB
		SFC	
		F	
Genotype	19, 38	13.20***	4.90***
Treatment	1, 2	14.19	29.83*
Treatment x Genotype	19, 38	0.90	1.41

*Significant at $P < 0.05$.
***Significant at $P < 0.001$.

Table 48. Short fiber content (%) of twenty cotton genotypes grown under dryland and irrigated conditions at College Station, TX in 2006.

Genotype	SFC
G. arboreum	13.80 a‡
Tamcot CAMD-E	10.10 b
Stv 213	9.58 bc
DP 90	9.38 bcd
Tamcot 22	9.33 bcd
DP 491	8.95 cde
DP 14	8.83 cdef
DP 50	8.80 cdefg
TAM 96WD-69s	8.63 cdefg
PM HS 26	8.58 cdefg
MD51ne	8.50 cdefg
TAM 89E-51	8.50 cdefg
SG 747	8.48 defg
TAM 94L-25	8.20 efgh
PSC 355	8.18 efgh
AllTex Atlas	7.95 efgh
Acala Maxxa	7.93 efgh
Acala 1517-99	7.78 fgh
FM 832	7.73 gh
Pima S-6	7.15 h
Mean	8.82
Standard deviation	1.37

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 49. Short fiber content (%) of twenty cotton genotypes grown under dryland and irrigated conditions at Lubbock, TX in 2006.

Genotype	SFC
G. arboreum	10.23 a‡
DP 14	9.05 b
Acala Maxxa	8.68 bc
DP 491	8.45 bcd
TAM 89E-51	8.43 bcd
TAM 96WD-69s	8.40 bcd
Tamcot CAMD-E	8.35 bcde
Tamcot 22	8.33 bcde
DP 90	8.30 bcde
AllTex Atlas	8.23 bcde
Stv 213	8.20 bcde
SG 747	8.00 cdef
DP 50	7.93 cdefg
FM 832	7.88 cdefg
MD51ne	7.83 cdefg
TAM 94L-25	7.73 defg
PM HS 26	7.45 efg
Acala 1517-99	7.25 fg
PSC 355	7.15 fg
Pima S-6	7.05 g
Mean	8.14
Standard deviation	0.71

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Fluorescence and Fiber Properties Correlations

Given that fluorescence values could be predictive of a cotton genotype's degree of resistance to stress and given the range in fiber properties across the genotypes included in this study, the relationships between fluorescence and fiber properties were explored using Pearson correlations. If a genotype was drought stress resistant then one could reasonably expect that genotype to suffer less from periodic droughts and therefore produce a better fiber product. However, that was not evident in these data. MIC measurements were not found to correlate with Fv'/Fm' values (Table 50). UHM correlated with Fv'/Fm' values in 2006 at CS at mid-bloom and late bloom under DL conditions and at LUB under DL conditions at late bloom. UI correlated with Fv'/Fm' values in 2006 at CS under IRR and DL conditions at mid and late bloom and at LUB under irrigation at late bloom. STR measurements correlated with Fv'/Fm' values in 2006 at LUB under DL conditions at mid and late bloom. ELO percentages did not correlate with Fv'/Fm' values under any year, location, treatment, growth stage combination. SFC correlated with Fv'/Fm' values in 2006 at CS under DL and IRR conditions at mid-bloom. More frequent correlations between Fv'/Fm' values and fiber properties do not appear to occur under particular irrigation and growth stage combinations.

Table 50. Pearson correlation coefficients for micronaire (units), upper half mean length (mm), uniformity index (%), strength (kN·m kg^{-1}), elongation (%), and short fiber content (%) versus Fv'/Fm' values measured at mid-bloom (MB) and late bloom (LB) for 19 cotton genotypes grown under irrigated (IRR) and dryland (DL) conditions at College Station, TX (CS) in 2005 and twenty cotton genotypes grown under irrigated and dryland conditions at College Station, TX and Lubbock, TX (LUB) in 2006 and 2007.

