

## SCREENING OF MAIZE (*ZEA MAYS* L.) GENOTYPES FOR DROUGHT TOLERANCE USING PHOTOSYNTHETIC PIGMENTS AND ANTI-OXIDATIVE ENZYMES AS SELECTION CRITERIA

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### Abstract

The present study was conducted to screen the drought tolerance in some promising maize genotypes viz. FH-1285, FH-949, FH-1292, FH-985, FH-1046, FH-1257, FH-922, FH-988, FH-1137 obtained from Ayub Agricultural Research Institute (AARI), and, Yousafwala hybrid, 3025w/6129, SWL-539516, YSC-15, P1543/2567600 developed by Maize Research Institute, Yousafwala, Sahiwal, Pakistan. The experiment was laid out in a Completely Randomized Design (CRD) with three replicates. Drought was applied at three leaf stage by maintaining three levels of irrigation i.e. 100% field capacity (full watering), 70% field capacity (mild drought stress) and 40% field capacity (severe drought stress). After 50 days of maintaining drought, plant sample was collected to record the growth and physio-biochemical parameters i.e. concentration of photosynthetic pigments, (Chl. *a*, Chl. *b*, total chl. and carotenoid content), anti-oxidative enzymes (SOD, POD, and CAT) and total soluble proteins. Drought stress severely hampered growth attributes that was clearly linked to a concurrent decrease in concentration of photosynthetic pigments at both mild and in particular at severe drought stress. Genotypes Yousafwala hybrid, P3164w/2403481 and FH-1137 showed less decrease in all growth parameters at both mild and severe drought levels indicating their resistant nature, whereas, genotypes FH-922, FH-985, FH-949 and FH-1257 were drought sensitive as they showed more than 50% growth reduction under severe drought stress. Genotypes P1543/2567600, YSC-15, FH-949 and FH-949 were considered moderately tolerant as they showed less decrease in growth parameters under mild drought conditions (70% field capacity), but under severe drought conditions (40% field capacity) a greater decrease in growth was recorded in the same genotypes. Antioxidant enzymes i.e. SOD, POD and CAT activity increased at both drought levels (70% and 40% field capacity) as compared to control plants (100% field capacity) accompanied by a concurrent increase in total soluble proteins in the genotypes Yousafwala hybrid, FH-1257, 3025w/6129, SWL-539516 and P3164w/2403481. Cluster analysis grouped the genotypes in distinct clusters indicating similarities among the various genotypes regarding their resistance to drought stress. The drought tolerant genotypes Yousafwala hybrid, P3164w/2403481 and FH-1137 are recommended for cultivation and improved crop yield in water deficit areas.

**Key words:** *Zea mays*; Drought tolerance; Photosynthetic pigments; Anti-oxidative enzymes; Screening.

### Introduction

Crop plants continuously face various biotic and abiotic stresses while growing under field conditions (Anjum *et al.*, 2011). Among these environmental stresses, water scarcity is a major abiotic factor that severely affects growth, development, metabolism and yield of plants (Shao *et al.*, 2009). Plants show adverse effects of drought stress when the supply of water to roots becomes low but transpirational rate becomes too high. This leads to decrease in water and turgor potentials that disturb the normal functioning of plants (Jaleel *et al.*, 2009). Drought stress also affects leaf water content that hinders cell enlargement and plant growth. Another direct effect of drought stress is stomatal closure at low water potentials that causes a reduction in CO<sub>2</sub> diffusion in leaves ultimately inhibiting photosynthesis and transpiration (Jason *et al.*, 2004).

The provision of sufficient supply of water is crucial for plants because it contributes to growth by maintaining developmental processes and plays a key role in crop production. Under water stress, plant growth decreases due to reduction in transpiration rate, membrane permeability and impaired nutrient transport that is a direct result of reduced water absorption by roots (Yang *et al.*, 2012). The ability of plants to tolerate

stress varies greatly in different species. Some sensitive plants cannot tolerate stress and therefore wilt and die. Some other plants can endure water stress by undergoing certain physiological changes in their tissues that maintain turgidity and water potential of the cell around normal ranges to maintain growth under stressful environments (Shaddad *et al.*, 2013)

Another immediate effect of drought stress is production of reactive oxygen species (ROS) during all types of abiotic stresses. During drought stress, many ROS are produced such as singlet oxygen, hydroxyl ions, superoxide radicals and hydrogen peroxide. These have deleterious effects on membrane system of plants (de Vasconcelos, 2020). Antioxidants, through their scavenging mechanism prevent the oxidative damage caused by these ROS. These antioxidants are classified into enzymatic and non-enzymatic antioxidants. Enzymatic antioxidants include superoxide dismutase (SOD), catalase (CAT), peroxidase (POD), glutathione reductase (GR), polyphenol oxidase (PPO) and ascorbate peroxidase (APX). Non-enzymatic antioxidants include  $\alpha$ -tocopherol,  $\beta$ -carotene, cysteine, glutathione and ascorbic acid (Soares *et al.*, 2019). All these antioxidants collectively work to neutralize the ROS and therefore play a defensive role during oxidative stress under drought stress (Farooq *et al.*, 2009).

Various physiological, molecular and genetic approaches are employed to cope with the drought stress and increase yield of agricultural crops. Other approaches include conventional and molecular breeding. However, all such approaches are very costly, time consuming and sometimes do not even help in developing desirable drought tolerance traits (Ahmar *et al.*, 2020). Under such circumstances, screening of available germplasm of agricultural crop using morphological, physiological and biochemical attributes are sought as a shotgun approach to identify stress tolerant genotypes (Wagaw, 2019; Riaz *et al.*, 2020). Cluster analysis is one of the methods employed in germplasm screening that relies on grouping genotypes on the basis of similarities and/or differences in their morphological, physiological, molecular and genetic attributes (Romesburg, 2004; Kaufman & Rousseeuw, 2009). The most commonly used clustering methods include WARD's minimum variance but advanced methods like SAHN can be a more effective approach to screen germplasm for drought tolerance based on growth, physiological and biochemical attributes (Day & Edelsbrunner, 1984; Roux, 2015).

