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Genetic variability in S_1 and S_2 maize (*Zea mays* L.) inbred lines under drought and irrigated conditions

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Abstract

Understanding genetic variation and its potential utilization in breeding programmes is essential for exploiting genetic variability among species and among varieties within a species. In the present investigation, 200 S_1 inbred lines of maize (*Zea mays* L.) were developed through ear-to-row progeny selection and evaluated along with nine parental lines and 16 checks during the post-rainy season of 2012 to assess genetic variability for different traits under drought and irrigated conditions. The experiment was conducted in a 15×15 lattice square design with two replications. Subsequently, 80 S_2 -generation selfed progenies, along with 12 inbred lines, three composite populations and five checks, were evaluated using a 10×10 lattice square design during the summer seasons of 2013–14 under normal and water-stress conditions. The analysis of variance revealed highly significant differences among genotypes for all 18 characters under drought conditions, whereas under irrigated conditions, 17 characters showed highly significant differences and one character showed a significant difference. Under drought conditions, high heritability coupled with high genetic advance as a percentage of the mean was observed for bulk cob weight, grain yield per plot, number of cobs per plant, anthesis–silking interval and number of kernels per row. Under irrigated conditions, high heritability coupled with high genetic advance as a percentage of the mean was recorded for bulk cob weight, grain yield per plot, cob length, number of kernels per row, number of cobs per plant, 100-seed weight and plant height. In the S_2 generation, the analysis of variance revealed highly significant differences for 17 characters, except relative water content at 60 and 90 days and number of kernel rows per cob. Under drought conditions, high heritability coupled with high genetic advance as a percentage of the mean was observed for grain yield per plot, bulk cob weight, anthesis–silking interval and grain yield per plant. Under non-stress conditions, highly significant differences were observed for seven characters, while four characters showed significant differences. High heritability coupled with high genetic advance as a percentage of the mean was recorded for grain yield per plot and bulk cob weight. These traits may therefore serve as useful selection criteria for improving grain yield in maize under both drought-stress and non-stress conditions.

Keywords: Drought, genetic variability, maize, heritability, genetic advance, grain yield, anthesis–silking interval

Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops worldwide and belongs to the tribe Maydeae of the family Poaceae. It is a monoecious, diploid species with a chromosome number of $2n = 20$ and is believed to have originated in the Americas. The crop has two closely related American relatives, *Tripsacum* (gamagrass) and teosinte (*Euchlaena*), the latter being considered its closest wild relative. The Asiatic members of the Maydeae include *Chionachne*, *Sclerachne*, *Coix*, *Trilobachne* and *Polytoca*. Maize is popularly known as the “Queen of Cereals” because of its high genetic yield potential, broad adaptability and diverse uses. As a C_4 plant, maize possesses high photosynthetic efficiency and can produce substantial biomass and grain yield across a wide range of agro-ecological environments. Maize is cultivated globally for food, feed and industrial purposes and plays a major role in supporting food security and agricultural economies. The crop is an important source of carbohydrates, proteins, oils and several industrially valuable products. Its grain is extensively used for human consumption, livestock and poultry feed, starch and oil production, biofuel, and a wide range of value-added industrial products.

With increasing population, expanding livestock and poultry industries, and growing demand for industrial raw materials, the global demand for maize is expected to continue increasing. Consequently, enhancing maize productivity and stability under diverse production environments has become a major objective of contemporary maize improvement programmes.

The increasing demand for maize must be addressed largely through improved productivity because opportunities for expanding cultivated land are limited by population growth, urbanization and environmental degradation. In many developing countries, maize production is constrained by a combination of abiotic and biotic stresses. Among these, drought is one of the most important environmental constraints affecting maize production, particularly in tropical and subtropical regions where a considerable proportion of the crop is grown under rainfed conditions. Drought stress may occur at any stage of crop development; however, its effects are particularly severe when it coincides with the flowering and grain-filling stages.

Maize is highly sensitive to water deficit during the reproductive phase. Drought stress during flowering can cause delayed silk emergence, increased anthesis-silking interval (ASI), poor pollen-silk synchrony and reduced fertilization. These effects ultimately result in a reduction in kernel number, kernel weight and grain yield. Water stress during grain filling further restricts assimilate production and translocation, thereby reducing final grain accumulation. The severity of drought-induced yield losses depends on the timing, duration and intensity of stress, as well as on the genetic constitution of the genotype and the prevailing environmental conditions. The increasing frequency and unpredictability of drought events associated with climate variability further emphasize the need to develop maize genotypes with improved drought tolerance and stable yield performance.

Drought tolerance in maize is a complex quantitative trait governed by several genes and influenced substantially by environmental conditions. Therefore, direct selection for grain yield under drought stress is often difficult because of strong genotype $\times$ environment interactions and reduced heritability under stressful conditions. The identification of secondary traits associated with drought adaptation can improve the efficiency of selection. Traits such as anthesis-silking interval, relative water content, chlorophyll retention, plant and ear height, number of cobs per plant, kernel number and grain yield have been widely considered important indicators of drought response and productivity. In particular, a shorter anthesis-silking interval, greater maintenance of leaf water status and chlorophyll content, and superior grain yield under water-limited conditions are generally associated with improved drought adaptation.

Genetic variability is the fundamental prerequisite for the genetic improvement of any crop. The success of a breeding programme depends largely on the availability of adequate genetic variation and the effective identification of superior genotypes within segregating populations. Estimates of genotypic and phenotypic coefficients of variation provide valuable information regarding the magnitude of variability present for important traits. However, the presence of variation alone does not necessarily indicate the effectiveness of selection. Heritability estimates, together with genetic advance, provide a better understanding of the relative contribution of genetic and environmental factors to the

expression of quantitative traits. High heritability coupled with high genetic advance as a percentage of the mean generally indicates the predominance of additive genetic effects and suggests that effective improvement may be achieved through phenotypic selection.

The development and evaluation of inbred lines through recurrent selection and selfing of superior plants represents an important strategy for generating improved genetic material in maize. Early-generation testing of segregating progenies under contrasting moisture regimes enables breeders to identify genotypes that combine desirable agronomic performance with drought adaptation. Evaluation under both stress and non-stress conditions is particularly important because genotypes that perform well under optimum moisture may not necessarily maintain their productivity under drought. Comparative assessment of genetic variability, heritability and genetic advance under contrasting moisture environments can therefore provide valuable information for designing effective selection strategies.

In view of the increasing importance of maize and the substantial yield losses associated with drought stress, the identification of genetically superior and drought-adapted breeding material is essential. Therefore, the present investigation was undertaken to assess the genetic variability, heritability and genetic advance for important morphological, physiological and yield-related traits in maize inbred populations evaluated under drought-stress and non-stress conditions. The study was aimed at identifying traits with a strong genetic basis and high selection potential for improving grain yield and drought tolerance in maize breeding programmes.

Water availability is one of the most important factors determining crop productivity per unit area. Although maize is relatively tolerant to water deficit during the early vegetative stages, water stress during the reproductive and grain-filling stages can severely reduce yield. The magnitude of yield reduction depends on the timing, duration and intensity of water stress, as well as on the genetic constitution of the genotype. Quaranta *et al.* (1998) ^[1] emphasized the importance of water availability for maximizing crop productivity. Khan *et al.* (2001) reported that increasing water stress adversely affected flowering time and grain yield in maize. Similarly, Tahir and Mehdi (2001) ^[2] observed significant reductions in 100-grain weight and grain yield per plant under water-limited conditions. Ramadoss *et al.* (2004) identified water stress and high temperature as major constraints to maize production and reported that drought reduced seed-set percentage, ultimately resulting in lower grain yield. Monneveux *et al.* (2005) ^[3] demonstrated significant genetic differences in yield performance under drought conditions, highlighting the potential for selection of drought-adapted genotypes. Zhang *et al.* (2008) ^[4] reported significant reductions in grain yield of maize inbred lines under drought stress, accompanied by delayed 50% silking. Hussain *et al.*, while evaluating maize inbred lines under normal and drought conditions, observed significant differences among genotypes for all the traits studied, indicating the presence of substantial genetic variability for drought response.