Year	Location	Treatment	Stage	N	MIC: Fv'/Fm' r	UHM: Fv'/Fm' r	UI: Fv'/Fm' r	STR: Fv'/Fm' r	ELO: Fv'/Fm' r	SFC: Fv'/Fm' r
2005	CS	DL	MB	19	0.0394	0.0154	-0.2039	0.3384	0.2452	0.1112
2005	CS	DL	LB	19	0.1323	-0.0689	-0.2201	0.0917	0.2856	-0.0082
2005	CS	IRR	MB	19	0.2264	0.2132	-0.1139	0.3342	-0.0800	-0.0437
2005	CS	IRR	LB	19	0.8685	0.2063	0.2015	0.1782	0.1018	-0.1441
2006	CS	DL	MB	20	0.0905	0.1499	-0.5225*	-0.1601	0.3469	0.4924*
2006	CS	DL	LB	20	-0.3797	0.5638**	0.0742	0.3837	0.0186	-0.1156
2006	CS	IRR	MB	20	0.3650	-0.0237	-0.7207***	-0.2044	0.2161	0.6643**
2006	CS	IRR	LB	20	-0.1564	0.5088*	-0.0390	0.4033	-0.1124	-0.0483
2006	LUB	DL	MB	20	-0.0990	0.3500	0.2724	0.5750**	-0.2541	-0.2558
2006	LUB	DL	LB	20	-0.0954	0.4603*	0.3184	0.4644*	0.0075	-0.3156
2006	LUB	IRR	MB	20	-0.0019	0.1740	-0.2978	0.3270	-0.1322	0.0336
2006	LUB	IRR	LB	20	0.2461	0.1381	-0.4640*	0.1918	0.0417	0.3482

*Significant at $P < 0.05$.
**Significant at $P < 0.01$.
*** Significant at $P < 0.001$.

Diallel

The diallel evaluation for combining ability for Fv'/Fm' involved six genotypes. Two of the genotypes, TAM 89E-51 and Tamcot 22 were generally consistent in their ranking for Fv'/Fm' values (Tables 3 and 5), indicating that they were drought susceptible and drought resistant, respectively. To further solidify that conclusion, individual plants expressing higher (hi) or lower (lo) values within each genotype were selected for this study. The resulting four entries along with DP 491 and Tamcot CAMD-E, which were assumed to be drought tolerant and drought susceptible, respectively, at the initiation of the study were combined in a half diallel fashion. Fv'/Fm' values did not differ among parents nor their F_1s at hour 3 or hour 5 and no GCA nor SCA effects were detected (Table 51). Differences between parents were perhaps not large enough to enable the detection of significant GCA and SCA effects (Tables 52 and 53).

Burke's method may allow scientists to verify tolerance and separate genotypes into broad groups but may not offer sufficient ability to differentiate between genotypes for breeding purposes. Further evaluation of more diverse germplasm may yield parents suitably divergent in their Fv'/Fm' values for further genetic evaluation. The ability to differentiate between genotypes in the diallel and in the progeny test discussed in the next section was likely hindered by the occurrence of 0.61 cm and 0.67 cm of rainfall occurring five days prior to sampling at CS and LUB, respectively. However, such events would confound breeding nurseries of any size sufficient to require field plantings. Though GxE interactions were present in this analysis, genotypic differences

and environmental interactions have been discussed in greater detail in previous sections.

Table 51. Analyses of variance of diallel crosses among 6 upland cotton genotypes for Fv'/Fm' measurements taken after 3 and 5 hours of incubation at College Station, TX and Lubbock, TX in 2007.

Source	df	Hour 3 Mean squares	Hour 5 Mean squares
Environments (E)	1	42.185**	51.958**
Error A	6	0.0054	0.0051
Genotypes (G)	20	0.0041**	0.0021*
Parents (P)	5	0.0079	0.0041
P vs F_1	1	0.0003	0.0006
F_1	14	0.0025	0.0014
GCA	5	0.0039	0.0012
SCA	9	0.0018	0.0017
G x E	20	0.0015	0.0023*
P x E	5	0.0031*	0.0044**
P vs F_1 x E	1	0.0029	0.0080**
F_1 x E	14	0.0012	0.0015
GCA x E	5	0.0015	0.0014
SCA x E	9	0.0010	0.0015
Error B	111	0.0013	0.0012

*, ** Significant at the 0.05 and 0.01 probability level, respectively.

Table 52. Mean hour 3 Fv'/Fm' of six upland cotton genotypes and one set of all possible single crosses among them measured at College Station, TX and Lubbock, TX in 2007.

Parent	TAM 89E-51hi	TAM 89E-51lo	TAMCOT 22hi	TAMCOT 22lo	DP 491	TAM CAMD-E
	Fv'/Fm'					
TAM 89E-51hi	0.272	0.229	0.247	0.252	0.215	0.257
TAM 89E-51lo		0.260	0.194	0.231	0.214	0.241
TAMCOT 22hi			0.205	0.200	0.230	0.222
TAMCOT 22lo				0.202	0.212	0.234
DP 491					0.199	0.214
TAM CAMD-E						0.237

Table 53. Mean hour 5 Fv'/Fm' of six upland cotton genotypes and one set of all possible single crosses among them measured at College Station, TX and Lubbock, TX in 2007.