The increase in population in the recent years has accelerated the demand for energy and food. However, environmental stresses such as water scarcity limits crop yield and poses a serious threat to agriculture (Malook *et al.*, 2014). Maize (*Zea mays* L.) is one of the crops highly sensitive to drought where yield can reduce by more than 50 percent under drought stress. Shortage of water is worsening in every growing season in most parts of the world having overwhelming effect on productivity of maize (Ludlow & Muchow, 1990). Keeping these aspects in view, it was hypothesized that drought stress should also have altered concentrations of photosynthetic pigments and modulated activities of anti-oxidative enzymatic defense system. Therefore, the drought tolerance potential of various maize genotypes can be identified through differences in their physiological, morphological and biochemical attributes by applying some effective screening approach like cluster analysis. Thus, the objectives of the present study were to compare the drought tolerance potential of 17 most commonly used maize hybrids/genotypes through cluster analysis and to recommend the most promising genotypes for cultivation in drought prone areas based on the findings reported in this study.

## Materials and Methods

Seventeen maize genotypes were screened for drought tolerance potential through Sequential Agglomerative Hierarchical Non-overlapping clustering technique (SAHN). Seeds of nine maize genotypes/hybrids [FH-922, FH-949, FH-985, FH-988, FH-1046, FH-1137, FH-1257, FH-1285, FH-1292] were obtained from Ayub Agricultural Research Institute (AARI), Faisalabad while eight genotypes [Pearl Basic, Yousafwala hybrid, 3025/6129, SWL-539516, YSC-15, P3164w/2403481, 34N41/2587599, P1543/2567600]

were collected from Maize and Millet Research Institute, Yousafwala, Sahiwal. The experiment was laid out in Completely Randomized Design (CRD) with three replications. Field capacity of soil was calculated according to gravimetric method and seeds were sown in plastic pots. Three levels of water stress i.e., 100, 70 and 40% of field capacity were maintained starting from three leaf stage of maize. After 50 days of drought maintenance, various morphological attributes, concentration of photosynthetic pigments and activities of anti-oxidative enzymes was determined.

**Morphological attributes:** Plants from each pot were randomly selected and cleaned with tap water. These plants were kept in paper bags and brought to laboratory for morphological attributes. Shoot and root weights, lengths, leaf number per plant and leaf area were determined by appropriate methods.

**Photosynthetic pigments:** Fresh leaves (0.1g) of plant were taken and ground in 10ml of 80% acetone solution. The plant extract was separated by centrifuging at 5000xg and the supernatant was shifted to new bottles. The absorbance of the supernatant was read in a spectrophotometer at 645 and 663nm and adjusted against 80% acetone as blank. The chlorophyll *a*, chlorophyll *b*, total chlorophyll were calculated by the formulae given by Arnon (1949) while those of carotenoids were calculated following Davis (1976).

**Anti-oxidative enzymes:** Super oxide dismutase (SOD) activity was determined using the procedure of Giannopolitis & Ries (1977). Catalase (CAT) and peroxidase (POD) activities were measured following the method of Chance & Macehly (1955). Total soluble proteins of leaves were estimated following Bradford method (Bradford, 1976).

**Statistical analysis:** The data were analyzed by using Analysis of Variance (ANOVA) technique and treatment means were compared by least significant difference (LSD) test at 5% probability level (Steel & Torrie, 1984).

**Cluster analysis:** In order to minimize the interference of un-related parameters, all variables were divided into 3 distinct groups i.e. *Morphological* (root and shoot fresh and dry weights); *Photosynthetic pigments* (Chl. *a*, Chl. *b* and total Chl.); and *Anti-oxidative enzymes* (SOD, POD, CAT, total proteins). The phonetic analysis and construction of phylogenetic trees was done using NtSys-pc program 2.11X (Rohlf, 2000). All 17 maize genotypes/hybrids were treated as operational taxonomic units (OTUs) and their morphological and physiological attributes were considered as variable characters. Pairwise distances on "interval data" of all pairs of maize genotypes were calculated using the average taxonomic distance (Sneath & Sokal, 1973). The distance matrix was used for UPGMA cluster analysis [Unweighted Pair-Group Method using Arithmetic Averages (Sneath & Sokal, 1973)] using the Sequential, Agglomerative,

Hierarchic and Non-overlapping (SAHN) method. The distinct branches of the trees so constructed were used to classify all 17 maize genotypes into identifiable clusters and sub-clusters based on genetic distance. Genotypes clustered in similar clusters had less genetic distance and hence were assumed to have comparable degree of drought tolerance.

## Results

Statistical analysis of the data revealed highly significant differences for various growth and morphological features of the all 17 genotypes under study. All growth attributes were drastically reduced with increasing level of water stress and more than 50% growth reduction was recorded at the highest level (40% field capacity) in maize genotypes FH-922, FH-985, FH-949 and FH-1257 making them the most susceptible. Genotypes like P3164w/2403481, FH-1137 and Yousafwala hybrid showed less decrease in most of the growth parameters under severe drought conditions. Although, genotypes P1543/2567600, YSC-15, FH-949 and FH-949 showed less decrease in growth parameters under mild drought conditions (70% field capacity), these genotypes showed greater decrease in growth under severe drought conditions (40% field capacity) (Figs. 1 & 2).

The concentration of photosynthetic pigment was also significantly affected by both levels of drought stresses. The highest decrease in carotenoid contents was recorded in FH-985. Moreover, genotypes FH-1046, FH-922 and FH-1137 showed significant decrease in both chlorophyll *a* and carotenoids, as well as, total chlorophyll at both mild and severe drought levels. Total chlorophyll, chlorophyll *a* and carotenoid contents showed lesser decrease in genotypes Yousafwala hybrid, 3025w/6129, SWL-539516 and P3164w/2403481 under drought conditions. In comparison, chlorophyll *b* contents showed less decrease in P3164w/2403481 and 3025w/6129 among all 17 genotypes under study, whereas, greater decrease was recorded in FH-922, FH-1137, FH-1046 and FH-985 (Fig. 3).

The activities of anti-oxidative enzymes (peroxidase, superoxide dismutase, catalase activities) and total soluble proteins were significantly modulated by drought treatment. The highest increase in peroxidase activity under both mild and severe drought conditions was recorded in 3025w/6129, whereas, FH-1046 showed the least increase. Other genotypes showing higher increase in peroxidase activity included Pearl Basic, FH-922, 34N41/2587599 and SWL-539516. Super oxide dismutase activity increased non-significantly in FH-985, FH-1046, FH-922, FH-988 and FH-1137. Genotypes Yousafwala hybrid, 3025w/6129, SWL-539516, 34N41/2587599 and P3164w/2403481 showed the highest increase. Catalase activity was non-significantly increased in FH-949 and FH-922. All other genotypes showed a significant increase in catalase activity with increase in drought level and higher increase was recorded in FH-1285, P3164w/2403481

and 3025w/6129. Total soluble proteins were significantly affected with increase in drought level in all 17 genotypes. The maximum increase in total soluble proteins with increase in drought stress was observed in Yousafwala hybrid, FH-1257, 3025w/6129, SWL-539516 and P3164w/2403481. Genotypes FH-1137, FH-1285, FH-1046 and FH-922 possessed the least soluble proteins in highest level of drought stress (Fig. 4).