The availability of diverse and genetically variable source populations is fundamental to the success of any crop improvement programme. Such populations provide valuable breeding material for generating and exploiting

genetic variability for desirable traits. The assessment of genetic variability, heritability and genetic advance in source populations helps determine the relative contribution of genetic and environmental factors to trait expression and provides an indication of the potential effectiveness of selection. Conventional maize breeding programmes largely rely on the development of inbred lines through repeated selfing of genetically diverse material, followed by their evaluation using appropriate biometrical and quantitative genetic approaches. The identification of superior lines at an early stage of breeding is particularly important for improving breeding efficiency and reducing the time and resources required for the development of drought-tolerant cultivars.

In the context of increasing water scarcity and the growing frequency of drought episodes, the development of maize genotypes capable of maintaining stable productivity under water-limited conditions has become a major breeding objective. Therefore, the present investigation was undertaken to assess the extent of genetic variability and the heritability of important agronomic, physiological and yield-related traits in maize populations evaluated under drought-stress and non-stress conditions. The study was specifically aimed at identifying superior breeding lines and traits with high selection potential that could be effectively utilized in breeding programmes for the development of high-yielding and drought-tolerant maize genotypes.

Material and Methods

Experimental Site and Weather Conditions

The investigation was conducted at the experimental fields of the Botanical Garden, Main Agricultural Research Station (MARS), University of Agricultural Sciences, Dharwad, Karnataka, India. The first experiment was conducted during the post-rainy season of 2012–2013. During the crop growth period, the minimum and maximum temperatures ranged from 14.8 to 29.5 °C, and a total rainfall of 201.1 mm was received.

A second experiment was conducted at the same location during the summer season of 2013–2014. During this crop growth period, the minimum and maximum temperatures ranged from 14.5 to 36.9 °C, with a total rainfall of 382 mm.

Evaluation of S₁ Generation under Stress and Non-Stress Conditions

A total of 200 S₁ -generation selfed seeds, together with nine parental genotypes and 16 checks, were evaluated as ear-to-row progenies during the post-rainy season of 2012–2013. The experiment was laid out in a 15×15 lattice square design with two replications under both managed drought-stress and non-stress conditions.

Under non-stress conditions, the genotypes received recommended agronomic practices and regular furrow irrigation at 10–12-day intervals throughout the crop growth period to prevent the development of moisture stress. Under managed drought-stress conditions, recommended agronomic practices were followed, but irrigation was provided only up to 20 days after sowing. No further irrigation was applied until harvest, thereby exposing the genotypes to moisture stress during the flowering and grain-filling stages. The stress and non-stress experiments were separated by a 4-m-wide buffer zone planted with maize to minimize the movement of irrigation water between the two experimental areas.

Each selfed seed was grown as an ear-to-row progeny in a single 4-m-long row. Under stress conditions, a spacing of 75 × 20 cm (inter-row × intra-row) was maintained, whereas under non stress conditions, the spacing was 60 × 30 cm. Two seeds were sown per hill and subsequently thinned to maintain one healthy plant per hill. Approximately 20 plants were maintained in each progeny row. Five competitive plants were randomly selected, tagged and used for recording observations. The mean values of the five plants were calculated for each trait and used for statistical analysis.

Evaluation of S₂ Generation under Stress and Non-Stress Conditions

A total of 80 S₂- generation selfed seeds, along with 12 inbred lines, three composite populations and five checks, were evaluated as ear-to-row progenies during the summer season of 2013–2014. The experiment was conducted in a 10 × 10 lattice square design with two replications under managed drought-stress and non-stress conditions.

Under non-stress conditions, the genotypes were maintained using recommended agronomic practices and regular furrow irrigation at 10–12-day intervals to ensure adequate moisture throughout the crop growth period. Under managed drought-stress conditions, recommended agronomic practices were followed, but irrigation was provided only up to 30 days after sowing. Thereafter, irrigation was withheld until harvest to impose moisture stress during the flowering and grain-filling stages. The stress and non-stress experiments were separated by a 4-m-wide buffer zone planted with maize.

Each progeny was grown in a single 4-m-long row. Inter-row and intra-row spacing of 75 × 20 cm was maintained under stress conditions, whereas 60 × 30 cm spacing was used under non stress conditions. Two seeds were dibbled per hill and subsequently thinned to retain one healthy plant per hill. Approximately 20 plants were maintained in each progeny row, from which five competitive plants were randomly selected and tagged for recording observations. The mean of the five plants was calculated for each trait and used in subsequent analyses.

Observations Recorded

Observations were recorded for the following morphological, physiological and yield-related traits: days to 50% anthesis, days to 50% silking, anthesis–silking interval (ASI), plant height (cm), ear height (cm), days to maturity, cob length (cm), cob girth (cm), number of cobs per plant, number of kernel rows per cob, number of kernels per row, shelling percentage, 100-seed weight (g), grain yield per plant (g), relative water content (RWC) and chlorophyll content.

Statistical Analysis

The data obtained for the evaluated traits were subjected to appropriate statistical analyses to estimate the magnitude of genetic variability and other genetic parameters under drought-stress and non-stress conditions. Statistical analyses were performed using WINDOSTAT version 8.0.

Results and Discussion

Performance and variability study of S inbred lines derived from the seven different population under stress and non stress conditions

Evaluation of 200 S_1 inbredlines was carried out under both stress (drought) and non stress (irrigated) conditions to isolate inbred lines for drought tolerance. Variability is very important for improvement of any trait. The nature and magnitude of variation for different traits apart from mean performance decides the worth of the cross for exploitation after hybridization. Adopting the procedures described in the material and methods phenotypic and genotypic variances were computed for different traits. In order to know the nature and magnitude of variances for divergent traits, genetic parameters viz., phenotypic and genotypic coefficients of variation, heritability in broad sense and genetic advance over mean were computed and presented in Table (2).

Analysis of variance

under stress the analysis of variance indicated highly significant differences for 18 characters except relative water content at 60 days and relative water content at 90 days (Table 1). whereas under non stress condition analysis of variance indicated highly significant differences for 17 characters and 1 character showed significant difference (chlorophyll content at 90 days) except chlorophyll content at 90 days and relative water content at 90 days (Table 1). There is a considerable variation in the mean values for all the traits as indicated by highly significant mean sum of squares.

Genetic variability parameters of S_1 progenies like mean, range and the components of genetic variability viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability and genetic advance as per cent mean (GAM) were worked out for the 20 quantitative characters under both stress and non stress conditions. Results obtained in the present investigation for each character is presented in Table (2).

Days to 50 per cent anthesis ranging from 54.0 to 79.0 with an average of 65.8 days (S_1 progenies) under stress condition. The variability parameters, like GCV (6.58%) and PCV (6.09%) exhibited low and S_1 progenies showed high heritability (85.5%) coupled with moderate genetic advance as per cent of mean (11.59%) under stress condition. it ranging from 59.0 to 80.0 with an average of 68.43 days (S_1) under non stress condition, The genetic variability components, viz., GCV (5.69%) and PCV (5.94%) exhibited low values and S_1 progenies showed high heritability (91.7%) coupled with moderate genetic advance as per cent of mean (11.23%) under non stress condition.

Days to 50 per cent silking ranging from 56.0 to 82.0 with an average of 68.2 days (S_1) under stress condition. The genetic variability components, viz., GCV (6.25%) and PCV (6.78%) exhibited low values and S_1 progenies showed high heritability (84.9%) coupled with moderate genetic advance as per cent of mean (11.86%) under stress condition. ranging from 61.0 to 84.0 with an average of 70.62 days (S_1) under non stress condition. The variability parameters, like GCV (5.63%) and PCV (5.92%) exhibited low values and S_1 progenies showed high heritability (90.5%) coupled with moderate genetic advance as per cent of mean (11.04%) under non stress condition.

Days to anthesis to silk interval ranging from 1.0 to 6.0 with an average of 2.4 days (S_1) under stress condition. The genetic variability components, viz., GCV (30.53%) and PCV (37.73%) exhibited high values and S_1 progenies showed high heritability (65.6%) coupled with high genetic advance as per cent of mean (50.93%) under stress

condition. ranging from 1.0 to 4.0 with an average of 2.19 days (S_1) under non stress condition, The genetic variability components, viz., GCV (21.48%) and PCV (30.38%) exhibited high values and S_1 progenies showed high and moderate heritability (50.0%) coupled with high genetic advance as per cent of mean (31.28%) non stress condition.