Parent	TAM 89E-51hi	TAM 89E-51lo	TAMCOT 22hi	TAMCOT 22lo	DP 491	TAM CAMD-E
	Fv'/Fm'					
TAM 89E-51hi	0.156	0.146	0.160	0.175	0.143	0.145
TAM 89E-51lo		0.176	0.122	0.143	0.145	0.149
TAMCOT 22hi			0.122	0.124	0.156	0.141
TAMCOT 22lo				0.125	0.128	0.158
DP 491					0.119	0.138
TAM CAMD-E						0.147

Progeny Test

Although TAM 89E-52 and Tamcot 22 were identified generally as drought susceptible and resistant, respectively, (Tables 3 and 5), overlapping variability for Fv'/Fm' values within these two genotypes grown under greenhouse conditions remained. Thus, 100 plants of each were grown and selfed seed from the 10% highest and lowest within each genotype harvested for progeny testing under field conditions in 2007. Genotype differences were found both at CS and LUB in 2007 among progeny test entries (Tables 54). TAM 89E-51 hi and low fluorescence selections were not different than the TAM 89E-51 check at CS or LUB, and Tamcot 22 hi and lo selections were not different than the Tamcot 22 check at CS or LUB (Tables 55 and 56). At CS, the TAM 89E-51hi progeny were significantly higher in Fv'/Fm' than the Tamcot 22lo but the other entries did not differ. However, at LUB, even these two entries were not different. The weakly significant genotype difference at LUB ($p=0.0439$) is not reflected in the genotypic mean separation.

Table 54. Variance analysis for Fv'/Fm' measurement taken after 5 hours of incubation of Tamcot 22 and TAM 89E-51 and high and low selections grown at College Station, TX, and Lubbock, TX in 2007.

Source	df	LUB Fv'/Fm'	CS
		F	
Genotype	5, 162	7.92***	2.35*

* Significant at the 0.05 probability level.
*** Significant at the 0.0001 probability level.

Table 55. Fv'/Fm' measurement taken after 5 hours of incubation of Tamcot 22 and TAM 89E-51 and high and low selections grown at College Station, TX, in 2007.

Source	Fv'/Fm'
TAM 89E-51hi	0.380 a‡
TAM 89E-51	0.370 ab
TAM 89E-51lo	0.362 ab
Tamcot 22	0.352 abc
Tamcot 22hi	0.283 bc
Tamcot 22lo	0.262 c
Mean	0.335
Standard deviation	0.049

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

Table 56. Fv'/Fm' measurement taken after 5 hours of incubation of Tamcot 22 and TAM 89E-51 and high and low selections grown at Lubbock, TX, in 2007.

Source	Fv'/Fm'
TAM 89E-51lo	0.109 a‡
Tamcot 22lo	0.104 a
TAM 89E-51	0.091 a
Tamcot 22hi	0.081 a
TAM 89E-51hi	0.081 a
Tamcot 22	0.067 a
Mean	0.089
Standard deviation	0.016

‡ Means followed by the same letter are not different according to Tukey-Kramer LSD ($P < 0.05$).

CONCLUSIONS

The field experiment testing twenty genotypes yielded results complicated by genotype x treatment and year x genotype interactions. The majority of genotypes did not perform similarly under DL and IRR conditions with respect to fluorescence, yield, and quality parameters. Since different years vary in precipitation and other climatological factors, it is difficult to classify genotypes consistently across years, especially if one is interested in traits related to abiotic stress tolerance. This protocol does not overcome these obstacles.

Some genotypes tend to have high fluorescence values and others tend to have low values but the protocol was not able to consistently rank genotypes or to differentiate between the eighteen upland types in the test. At best, the data from this experiment suggest that this procedure might broadly categorize genotypes for some stress factor but it does not appear to be applicable as a predictive tool for single plant selection. Expanding the number of genotypes tested may elucidate greater diversity among upland types for fluorescence values. Testing under extreme arid conditions may aid the ability to separate genotypes since more significant differences were found under DL conditions in the 2005 tests.

Breeders have not developed distinctive drought tolerant and drought susceptible phenotypes. Perhaps when that occurs, this procedure can be modified to be a useful tool for breeders to select for abiotic stress resistance. This protocol also should be evaluated for the impact of heat, wind, or other abiotic stress, and for biotic stress such as insects or diseases on values obtained.

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