### Clustering of genotypes for drought tolerance based on SAHN analysis:

Cluster analysis of the seventeen genotypes on the basis of growth attributes showed three major groups. Group I contained only two genotypes FH-1137 and P1543/2567600 categorized as less drought tolerant (7.03 distance coefficient). Of the remaining 15 genotypes, Group II consisting of FH-985, FH-922 and Pearl Basic branched off at distance coefficient of 4.26 and showed susceptibility to drought. The third group (branching off at 3.19 distance coefficient) consisted of several sub-groups containing drought tolerant Yousafwala hybrid, and, moderately tolerant 3025w/6129 and SWL-539516. P3164w/2403481 branched off separately in sub-group IIIa followed by FH-949, FH-1292 and 34N41/2587599 (sub-group IIIb) all three of which showed tolerance to mild drought but susceptibility to severe drought. Sub-group IIIc branched off at a distance coefficient of 2.76 and consisted of the susceptible and moderately susceptible genotypes FH-1257, FH-988 and FH-1046. The last sub-group comprised of YSC-15 and FH-1285 both of which were categorized as moderately tolerant genotypes (Fig. 5).

All seventeen maize genotypes were grouped into three major groups on the basis of photosynthetic pigments. Group I (distance coefficient 0.10) consisted of 3025w/6129, YSC-15 and FH-949. Group II comprised of FH-949, FH-922, FH-1137, FH-1046, FH-985 and FH-1292 all categorized as drought sensitive showed significant decrease in pigment contents under drought stress. Genotypes 34N41/2587599, P3164w/2403481, Pearl Basic, Yousafwala hybrid, SWL-539516, P1543/2567600, FH-1257 and FH-1285 were included in group III, most of them showing lesser decrease in pigment contents under drought stress and hence were identified as drought tolerant genotypes (Fig. 6).

Clustering of the different maize genotypes for drought tolerance based on activities of anti-oxidative enzymes grouped two drought tolerant maize genotypes Yousafwala hybrid and FH-1046 into a distinct separate group (0.34 distance coefficient). Out of the remaining 15 genotypes, another branch consisting of FH-1285 and FH-1292, both showing decrease in soluble proteins under drought stress, separated at distance coefficient 0.27. The second and largest group was further subdivided into several groups of which IIa, IIb2 and IIc2 consisted of genotypes with significant decrease in protein contents in response to drought stress. Sub-groups IIb1 and IIc1 contained genotypes showing an increase in protein contents with increasing severity in drought stress (Fig. 7).

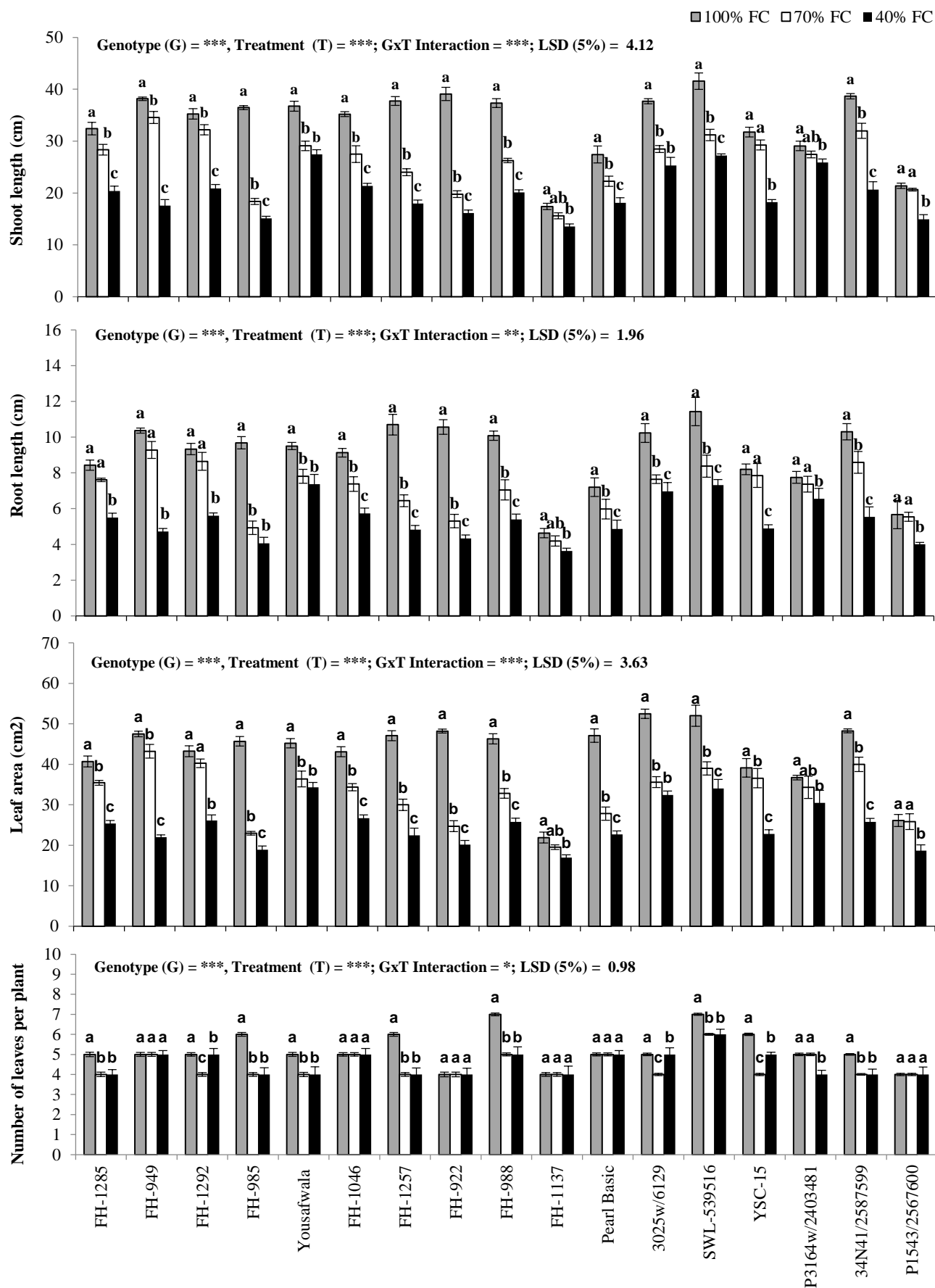


Fig. 1. Effect of various field capacity levels on shoot and root lengths, leaf area and number of leaves per plant in different maize hybrids (*Zea mays* L.).