At 60 days after sowing chlorophyll content ranging from 29.8 to 56.8% with an average of 39.9 % (S_1) under stress condition. Genetic components of both GCV (5.19%) and PCV (8.07%) were low, and S_1 progenies showed moderate heritability (41.3%) coupled with low genetic advance as per cent of mean (6.87%) under stress. ranging from 28.6 to 49.8% with an average of 42.6 % (S_1) under non stress condition. The variability parameters, like GCV (2.94%) and PCV (6.27%) exhibited low values, S_1 progenies showed moderate heritability (21.9%) coupled with low genetic advance as per cent of mean (2.83%) non stress conditions.

At 90 days after sowing chlorophyll content ranging from 23.0 to 53.5% with an average of 38.5 % (S_1) under stress condition. The genetic variability components, viz., GCV (8.06%) and PCV (11.65%) exhibited low and moderate values, S_1 progenies showed moderate heritability (47.8%) coupled with moderate genetic advance as per cent of mean (11.48%) under stress, ranging from 26.7 to 45.8% with an average of 36.5% (S_1) under non stress condition. Genetic components of both GCV (3.04%) and PCV (7.69%) were low and S_1 progenies showed low heritability (15.7%) coupled with low genetic advance as per cent of mean (2.48%) non stress condition.

Relative water content at 60 days ranging from 0.49 to 0.99% with an average of 0.70 % (S_1) under stress condition. The genetic variability components, viz., GCV (2.83%) and PCV (9.62%) exhibited low values and S_1 progenies showed low heritability (8.7%) coupled with low genetic advance as per cent of mean (1.71%) under stress. ranging from 0.42 to 0.94% with an average of 0.73% (S_1) under non stress condition, variability components of both GCV (7.87%) and PCV (8.97%) were low and S_1 progenies showed high heritability (77.0%) coupled with moderate genetic advance as per cent of mean (14.22%) non stress condition.

Relative water content at 90 days ranging from 0.33 to 0.77% with an average of 0.57 % (S_1) under stress condition. Genetic components of both GCV (1.94%) and PCV (8.04%) were low, S_1 progenies showed moderate heritability (47.0%) coupled with low genetic advance as per cent of mean (7.54%) under stress. ranging from 0.30 to 0.76% with an average of 0.47% (S_1) under non stress condition. The genetic variability components, viz., GCV (4.92%) and PCV (12.16) exhibited low and moderate values and S_1 progenies showed low heritability (16.4%) coupled with low genetic advance as per cent of mean (4.10%) non stress condition.

Plant height ranging from 103.0 to 263.6cm with an average of 189.7 cm (S_1) under stress condition. The genetic variability components, viz., GCV (9.99%) and PCV (12.12%) exhibited low and moderate values, and S_1 progenies showed high heritability (68.0%) coupled with moderate genetic advance as per cent of mean (16.98%) under stress. ranging from 119.6 to 269.8 cm with an average of 196.0 cm (S_1) under non stress condition. Genetic components of both GCV (11.41%) and PCV (12.18%) were moderate and S_1 progenies showed high heritability

(87.7%) coupled with high genetic advance as per cent of mean (22.03%) non stress condition.

Ear height ranging from 42.2 to 130.0cm with an average of 85.9 cm (S_1) under stress condition. Genetic components of both GCV (13.06%) and PCV (16.05%) were moderate and S_1 progenies showed high heritability (66.2%) coupled with high genetic advance as per cent of mean (22.88%) under stress. ranging from 33.6 to 129.9 cm with an average of 104.3 cm (S_1) under non stress condition. The genetic variability components, viz., GCV (10.70%) and PCV (13.74%) exhibited moderate values and S_1 progenies showed high heritability (60.7%) coupled with moderate genetic advance as per cent of mean (17.18%) non stress condition.

Days to maturity ranging from 104.0 to 136.0 with an average of 120.8 days (S_1) under stress condition. The variability components of both GCV (3.67%) and PCV (4.76%) were low, and S_1 progenies showed moderate heritability (59.4%) coupled with low genetic advance as per cent of mean (5.83%) under stress. ranging from 104.0 to 134.0 with an average of 120.8 days (S_1) under non stress condition. Genetic components of both GCV (2.76%) and PCV (3.90%) were low and S_1 progenies showed moderate heritability (50.3%) coupled with low genetic advance as per cent of mean (4.04%) non stress condition.

Cob length ranging from 7.0 to 20.7cm with an average of 13.2 cm (S_1) under stress condition. The genetic variability components, viz., GCV (11.87%) and PCV (14.98%) exhibited moderate values, S_1 progenies showed high heritability (62.8%) coupled with moderate genetic advance as per cent of mean (19.37%) under stress. ranging from 10.7 to 24.1 cm with an average of 17.6 cm (S_1) under non stress condition. The genetic variability components, viz., GCV (12.28%) and PCV (12.46%) exhibited moderate values and S_1 progenies showed high heritability (97.1%) coupled with high genetic advance as per cent of mean (24.93%) non stress condition.

Cob girth ranging from 1.18 to 5.0cm with an average of 3.8 cm (S_1) under stress condition. Genetic components of both GCV (8.16%) and PCV (11.95%) were low and moderate and S_1 progenies showed moderate heritability (46.6%) coupled with moderate genetic advance as per cent of mean (11.48%) under stress. ranging from 3.25 to 5.3 cm with an average of 4.4 cm (S_1) under non stress condition. Genetic components of both GCV (6.85) and PCV (7.58) were low values and S_1 progenies showed high heritability (81.6%) coupled with moderate genetic advance as per cent of mean (12.74%) non stress condition

Number of kernel rows per cob ranging from 6.0 to 19.6 with an average of 13.5 (S_1) under stress condition. The variability components of both GCV (7.50%) and PCV (9.99%) were low and S_1 progenies showed moderate heritability (56.5%) coupled with moderate genetic advance as per cent of mean (11.62%) under stress. ranging from 12.0 to 18.0 with an average of 14.7 (S_1) under non stress condition. The variability components of both GCV (4.68%) and PCV (7.24%) were low and S_1 progenies showed moderate heritability (41.7%) coupled with low genetic advance as per per cent of mean (6.23%) non stress condition.

Number of kernels per row ranging from 9.0 to 49.8 with an average of 25.8 (S_1) under stress condition. The genetic variability components, viz., GCV (15.99%) and PCV (19.85%) exhibited moderate values, S_1 progenies showed

high heritability (64.9%) coupled with high genetic advance as per cent of mean (26.53%) under stress. ranging from 18.5 to 48.59 with an average of 34.1 (S_1) under non stress condition. The genetic variability components, viz., GCV (15.90%) and PCV (16.18%) exhibited moderate values and S_1 progenies showed high heritability (96.6%) coupled with high genetic advance as per cent of mean (32.2%) non stress condition.

Number of cobs ranging from 2.0 to 39.0 with an average of 13.0 (S_1) under stress condition. Genetic components of both GCV (30.91%) and PCV (36.20%) were high and S_1 progenies showed high heritability (72.9%) coupled with high genetic advance as per cent of mean (54.36%) under stress. ranging from 1.0 to 16.0 with an average of 7.90 (S_1) under non stress condition. Genetic components of both GCV (32.99%) and PCV (33.92%) were moderate and S_1 progenies showed high heritability (94.6%) coupled with high genetic advance as per cent of mean (66.11%) non stress condition.

Bulk cob weight ranging from 59.0 to 2741g with an average of 916.7 (S_1) under stress condition. The variability components of both GCV (48.36%) and PCV (53.47%) were high, S_1 progenies showed high heritability (81.8%) coupled with high genetic advance as per cent of mean (90.09%) under stress. ranging from 52.0 to 2748 g with an average of 885 g (S_1) under non stress condition. The variability components of both GCV (49.33%) and PCV (49.65%) were high and S_1 progenies showed high heritability (98.7%) coupled with high genetic advance as per cent of mean (100.96%) non stress condition.

Grain weight per plot ranging from 0.03 to 2.12kg with an average of 0.68kg (S_1) under stress condition. The genetic variability components, viz., GCV (45.14%) and PCV (51.19%) exhibited high values and S_1 progenies showed high heritability (77.70%) coupled with high genetic advance as per cent of mean (81.99%) under the stress condition.

Ranging from 0.04 to 2.37 kg with an average of 0.70kg (S_1) under non stress condition. The genetic variability components, viz., GCV (54.55%) and PCV (55.03%) exhibited high values and high heritability (98.30%) under the non stress condition.