SE are shown on each bar. Means sharing same letters within genotypes are non-significant. Results of ANOVA shows significance by \*, \*\*, \*\*\* at 0.05; 0.01 and 0.001, respectively; ns is non-significant.

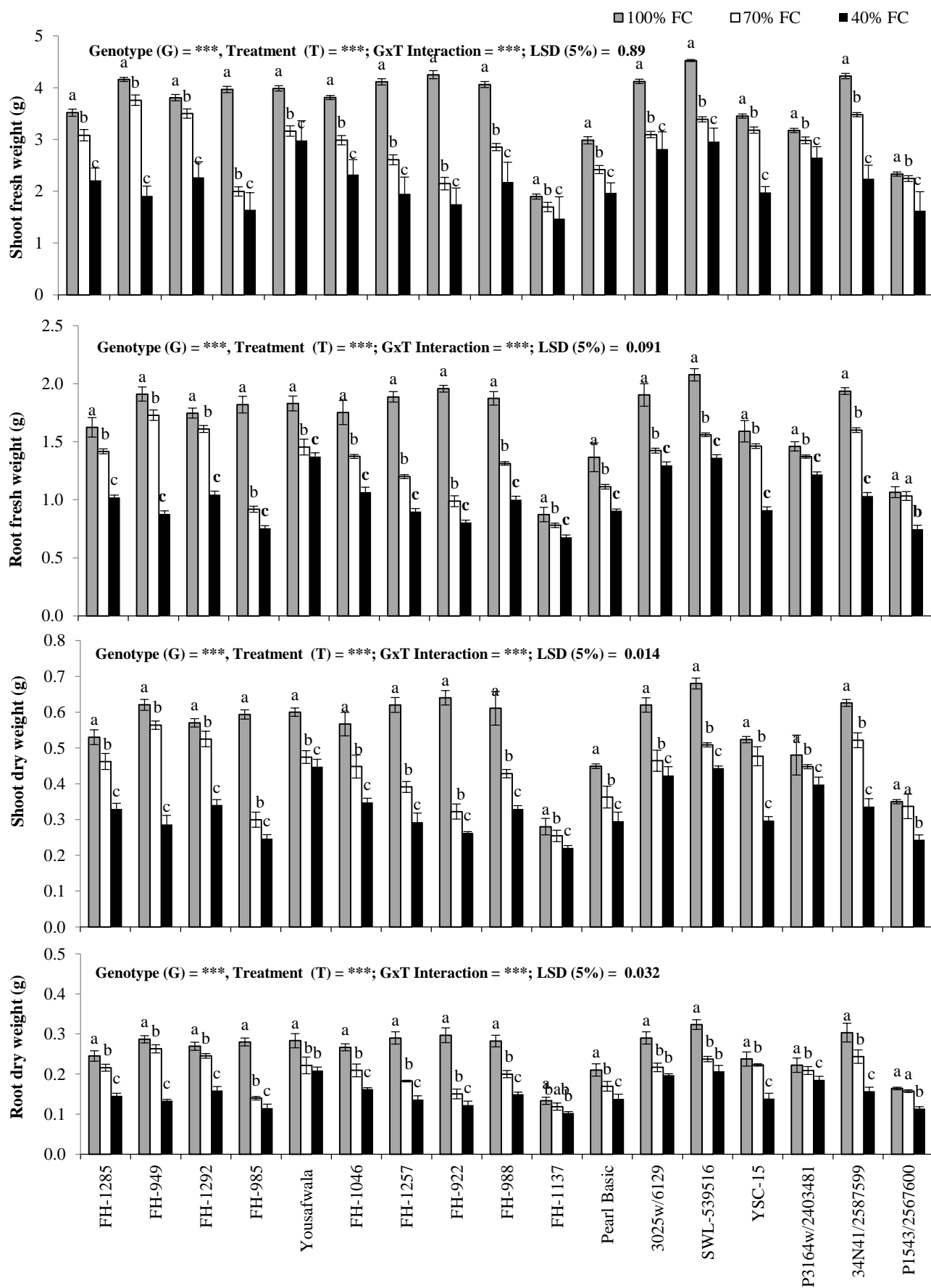


Fig. 2. Effect of various field capacity levels on shoot and root fresh and dry weights of different maize hybrids (*Zea mays* L.). SE are shown on each bar. Means sharing same letters within genotypes are non-significant. Results of ANOVA shows significance by \*, \*\*, \*\*\* at 0.05; 0.01 and 0.001, respectively; ns is non-significant.