Grain weight per plant ranging from 4.0 to 151.3g with an average of 51.8 (S_1) under stress condition. The genetic variability components, viz., GCV (25.02%) and PCV (34.72%) exhibited high values, S_1 progenies showed moderate heritability (51.8%) coupled with high genetic advance as per cent of mean (37.08%) under the stress condition. ranging from 24.5 to 188.5 g with an average of 84.0g (S_1) under non stress condition. The genetic variability components, viz., GCV (25.88%) and PCV (27.43%) exhibited high values and high heritability (89.0%) coupled with high genetic advance as per cent of mean (50.29%).

Hundred seed weight ranging from 11.9 to 34.5g with an average of 20.4 (S) under stress condition. The variability components of both GCV (10.93%) and PCV (15.40%) were moderate and S_1 progenies showed moderate heritability (50.4%) coupled with moderate genetic advance as per cent of mean under stress (15.98). ranging from 13.24 to 35.6 g with an average of 22.9 g (S_1) under non stress condition. The variability components of both GCV (15.60%) and PCV (16.11%) were moderate and S_1 progenies showed high heritability (93.7%) and high genetic

advance as per cent of mean under non stress conditions (31.1%).

Shelling per centage ranging from 30.1 to 98.5 % with an average of 74.4 % (S_1) under stress condition. Genetic components of both GCV (4.5%) and PCV (9.77%) were low, S_1 progenies showed low heritability (21.8%) coupled with low advance as per cent of mean (4.39 %) under stress, ranging from 41.0 to 98.1 % with an average of 77.3% (S_1) under non stress condition. Genetic components of both GCV (9.66%) and PCV (10.98%) were low and moderate and S_1 progenies showed high heritability (77.3%) with moderate genetic advance as per cent of mean (17.49 %) under on stress condition.

Under stress condition the GCV and PCV were high for bulk cob weight (48.36% and 53.47%, respectively), grain yield per plot (45.14% and 51.19%, respectively), anthesis to silk interval (30.53% and 37.73%, respectively), number of cobs (30.91% and 36.20%, respectively) and grain yield per plant (25.02% and 34.72%, respectively), whereas under non stress condition grain yield per plot (54.56% and 55.03%, respectively), bulk cob weight (49.33% and 49.65%, respectively), number of cobs (33% and 33.92%, respectively), anthesis to silk interval (21.48% and 30.38%, respectively) and grain yield per plant (25.88% and 27.43%, respectively) Mani *et al.* (1999b), Choudhary and Choudhary (2002), Muhammad Rafique *et al.* (2004) [5], Om Prakash *et al.* (2006) [6], Prashanth M. (2008) [7], Alake *et al.* (2008), Kuchanur, P. H., (2010) and Salman S., (2011) [8]. Noticed similar results. The high variability values among the inbred lines suggest that there is lot of scope for selection of high yielding superior inbred lines.

Moderate values of genotypic coefficient of variation and phenotypic coefficient of variation under stress condition were noticed number of kernels per row, ear height, 100-seed weight, cob length and plant height under stress condition, whereas under non stress condition number of kernels per row, 100-seed weight, ear height, cob length and plant height Similar results of moderate GCV and PCV were noticed by Mani *et al.* (1996b), Chaudhary *et al.* (2002), Kumar *et al.* (2006), Om Prakash *et al.* (2006) [6], Prashanth M. (2008) [7], Alake *et al.* (2008), Kuchanur, P. H., (2010) and Salman S., (2011) [8].

Under stress condition cob girth and chlorophyll content at 90 days the GCV was low and PCV was moderate. For number of kernel rows per cob, shelling percentage, relative water content at 60 days, chlorophyll content at 60 days, relative water content at 90 days, 50 per cent silking, 50 per cent anthesis and days to maturity the GCV and PCV was low. Whereas, under non stress condition relative water content at 90 days and shelling percentage the GCV was low and PCV was moderate. For relative water content at 60 days, chlorophyll content at 90 days, cob girth, number of kernel rows per cob, chlorophyll content at 60 days, 50 per cent anthesis, 50 per cent silking and days to maturity the GCV and PCV was low. Mani *et al.* (1996b), Om Prakash *et al.* (2006) [6], Kumar *et al.* (2006), Prashanth M. (2008) [7], Alake *et al.* (2008) and Kuchanur, P. H., (2010) reported similar results.

High heritability values under stress condition for 50 per cent anthesis, 50 per cent silking, bulk cob weight, grain yield per plot, number of cobs, plant height, ear height, anthesis to silking interval, number of kernels per row, and cob length, whereas under non stress condition high heritability values for bulk cob weight, grain yield per plot, cob length, number

of kernels per row, number of cobs, 100-seed weight, 50 per cent anthesis, 50 per cent silking, grain yield per plant, plant height, cob girth, shelling percentage, relative water content at 60 days and ear height revealed that variation in these characters is largely controlled by heritable factors. Similar results for high heritability was reported by Sumathi *et al.* (2005) [9], Prashanth M. (2008) [7], Alake *et al.* (2008), Kuchanur, P. H., (2010) and Salman S., (2011) [8].

Moderate heritability values under stress condition for days to maturity, number of kernel rows per cob, grain yield per plant, 100-seed weight, chlorophyll content at 90 days, relative water content at 90 days, cob girth and chlorophyll content at 60 days, under non stress condition moderate heritability values for days to maturity, anthesis to silking interval and number of kernel rows per cob showed that both genetics and environment played equal roles in the expression of these traits.

under stress condition shelling percentage and relative water content at 60 days low heritability it was influenced mostly by environment rather than genetic constitution, under non stress condition chlorophyll content at 60 days, relative water content at 90 days and chlorophyll content at 90 days The results suggest that the yield components in maize are less influenced by environmental conditions. High heritability values for these traits indicate that the variation observed was mainly under genetic control and less influenced by environment. The characters showing high GCV and high heritability can be considered for selection. Similar results for moderate and low heritability was reported by Prashanth M. (2008) [7], Alake *et al.* (2008) and Kuchanur, P. H.

High genetic advance as per cent mean under stress condition was noticed for bulk cob weight, grain yield per plot, number of cobs, Anthesis to silking interval, grain yield per plant, number of kernels per row and ear height, whereas under non stress condition high genetic advance as per cent mean was noticed for number of cobs, grain yield per plant number of kernels per row, anthesis to silking interval, 100-seed weight, cob length and plant height indicative of additive gene action, Singh and Marayanan, (1993) and Kuchanur, P. H., (2010). Thus, the heritability estimates will be reliable if accompanied by high genetic advance. reported similar results of high heritability coupled with high genetic advance by Mani *et al.* (1996b), Kumar *et al.* (2006), Om Prakash *et al.* (2006) [6], Kumar *et al.* (2006), Prashanth M. (2008) [7], Alake *et al.* (2008), Kuchanur, P. H., (2010) and Salman S., (2011) [8]. Whereas under non stress condition grain yield per plot and bulk cob weight were indicating higher variances in the parents as compared to S_1 progenies. Hence, the genetic parameters were non estimable in these two characters,

Evaluation of 80 S_2 inbred lines was carried out during rabi season of 2013-14 under stress (drought) and under irrigated conditions to isolate inbred lines for drought tolerance. Variability is very important for improvement of any trait. The nature and magnitude of variation for different traits apart from mean performance decides the worth of the cross for exploitation after hybridization. Adopting the procedures described in the material and methods phenotypic and genotypic variances were computed for different traits. In order to know the nature and magnitude of variances for divergent traits, genetic parameters viz., phenotypic and genotypic coefficients of variation, heritability in broad sense and genetic advance over mean were computed and presented in Table (4).

The analysis of variance under stress condition indicated highly significant differences for 17 characters except relative water content at 60 days, relative water content at 90 days and number of kernel rows per cob (Table 3). There is a considerable variation in the mean sum of square values for all the 17 traits. Under non stress condition the analysis of variance indicated highly significant differences for 7 characters and 4 character showed significant difference except chlorophyll content at 60 days, chlorophyll content at 90 days, relative water content at 60 days, days to maturity, plant height, ear height, cob girth, number of kernel rows per cob and number of kernels per row (Table 3). There is a considerable variation in the mean values for 11 traits as indicated by significant mean sum of squares.