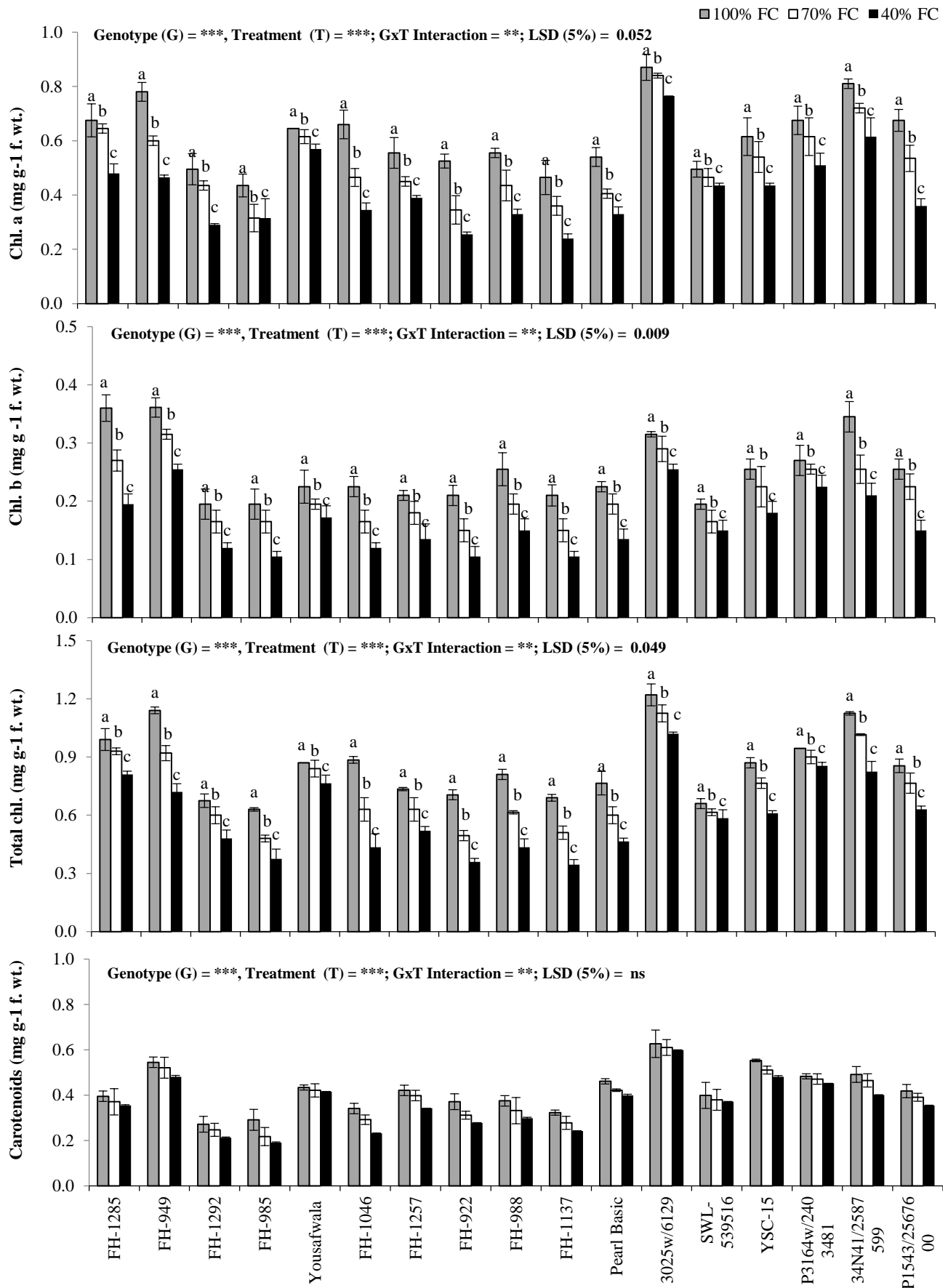


Fig. 3. Effect of various field capacity levels on concentration of photosynthetic pigments in different maize hybrids (*Zea mays* L.). SE are shown on each bar. Means sharing same letters within genotypes are non-significant. Results of ANOVA shows significance by \*, \*\*, \*\*\* at 0.05; 0.01 and 0.001, respectively; ns is non-significant.

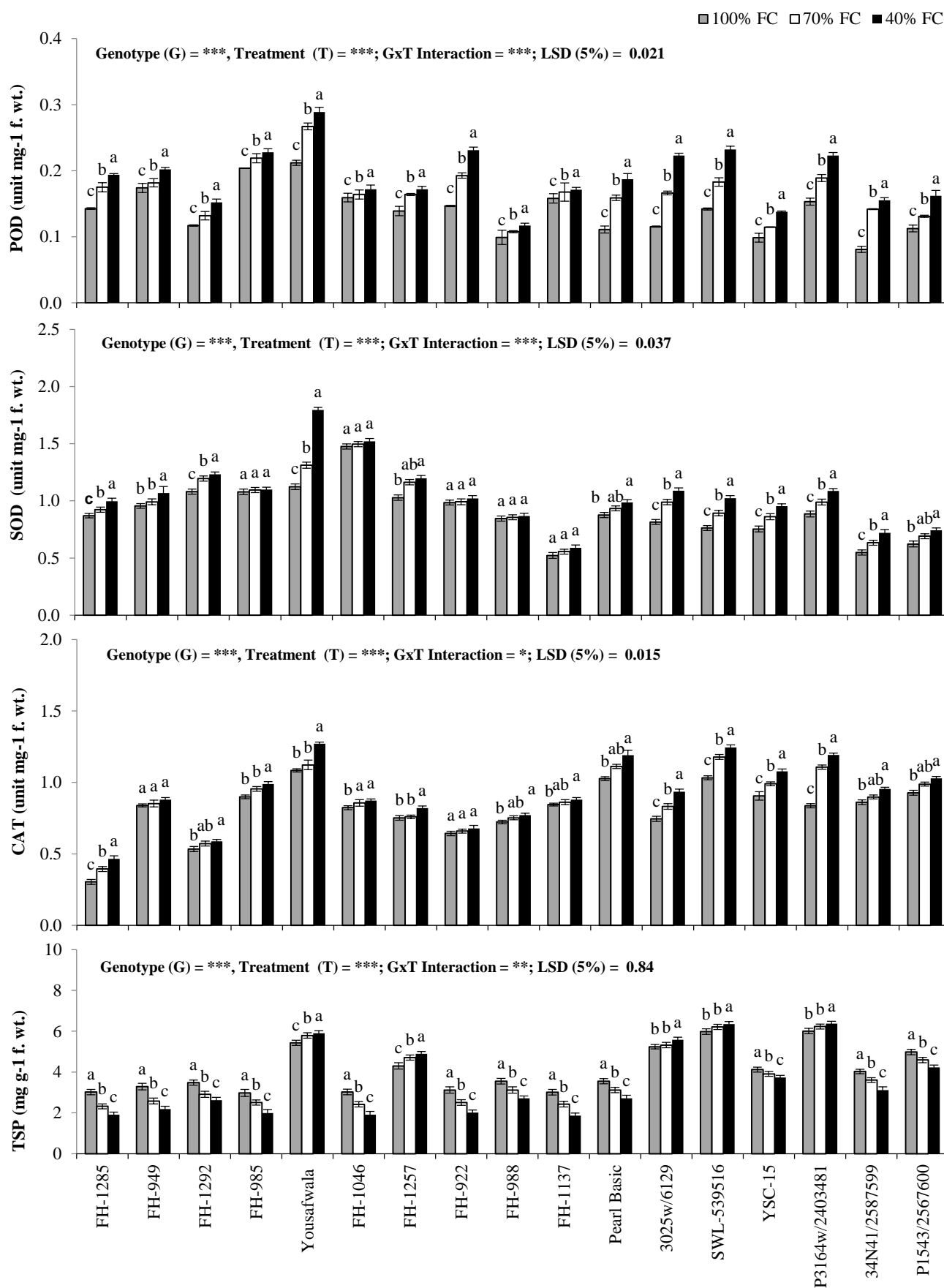


Fig. 4. Effect of various field capacity levels on activities of enzymatic antioxidants (SOD, POD and CAT), and total soluble proteins (TSP) in different maize hybrids (*Zea mays* L.). SE are shown on each bar. Means sharing same letters within genotypes are non-significant. Results of ANOVA shows significance by \*, \*\*, \*\*\* at 0.05; 0.01 and 0.001, respectively; ns is non-significant.