Genetic variability parameters of S_2 progenies like mean, range and the components of genetic variability viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability and genetic advance as per cent mean (GAM) were worked out for the 20 quantitative characters. Results obtained in the present investigation for each character is presented in Table (4).

Days to 50 per cent anthesis ranging from 53.0 to 78.0 with an average of 64.91 days (S_2) under stress condition. The variability parameters, like GCV (5.43%) and PCV (6.36%) exhibited low and S_2 progenies showed high heritability (73.0%) coupled with low genetic advance as per cent of mean (9.57%) under stress condition, it ranging from 60.0 to 81.0 with an average of 69.46 days (S_2) under non stress condition. The genetic variability components, viz. GCV (4.98%) and PCV (5.27%) exhibited low values and S_2 progenies showed high heritability (89.3%) coupled with low genetic advance as per cent of mean (9.7%) under non stress condition.

Days to 50 per cent silking ranging from 54.0 to 85.0 with an average of 67.32 days (S_2) under stress condition. The genetic variability components, viz., GCV (5.63%) and PCV (6.56%) exhibited low values and S_2 progenies showed high heritability (73.7%) coupled with low genetic advance as per cent of mean (9.97%) under stress condition, it ranging from 63.0 to 82.0 with an average of 71.1 days (S_2) under non stress condition. The variability parameters, like GCV (4.72%) and PCV (5.07%) exhibited low values and S_2 progenies showed high heritability (86.6%) coupled with low genetic advance as per cent of mean (9.05%) under non stress condition

Days to anthesis to silk interval ranging from 1.0 to 7.0 with an average of 2.41 days (S_2) under stress condition. The genetic variability components, viz., GCV (34.22%) and PCV (41.42%) exhibited high values and S_2 progenies showed high heritability (68.2%) coupled with low genetic advance as per cent of mean (58.24%) under stress. It ranging from 1.0 to 4.0 with an average of 1.64 days (S_2) under non stress condition. The genetic variability components, viz., GCV (16.30%) and PCV (26.74%) exhibited moderate and high values, S_2 progenies showed moderate heritability (37.2%) coupled with high genetic advance as per cent of mean (20.48%) non stress conditions. At 60 days after sowing chlorophyll content ranging from 31.6 to 48.9% with an average of 41.9% (S_2) under stress condition. Genetic components of both GCV (7.34%) and PCV (7.55%) were low and S_2 progenies showed high heritability (94.7%) coupled with moderate and low genetic advance as per cent of mean (14.72%) under stress, it

ranging from 31.8 to 52.7% with an average of 44.7% (S_2) under non stress condition. The variability parameters, like GCV (2.54) and PCV (6.61) exhibited low values, S_2 progenies showed low heritability (14.8%) coupled with low genetic advance as per cent of mean (2.01%) non stress condition.

At 90 days after sowing chlorophyll content ranging from 23.1 to 47.9 %with an average of 37.4% (S_2) under stress condition. The genetic variability components, viz., GCV (7.03%) and PCV (8.72%) exhibited low and S_2 progenies showed high heritability (65.5%) coupled with low genetic advance as per cent of mean (11.68%) under stress, it ranging from 23.0 to 50.1 %with an average of 38.2% (S_2) under non stress condition. Genetic components of both GCV (3.09%) and PCV (7.93%) were low and S_2 progenies showed low heritability (15.2%) coupled with low genetic advance as per cent of mean (2.47%) non stress condition

Relative water content at 60 days ranging from 0.3 to 0.94 %with an average of 0.69% (S_2) under stress condition. The genetic variability components, viz., GCV (5.66%) and PCV (9.77%) exhibited low values and S_2 progenies showed low heritability (7.8%) coupled with moderate genetic advance as per cent of mean (15.7%) under stress, it ranging from 0.5 to 0.98 %with an average of 0.76% (S_2) under non stress condition. variability components of both GCV (2.63%) and PCV (6.86%) were low and S_2 progenies showed low heritability (14.7%) coupled with low genetic advance as per cent of mean (2.07%) non stress condition.

Relative water content at 90 days ranging from 0.24 to 0.86 %with an average of 0.58 % (S_2) under stress condition. Genetic components of both GCV (2.48%) and PCV (9.75%) were low and S_2 progenies showed moderate heritability (50.0%) coupled with moderate genetic advance as per cent of mean (10.12%) under stress, It ranging from 0.28 to 0.81 %with an average of 0.52% (S_2) under non stress condition. The genetic variability components, viz., GCV (8.66%) and PCV (15.32) exhibited low and moderate values, S_2 progenies showed moderate heritability (32.0%) coupled with moderate genetic advance as per cent of mean (10.09%) non stress condition.

Plant height ranging from 112.3 to 278.0 cm with an average of 202.3cm (S_2) under stress condition. The genetic variability components, viz., GCV (7.44%) and PCV (10.47%) exhibited low and moderate values and S_2 progenies showed high heritability (50.5%) coupled with moderate genetic advance as per cent of mean (10.89%) under stress, It ranging from 128.8to 277.9 cm with an average of 21.1cm (S_2) under non stress condition. Genetic components of both GCV (3.33%) and PCV (9.27%) were low and S_2 progenies showed low heritability (12.9%) coupled with low genetic advance as per cent of mean (2.46%) non stress condition.

Ear height ranging from 44.4 to 132.0 cm with an average of 91.1cm (S_2) under stress condition. Genetic components of both GCV (9.28%) and PCV (13.72%) were low and moderate values and S_2 progenies showed moderate heritability (45.8%) coupled with moderate genetic advance as per cent of mean (12.93%) under stress, It ranging from 33.8to 191.9 cm with an average of 120.5cm (S_2) under non stress condition. The genetic variability components, viz., GCV (9.21%) and PCV (18.20%) exhibited low and moderate values, S_2 progenies showed low heritability (25.6%) coupled with low genetic advance as per cent of mean (9.59%) non stress condition.

Days to maturity ranging from 102.0 to 139.0 with an average of 122.0 days (S_2) under stress condition. The variability components of both GCV (3.46%) and PCV (4.92%) were low S_2 progenies showed moderate heritability (49.6%) coupled with low genetic advance as per cent of mean (5.03%) under both stress, It ranging from 100.0 to 135.0 with an average of 121.2 days (S_2) under non stress condition. components of both GCV (2.08%) and PCV (4.09%) were low and S_2 progenies showed low heritability (25.9%) coupled with low genetic advance as per cent of mean (2.18%) non stress condition.

Cob length ranging from 9.8 to 20.3cm with an average of 14.7cm (S_2) under stress condition. The genetic variability components, viz. GCV (7.47%) and PCV (10.85%) exhibited low and moderate values and S_2 progenies showed moderate heritability (47.4%) coupled with moderate genetic advance as per cent of mean (10.6%) under stress, It ranging from 12.4 to 24.9 cm with an average of 17.4cm (S_2) under non stress condition. The genetic variability components, viz. GCV (6.21%) and PCV (10.31%) exhibited low and moderate values, S_2 progenies showed moderate heritability (36.2%) coupled with low genetic advance as per cent of mean (7.7%) non stress condition.

Cob girth ranging from 2.0 to 5.2 cm with an average of 4.16cm (S_2) under stress condition. Genetic components of both GCV (6.44%) and PCV (10.01%) were low and moderate and S_2 progenies showed high heritability (41.4%) coupled with low genetic advance as per cent of mean (8.53%) under stress, it ranging from 3.5 to 5.2 cm with an average of 4.4cm (S_2) under non stress condition. Genetic components of both GCV (2.61) and PCV (5.23) were low values and S_2 progenies showed low heritability (25%) coupled with low genetic advance as per cent of mean (2.69%) non stress condition.

Number of kernel rows per cob ranging from 10.2 to 18.9 with an average of 14.27 (S_2) under stress condition. The variability components of both GCV (2.25%) and PCV (6.67%) were low and S_2 progenies showed low heritability (11.4%) coupled with low genetic advance as per cent of mean (1.56%) under stress, It ranging from 12.0 to 16.0 with an average of 14.3 (S_2) under non stress condition. The variability components of both GCV (1.81%) and PCV (4.93%) were low and S_2 progenies showed low heritability (13.4%) coupled with low genetic advance as per cent of mean (1.36%) non stress condition.