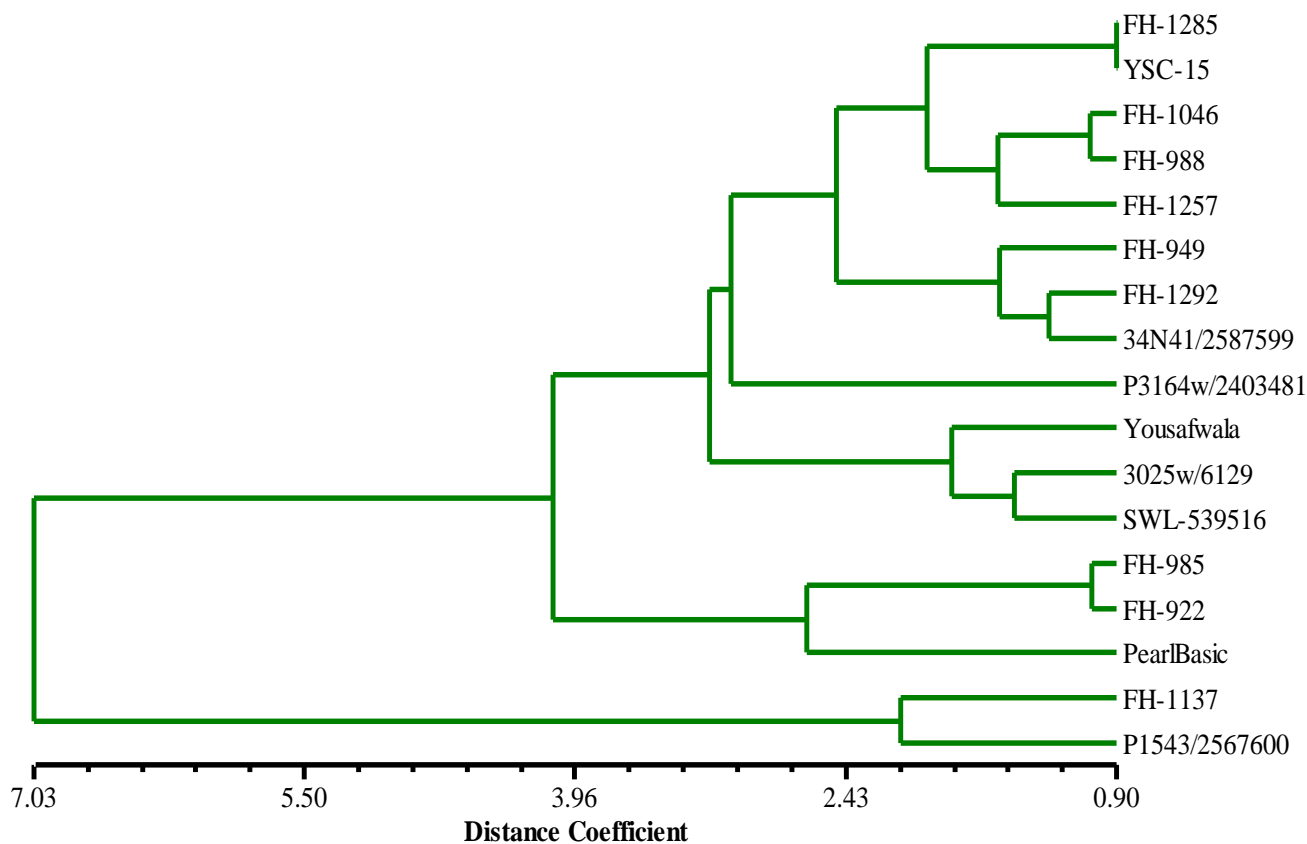


Fig. 5. Clustering of different maize genotype constructed by distance coefficients for drought tolerance based on growth attributes. Genotypes with less distance (or higher similarity) are grouped together indicating close resemblance in observed parameters.