Number of kernels per row ranging from 14.8 to 44.8 with an average of 31.1 (S_2) under stress condition. The genetic variability components viz., GCV (9.25%) and PCV (13.16%) exhibited low and moderate values, under stress S_2 progenies showed moderate heritability (49.4%) with moderate genetic advance as per cent of mean (13.4%), It ranging from 12.0 to 49.8 with an average of 36.3 (S_2) under non stress condition. The genetic variability components, viz., GCV (5.45%) and PCV (11.56%) exhibited low and moderate values, under non stress conditions S_2 progenies showed low heritability (22.2%) and low genetic advance as per cent of mean (5.29%).

Number of cobs ranging from 4.0 to 26.0 with an average of 12.4 (S_2) under stress condition. Genetic components of both GCV (22.60%) and PCV (24.61%) were high and S_2 progenies showed high heritability (84.4%) coupled with high genetic advance as per cent of mean (42.77%) under stress, it ranging from 2.0 to 26.0 with an average of 10.2 (S_2) under non stress condition. Genetic components of both

GCV (24.42%) and PCV (33.11%) were moderate and S_2 progenies showed moderate heritability (54.4%) coupled with high genetic advance as per cent of mean (37.11%) non stress condition.

Bulk cob weight ranging from 114 to 2237.0 with an average of 948.2g (S_2) under stress condition. The variability components of both GCV (34.99%) and PCV (36.46%) were high, S_2 progenies showed high heritability (92.1%) coupled with high genetic advance as per cent of mean (69.16%) under stress, it ranging from 218.0 to 3318.0 g with an average of 16580g (S_2) under non stress condition. The variability components of both GCV (42.04%) and PCV (42.27%) were high and S_2 progenies showed high heritability (98.9%) coupled with high genetic advance as per cent of mean (86.14%) non stress condition.

Grain weight per plot ranging from 0.09 to 1.92 kg with an average of 0.72kg (S_1) under stress condition. The genetic variability components, viz., GCV (38.52%) and PCV (40.68%) exhibited high values and S_1 progenies showed high heritability (92.10%) coupled with high genetic advance as per cent of mean (69.16%) under the stress condition. it ranging from 0.16 to 2.94 kg with an average of 1.32 kg (S_2) under non stress condition. The genetic variability components, viz., GCV (45.83%) and PCV (46.19%) exhibited high values and high heritability (98.30%) coupled with high genetic advance as per cent of mean (93.69%) under the non stress condition.

Grain weight per plant ranging from 19.5 to 79.9g with an average of 55.5g (S_2) under stress condition. The genetic variability components, viz., GCV (18.93%) and PCV (20.72%) exhibited moderate and high values, S_2 progenies showed high heritability (83.5%) coupled with high genetic advance as per cent of mean (35.64%) under stress, it ranging from 36.8 to 233.6 g with an average of 127.0g (S_2) under non stress condition. The genetic variability components, viz., GCV (16.79%) and PCV (25.40%) exhibited moderate and high values, S_2 progenies showed moderate heritability (43.7%) coupled with high genetic advance as per cent of mean (22.86%) non stress condition.

Hundred seed weight ranging from 13.6 to 35.9g with an average of 22.8g (S_2) under stress condition. The variability components of both GCV (9.95%) and PCV (14.24%) were low and moderate. Under stress S_2 progenies exhibited moderate heritability (48.8%) and genetic advance as per cent of mean (14.32%), it ranging from 12.3 to 37.6 g with an average of 23.7g (S_2) under non stress condition. The variability components of both GCV (9.88%) and PCV (15.78%) were low and moderate values, S_2 progenies exhibited moderate heritability (39.2%) with moderate genetic advance as per cent of mean (12.74%) under the non stress situation.

Shelling per centage ranging from 31.5 to 93.2 % with an average of 74.9 % (S_2) under stress condition. Genetic components of both GCV (6.91%) and PCV (8.38%) were low and S_2 progenies showed high heritability (67.9%) coupled with moderate genetic advance as per cent of mean (11.73% under stress. It is ranging from 41.0 to 94.5% with an average of 77.0% (S_2) under non stress condition. Genetic components of both GCV (10.18%) and PCV (11.27%) were moderate and S_2 progenies showed high heritability (81.5%) coupled with moderate genetic advance as per cent of mean (18.94%) non stress condition.

The GCV and PCV were high for anthesis to silk interval (34.22% and 41.43%, respectively), grain yield per plot

(38.53% and 40.69%, respectively), bulk cob weight (34.99% and 36.47%, respectively) and number of cobs (22.61% and 24.61%, respectively) under stress condition, whereas under non stress condition the GCV and PCV were high for grain yield per plot (45.83% and 46.19%, respectively), bulk cob weight (42.04% and 42.27%, respectively), number of cobs (24.42% and 33.11%, respectively). Mani *et al.* (1996b), Choudhary and Choudhary (2002), Om Prakash *et al.* (2006) ^[6], Prashanth M., (2008) ^[7] and Kuchanur, P. H., (2010) noticed similar results. The high variability values among the inbred lines suggest that there is lot of scope for selection of high yielding superior inbred lines.

Moderate values of genotypic coefficient of variation and phenotypic coefficient of variation under stress condition were noticed for grain yield per plant. And, for 100-seed weight, ear height, number of kernels per row, cob length, plant height and cob girth the GCV was low and PCV was moderate. For relative water content at 60 days, relative water content at 90 days, chlorophyll content at 90 days, shelling percentage, chlorophyll content at 60 days, number of kernel rows per cob, 50 per cent silking, 50 per cent anthesis and days to maturity the GCV and PCV was low.

Whereas under non stress condition the GCV moderate and PCV high were high for anthesis to silk interval and grain yield per plant, moderate values of genotypic coefficient of variation and phenotypic coefficient of variation were noticed for shelling percentage. Similar results of moderate GCV and PCV were noticed by Mani *et al.* (1996b), Chaudhary *et al.* (2002), Kumar *et al.* (2006), Om Prakash *et al.* (2006) ^[6] Prashanth M., (2008) ^[7] and Kuchanur, P. H., (2010). Whereas, for ear height, 100-seed weight, relative water content at 90 days, number of kernels per row and cob length the GCV was low and PCV was moderate. For plant height, chlorophyll content at 90 days, relative water content at 60 days, chlorophyll content at 60 days, 50 per cent anthesis, cob girth, 50 per cent silking, number of kernel rows per cob and days to maturity the GCV and PCV was low. Mani *et al.* (1996b) and Om Prakash *et al.* (2006) ^[6] reported similar results.

High heritability values under stress condition for chlorophyll content at 60 days, bulk cob weight, grain yield per plot, number of cobs, grain yield per plant, relative water content at 60 days, 50 per cent anthesis, 50 per cent

silking, anthesis to silking interval, shelling percentage and chlorophyll content at 90 days. Moderate heritability values for plant height, relative water content at 90 days, days to maturity, number of kernels per row, 100-seed weight, cob length ear height and cob girth. And, for number of kernel rows per cob low heritability.

whereas under non stress condition high heritability values for bulk cob weight, grain yield per plot, 50 per cent anthesis, 50 per cent silking and shelling percentage revealed that variation in these characters is largely controlled by heritable factors. Similar results for high heritability was reported by Sumathi *et al.* (2005) ^[9], Alake *et al.* (2008) and Kuchanur, P. H., (2010). Moderate heritability values for number of cobs, grain yield per plant, 100-seed weight, anthesis to silking interval, cob length and relative water content at 90 days showed that both genetics and environment played equal roles in the expression of these traits. Whereas, for days to maturity, ear height, cob girth, number of kernels per row, chlorophyll content at 90 days, chlorophyll content at 60 days, relative water content at 60 days, number of kernel rows per cob and plant height low heritability it was influenced mostly by environment rather than genetic constitution. High heritability values for these traits indicate that the variation observed was mainly under genetic control and less influenced by environment. The characters showing high GCV and high heritability can be considered for selection similar results were found by Mani *et al.* (1996b), Chaudhary *et al.* (2002), Kumar *et al.* (2006), Om Prakash *et al.* (2006) ^[6] Prashanth M., (2008) ^[7] and Kuchanur, P. H., (2010)..

Under stress condition high genetic advance as per cent mean was noticed for grain yield per plot, bulk cob weight, anthesis to silking interval, number of cobs and grain yield per plant. High genetic advance as per cent mean was noticed under non stress condition for grain yield per plot, bulk cob weight, number of cobs, grain yield per plant and anthesis to silking interval indicative of additive gene action (Singh and Marayanan, 1993). Thus, the heritability estimates will be reliable if accompanied by high genetic advance. reported similar results of high heritability coupled with high genetic advance by Mani *et al.* (1996b), Kumar *et al.* (2006), Om Prakash *et al.* (2006) ^[6] Prashanth M., (2008) ^[7] and Kuchanur, P. H., (2010).

Table 1: Analysis of variance for twenty characters in 200 S₁ progenies of maize inbred lines under stress and nonstress situation

Characters	Sources of Variance											
	Under stress condition						Under nonstress condition					
	Replication MSS	Treatments (Adjusted) MSS	Blocks within Reps (adj.)	Interblock error	CD at 5%	CD at 1%	Replication MSS	Treatments (Adjusted) MSS	Blocks within Reps (adj.)	Interblock error	CD at 5%	CD at 1%
DF	1	224	28	196			1	224	28	196		
50% Tasseling(days)	1.87	1.642**	0.52	0.57	1.48	1.10	9.68	0.886**	0.44	0.44	1.31	1.73
50% Silking (days)	76.06	37.597**	3.64	5.72	4.61	6.07	0.11	33.137**	3.10	2.72	3.28	4.33
Anthesis silk interval (days)	62.72	42.781**	4.30	6.75	5.00	6.60	7.74	35.029**	4.22	3.20	3.60	4.75
Chlorophyll @ 60 days	0.07	20.867**	17.86	11.45	6.90	9.10	920.41	14.331*	6.61	11.84	6.59	8.69
Chlorophyll @ 90 days	705.73	40.308**	13.88	22.05	9.04	11.91	5.60	15.81	7.69	14.13	7.19	9.48
Relative water content @ 60 days	0.002	0.009	0.004	0.009	0.180	0.237	0.15	0.008**	0.002	0.002	0.087	0.115
Relative water content @ 90 days	0.265	0.004	0.010	0.004	0.132	0.174	0.39	0.01	0.012	0.005	0.147	0.193
Plant height (cm)	2386.90	1058.113**	351.80	336.80	36.29	47.87	9116.10	1141.625**	152.72	138.34	23.35	30.79

Ear height (cm)	1905.46	380.585**	122.31	129.63	22.36	29.47	10925.18	410.813**	157.48	161.37	25.03	33.00
Days to maturity (days)	679.58	66.354**	53.53	23.13	10.23	13.50	355.56	44.484**	30.28	20.95	9.27	12.23
Cob length (cm)	5.53	7.83**	1.02	3.19	3.36	4.44	58.45	9.687**	0.38	0.27	1.04	1.37
Cob girth (cm)	7.58	0.415**	0.53	0.22	0.93	1.22	0.37	0.223**	0.03	0.04	0.40	0.53
Number of Kernel rows per cob	0.63	3.688**	1.57	1.61	2.50	3.29	2.28	2.282**	0.63	1.43	2.27	3.00
Number of Kernels per row	0.55	52.843**	11.80	19.52	8.49	11.19	308.15	60.963**	2.34	2.04	2.84	3.75
Number of cobs	27.88	44.879**	7.59	12.82	6.87	9.06	18.40	14.508**	1.34	0.70	1.74	2.30
Bulk cob weight (g)	394212.80	481558.549**	75164.79	89498.34	583.60	769.39	618123.74	386755.861**	3651.17	5176.93	139.15	183.45
Grain yield per plot (kg)	454545.48	241665.709**	42379.38	55509.37	457.37	602.97	201358.58	298885.73**	4969.80	5165.85	141.30	186.28
Grain yield per plant (g)	0.46	0.0242**	0.04	0.06	0.46	0.60	0.20	0.299**	0.01	0.01	0.14	0.19
100-Seed weight (g)	240.36	19.831**	5.99	10.40	6.18	8.15	338.82	27.395**	2.83	1.57	2.59	3.42
Shelling (%)	117.52	7211.969**	6327.53	3959.86	128.66	169.69	543.82	144.419**	19.42	34.69	11.28	14.88

Table 2: Estimation of genetic variability parameters in 200 S₁ progenies of maize inbred lines under stress and non stress situation

Characters	Under stress condition							Under nonstress condition						
	Range			GCV%	PCV%	h ² (Broad Sense)	GAM 5%	Mean	Min.	Max.	GCV%	PCV%	h ² (Broad Sense)	GAM 5%
	Mean	Min.	Max.											
50% Tasseling(days)	65.82	54.00	79.00	6.09	6.58	85.50	11.60	68.43	59.00	80.00	5.70	5.95	0.92	11.23
50% Silking (days)	68.20	56.00	82.00	6.25	6.78	84.90	11.86	70.62	61.00	84.00	5.64	5.93	0.91	11.05
Anthesis silk interval (days)	2.40	1.00	6.00	30.54	37.73	65.60	50.93	2.19	1.00	4.00	21.48	30.38	0.50	31.28
Chlorophyll @ 60 days	39.98	29.80	56.80	5.19	8.07	41.30	6.87	42.63	28.60	49.80	2.94	6.28	0.22	2.84
Chlorophyll @ 90 days	38.52	23.00	53.56	8.06	11.65	47.80	11.48	36.54	26.70	45.80	3.05	7.69	0.16	2.49
Relative water content @ 60 days	0.70	0.49	0.99	2.83	9.62	8.70	1.72	0.73	0.42	0.94	7.87	8.97	0.77	14.23
Relative water content @ 90 days	0.57	0.33	0.77	1.94	8.04	47.00	7.54	0.47	0.30	0.76	4.92	12.16	0.16	4.11
Plant height (cm)	189.71	103.00	263.60	10.00	12.12	68.00	16.98	196.05	119.60	269.80	11.41	12.19	0.88	22.02
Ear height (cm)	85.93	42.20	130.00	13.06	16.05	66.20	21.89	104.31	33.60	129.90	10.71	13.74	0.61	17.19
Days to maturity (days)	120.86	104.00	136.00	3.67	4.76	59.40	5.83	120.87	104.00	134.00	2.77	3.90	0.50	4.04
Cob length (cm)	13.20	7.00	20.75	11.87	14.98	62.80	19.38	17.66	10.75	24.15	12.28	12.46	0.97	24.94
Cob girth (cm)	3.81	1.18	5.05	8.17	11.95	46.60	11.49	4.40	3.25	5.30	6.85	7.58	0.82	12.75
Number of Kernel rows per cob	13.59	6.00	19.60	7.51	9.99	56.50	11.62	14.74	12.00	18.00	4.68	7.25	0.42	6.23
Number of Kernels per row	25.89	9.00	49.80	15.99	19.85	64.90	26.53	34.11	18.50	48.59	15.91	16.19	0.97	32.20
Number of cobs	13.08	2.00	39.00	30.91	36.20	72.90	54.37	7.94	1.00	16.00	33.00	33.92	0.95	66.11
Bulk cob weight (g)	917.62	59.00	2741.00	48.36	53.47	81.80	90.10	885.63	52.00	2748.00	49.33	49.65	0.99	-
Grain yield per plot (kg)	0.68	0.03	2.12	45.14	51.19	77.70	82.00	0.70	0.04	2.37	54.56	55.03	0.98	-
Grain yield per plant (g)	51.81	4.07	151.34	25.00	34.72	51.80	37.08	84.02	24.50	188.58	25.88	27.43	0.89	50.30
100-Seed weight (g)	20.44	11.93	34.51	10.93	15.40	50.40	15.98	22.96	13.24	35.67	15.60	16.12	0.94	31.11
Shelling (%)	74.40	30.16	98.56	4.57	9.77	21.80	4.40	77.33	41.02	98.15	9.66	10.99	0.77	17.50

Table 3: Analysis of variance for twenty characters in 200 S₁ progenies of maize inbred lines under stress and nonstress situation