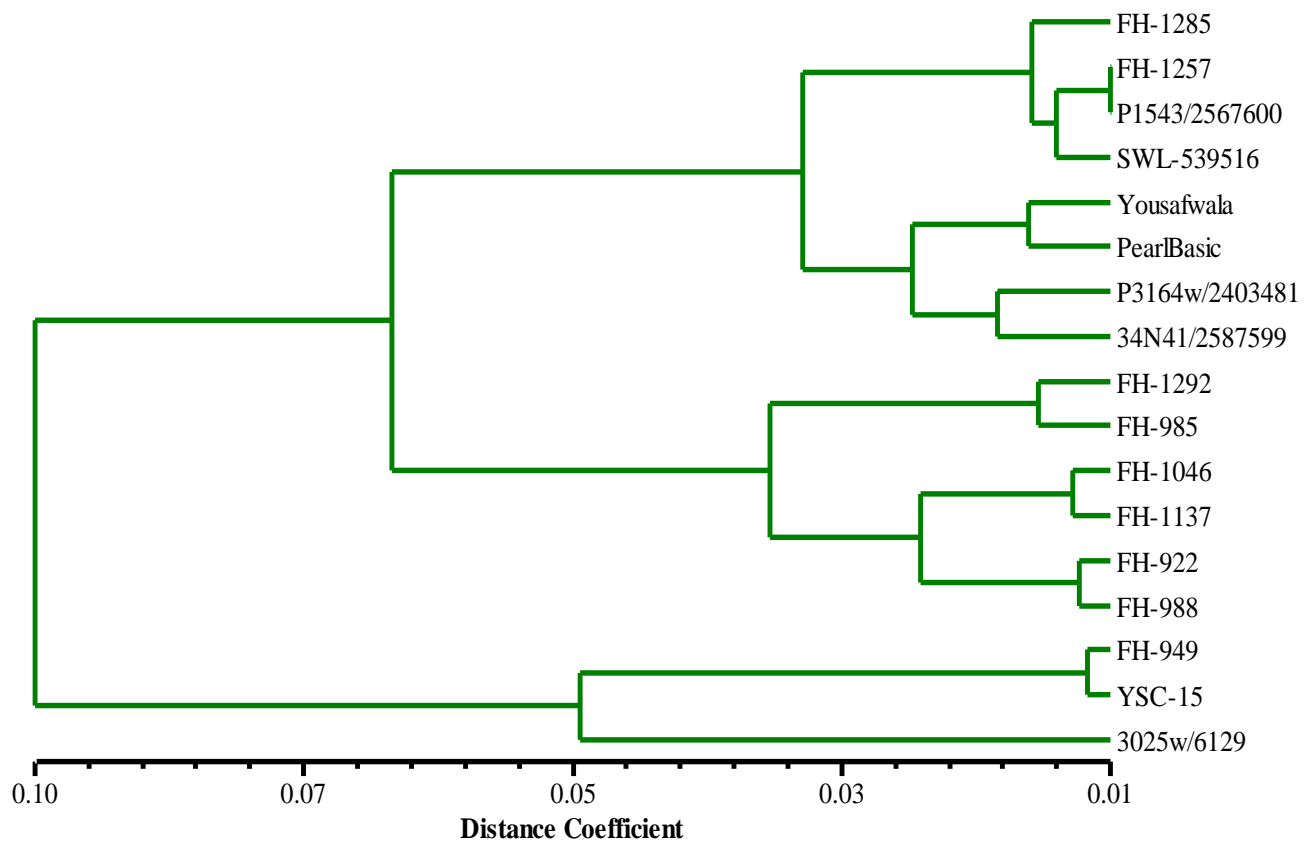


Fig. 6. Clustering of different maize genotype constructed by distance coefficients for drought tolerance based on concentration of photosynthetic pigments. Genotypes with less distance (or higher similarity) are grouped together indicating close resemblance in observed parameters.



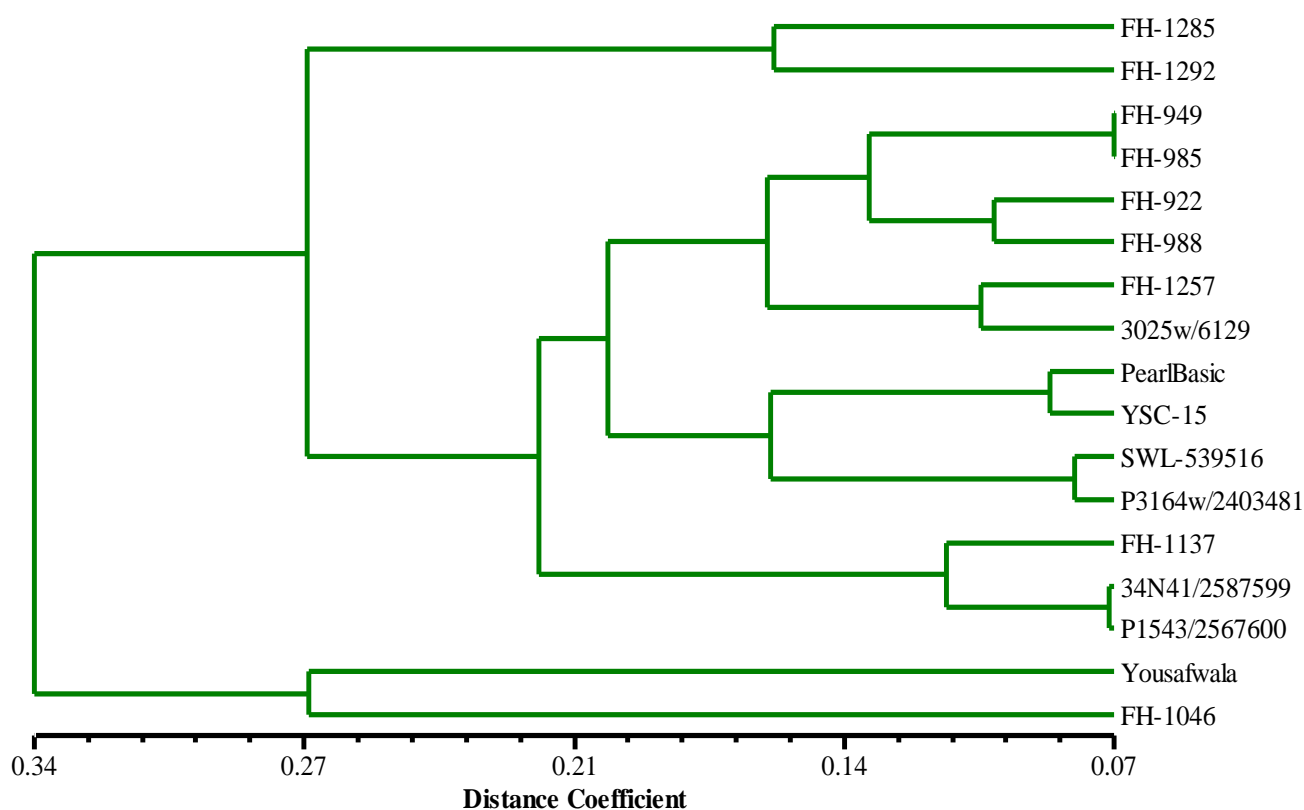


Fig. 7. Clustering of different maize genotype constructed by distance coefficients for drought tolerance based on activities of anti-oxidative enzymes. Genotypes with less distance (or higher similarity) are grouped together indicating close resemblance in observed parameters.

## Discussion

Drought stress is a major limiting factor in crop production. Changes in morphological attributes are the ultimate determinants of stress effects on plants (Jaleel *et al.*, 2009). A clear effect of drought stress on various morphological attributes of maize (*Zea mays* L.) genotypes was observed as these parameters were significantly affected by watering at different levels of field capacity (100% FC, 70% FC, and 40% FC). A significant effect of drought stress on leaf development was observed in maize genotypes used in this study. A highly significant variation both in leaf area and leaf number was observed between normal and drought stress conditions. Number of leaves reduced under water stress as compared to control. In past studies, Patharkar & Walker (2016) reported an increased leaf abscission under water deficient conditions resulting in reduction in cell division and cell expansion and ultimately impairing development of plant leaves. In current study as well, leaf area of different maize genotypes varied significantly between different stress levels (Granier *et al.*, 2006; Ali *et al.*, 2020). These findings show that the reduction in leaf area was a major modification to avoid evapotranspiration loss (Araus, 2012) and to increase water use efficiency which helps the plant to tolerate water stress (Riaz *et al.*, 2010).