Characters	Sources of Variance											
	Under stress condition						Under nonstress condition					
	Replication MSS	Treatments (Adjusted) MSS	Blocks within Reps (adj.)	Interblock error	CD at 5%	CD at 1%	Replication MSS	Treatments (Adjusted) MSS	Blocks within Reps (adj.)	Interblock error	CD at 5%	CD at 1%
DF	1	99	18	81			1	99	18	81		
50% Tasseling(days)	42.32	34.085**	9.51	9.12	6.03	8.00	21.78	26.876**	5.29	2.35	3.38	4.48
50% Silking (days)	35.28	39.096**	11.37	10.04	6.38	8.46	19.22	26.071**	5.28	3.10	3.72	4.93
Anthesis silk interval (days)	0.32	1.994**	0.25	0.72	1.58	2.09	0.08	0.385*	0.22	0.25	0.98	1.29
Chlorophyll @ 60 days	24.63	20.029**	0.79	1.13	2.05	2.71	20.21	17.48	18.56	14.08	7.68	10.18
Chlorophyll @ 90 days	1.21	21.356**	13.60	6.11	5.44	7.21	1.75	18.41	12.43	16.33	7.84	10.38
Relative water	108.12	90.18	38.93	138.59	21.78	28.83	0.01	0.01	0.02	0.01	0.13	0.18

content @ 60 days												
Relative water content @ 90 days	665.36	63.48	19.98	78.18	16.31	21.59	0.01	0.013*	0.01	0.01	0.19	0.25
Plant height (cm)	2829.78	899.116**	478.09	438.01	41.99	55.67	968.44	773.98	762.04	654.46	51.66	68.48
Ear height (cm)	41.99	312.604**	158.70	172.00	25.84	34.20	3422.95	962.63	977.92	658.09	53.25	70.60
Days to maturity (days)	359.12	72.207**	33.57	36.98	11.97	15.84	737.28	49.44	40.96	35.66	12.04	15.96
Cob length (cm)	128.02	5.147**	2.73	2.70	3.27	4.34	5.65	6.48*	3.12	4.36	4.03	5.34
Cob girth (cm)	2.01	0.348**	0.16	0.21	0.90	1.19	0.55	0.11	0.10	0.15	0.73	0.97
Number of Kernel rows per cob	4.58	1.81	1.21	1.69	2.51	3.33	0.50	1.00	0.25	1.00	1.84	2.44
Number of Kernels per row	290.07	33.703**	18.32	16.77	8.22	10.89	173.17	35.41	47.19	23.18	10.44	13.84
Number of cobs	156.65	18.734**	1.75	3.19	3.40	4.49	76.88	22.954**	30.91	5.92	6.44	8.53
Bulk cob weight (g)	1596080.51	239136.647**	8962.29	21201.22	273.33	361.80	757926.72	10041.16**	10041.16	10776.65	204.70	270.95
Grain yield per plot (kg)	1.06	0.173**	0.01	0.02	0.27	0.35	0.15	0.778**	0.01	0.01	0.23	0.30
Grain yield per plant (g)	1276.24	265.146**	35.20	45.64	13.12	17.37	37312.94	2082.591**	3755.46	598.99	68.14	90.34
100-Seed weight (g)	131.38	21.236**	5.52	12.05	6.54	8.66	300.15	28.189*	22.95	15.85	8.24	10.92
Shelling (%)	52.55	79.028**	14.31	27.80	9.99	13.22	369.40	150.877**	10.36	31.76	10.48	13.87

Table 4: Estimation of genetic variability parameters in 200 S₁ progenies of maize inbred lines under stress and non stress situation

Characters	Under stress condition								Under nonstress condition							
	Range			GCV%	PCV%	h ² (Broad Sense)	GAM 5%					GCV%	PCV%	h ² (Broad Sense)	GAM 5%	
	Mean	Min.	Max.						Mean	Min.	Max.					
50% Tasseling(days)	64.91	53.00	78.00	5.44	6.36	73.00	9.57		69.46	60.00	81.00	4.987	5.278	89.30	9.706	
50% Silking (days)	67.32	54.00	85.00	5.64	6.57	73.70	9.97		71.10	63.00	82.00	4.726	5.078	86.60	9.059	
Anthesis silk interval (days)	2.41	1.00	7.00	34.22	41.43	68.20	58.24		1.64	1.00	4.00	16.306	26.741	37.20	20.484	
Chlorophyll @ 60 days	41.91	31.64	48.92	7.35	7.55	94.70	14.73		44.72	31.80	52.70	2.544	6.611	14.80	2.016	
Chlorophyll @ 90 days	37.47	23.16	47.91	7.03	8.72	65.00	11.68		38.22	23.00	50.10	3.091	7.939	15.20	2.479	
Relative water content @ 60 days	0.69	0.30	0.94	5.66	9.77	78.00	15.73		0.76	0.50	0.98	2.63	6.865	14.70	2.076	
Relative water content @ 90 days	0.58	0.24	0.86	2.48	9.75	50.00	10.12		0.52	0.28	0.81	8.667	15.327	32.00	10.097	
Plant height (cm)	202.33	112.30	278.00	7.45	10.48	50.50	10.90		212.14	128.80	277.90	3.333	9.273	12.90	2.467	
Ear height (cm)	91.12	44.40	132.02	9.28	13.72	45.80	12.93		120.52	33.80	191.90	9.21	18.204	25.60	9.599	
Days to maturity (days)	122.05	102.00	139.00	3.47	4.92	49.60	5.03		121.29	100.00	135.00	2.087	4.099	25.90	2.188	
Cob length (cm)	14.77	9.80	20.31	7.48	10.86	47.40	10.61		17.45	12.43	24.90	6.21	10.316	36.20	7.7	
Cob girth (cm)	4.16	2.00	5.20	6.44	10.02	41.40	8.54		4.44	3.50	5.20	2.617	5.236	25.00	2.695	
Number of Kernel rows per cob	14.27	10.20	18.90	2.25	6.67	11.40	1.57		14.31	12.00	16.00	1.81	4.936	13.40	1.367	
Number of Kernels per row	31.18	14.80	44.80	9.26	13.17	49.40	13.40		36.39	12.02	49.89	5.45	11.564	22.20	5.292	
Number of cobs	12.44	4.00	26.00	22.61	24.61	84.40	42.78		10.23	2.00	26.00	24.426	33.116	54.40	37.114	
Bulk cob weight (g)	948.20	114.00	2237.00	34.99	36.47	92.10	69.16		1658.64	218.00	3318.00	42.047	42.276	98.90	86.147	
Grain yield per plot (kg)	0.72	0.09	1.92	38.53	40.69	89.70	75.15		1.32	0.16	2.94	45.835	46.192	98.50	93.69	
Grain yield per plant (g)	55.56	19.54	79.91	18.94	20.72	83.50	35.65		127.00	36.86	233.60	16.793	25.408	43.70	22.863	
100-Seed weight (g)	22.88	13.68	35.97	9.95	14.24	48.80	14.33		23.78	12.34	37.67	9.884	15.785	39.20	12.749	
Shelling (%)	74.93	31.50	93.27	6.91	8.39	67.90	11.74		77.01	41.02	94.53	10.184	11.279	81.50	18.942	

Conclusion

The present investigation demonstrated substantial genetic variability for important agronomic, physiological and yield-related traits in maize under both drought-stress and non-stress conditions. Under drought stress, high heritability coupled with high genetic advance as a percentage of the mean was observed for bulk cob weight, grain yield per plot, number of cobs per plant, anthesis–silking interval and number of kernels per row. Under non-stress conditions, the same combination of high heritability and high genetic advance was recorded for bulk cob weight, grain yield per

plot, cob length, number of kernels per row, number of cobs per plant, 100-seed weight and plant height.

The association of high heritability with high genetic advance suggests that these traits are predominantly governed by additive genetic effects and can therefore be effectively improved through selection. Accordingly, these traits may serve as useful selection criteria in maize breeding programmes aimed at improving grain yield and drought adaptation. The superior inbred lines identified in the present study may provide valuable genetic resources for the development of high-yielding, drought-tolerant maize

hybrids and varieties, particularly for cultivation under water-limited environments.

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40. Table 1: Analysis of variance for twenty characters in 200 S₁ progenies of maize inbred lines under stress and non-stress situations.
41. Table 2: Estimation of genetic variability parameters in 200 S₁ progenies of maize inbred lines under stress and non-stress situations.
42. Table 3: Analysis of variance for twenty characters in 200 S₁ progenies of maize inbred lines under stress and non-stress situations.
43. Table 4: Estimation of genetic variability parameters in 200 S₁ progenies of maize inbred lines under stress and non-stress situations.