Maintenance of shoot and root elongations are plant growth characteristics considered as key indicators of drought tolerance of crop plants. The higher root and shoot fresh weight as observed in drought tolerant genotypes suggested that these genotypes maintained

better root growth to absorb more water that help survival under harsh environmental conditions (Ali *et al.*, 2014). In other studies, Khodarahmpour (2011) reported that reduction in shoot elongation was greater than root elongation under water stress in maize at seedling stage. Considering this, root growth is an important characteristic of plants to tolerate environmental stresses because roots are the main organ to meet the transpirational demand of a plant and play a key role in water availability to plants (Liu & Huang, 2000).

The concentration of photosynthetic pigment including chlorophyll *a*, chlorophyll *b*, total chlorophyll and carotenoids were adversely affected by both levels of irrigation i.e. 70% field capacity (mild drought stress) and 40% field capacity (severe drought stress) as compared to control plants. A significantly higher decrease in carotenoid content was observed in FH-985, FH-1046, FH-922 and FH-1137 genotypes indicating higher sensitivity to drought stress. These varieties showed 34.3%, 31.9%, 25.06% and 25% respective decrease in carotenoid contents compared with controls. A similar decrease in carotenoid content during both mild and severe drought stress in maize plants was recorded by Jaleel *et al.*, (2009). These photosynthetic pigments are of immense importance for plants because they capture sunlight for photosynthesis. Any reduction in photosynthetic pigments directly reduces rate of photosynthesis in plants (Murtaza *et al.*, 2016). Greater reduction in chlorophyll *a*, chlorophyll *b* and total chlorophyll was also recorded in FH-922, FH-1137, FH-1046 and FH-985 at both levels of drought stress showing that these varieties were highly susceptible to drought.

The photosynthetic pigments in these varieties at 40% irrigation level decreased up to 40-50% as compared to their respective control plants. In some other genotypes (genotypes Yousafwala hybrid, 3025w/6129, SWL-539516 and P3164w/2403481), the photosynthetic pigment showed less decrease indicating their higher contribution to drought tolerance. In some past studies, it has been observed that during severe drought, leaves of plants undergo yellowing due to reduction in photosynthetic pigments because of chlorophyll break down in leaves. Under such conditions, leaves undergo chlorosis indicating higher susceptibility of those genotypes to drought stress (Khani & Heidari, 2007; Efeoğlu *et al.*, 2009).

Drought stress results in higher production of reactive oxygen species (ROS) which severely damage plant cells. Plants produce many antioxidant enzymes to cope with adverse effects of these ROS (Goodarzian-Ghahfarokhi *et al.*, 2016). In the present study the activity of antioxidant enzymes POD, CAT and SOD increased at both levels of drought stress (watering at 70% and 40% field capacity) in all 17 maize genotypes. The activity of POD highly increased in drought-tolerant genotypes than the sensitive ones (Wang *et al.*, 2009). In this study as well, the highest increase in peroxidase activity under both mild and severe drought conditions was recorded in 3025w/6129, whereas, FH-1046 showed the least increase in POD activity. Other genotypes showing higher increase in peroxidase activity included Pearl Basic, FH-922, 34N41/2587599 and SWL-539516. Lesser increase in POD under drought stress was recorded in FH-949, FH-985, FH-1046, and FH-1137 as compared to control plants. Under stress conditions low antioxidant activity would be insufficient to scavenge the ROS produced because of oxidative stress resulting in damage to the plants that explains the inability of sensitive genotypes to withstand against deleterious effects of drought stress (Tuna *et al.*, 2013).

A non-significant increase in SOD activity was recorded in FH-922, FH-1046, FH-988, FH-1137 and FH-985 at both levels of drought stress in comparison to control plants indicating that these genotypes were highly susceptible to both levels of irrigation (70% and 40% field capacity). All other genotypes showed statistically significant increase in SOD activity (in Yousafwala hybrid, 3025w/6129, SWL-539516, 34N41/2587599 and P3164w/2403481) indicating that these genotypes were resistant to drought stress. The results for increase in SOD activity were similar to other research work reported on wheat (Csiszar *et al.*, 2005), licorice (Pan *et al.*, 2006), cowpea (Manivannan *et al.*, 2007) and sunflower (Gunes *et al.*, 2008). Another important reactive oxygen species produced under stress conditions is hydrogen peroxide which is damaging for plants. The function of CAT enzyme is to scavenge hydrogen peroxide (Feierabend, 2005). Catalase activity increased non-significantly in FH-949 and FH-922. Other genotypes i.e. FH-1285, P3164w/2403481 and 3025w/6129 showed a significant increase in catalase activity with increase in severity of drought. Genotypes Yousafwala hybrid, 3025w/6129, SWL-539516 and YSC-15 showed moderate but statistically significant

increase in CAT activity as compared to their respective controls. The results indicated that these genotypes have the ability to resist drought stress at both at 70% field capacity (mild stress) as well as 40% field capacity (severe stress) (Abedi *et al.*, 2010)

Drought stress decreased total soluble proteins which showed a direct relationship with reduction in photosynthetic pigments. With reduction in photosynthetic pigments, sufficient protein material cannot be synthesized due to impairment of secondary metabolic pathways of protein synthesis (Khani & Heidari, 2007). In the present study, the amount of total soluble proteins increased under drought stress in some genotypes of maize (Yousafwala hybrid, FH-1257, 3025w/6129, SWL-539516 and P3164w/2403481) even under severe drought (40%) indicating high capability of these genotypes to main protein synthesis under drought stress. Other cultivars showed decrease in total soluble proteins during both level of drought stress as compared to control plants. Such reduction in total soluble proteins in sensitive genotypes might be caused by oxidative damage resulting from severe drought stress (Couée *et al.*, 2006).

The results of cluster analysis also grouped these genotypes in a meaningful manner, which could be due to similarities or differences in their genetic makeup resulting in their specific responses to drought stress. Genotypes Yousafwala hybrid, P3164w/2403481 and FH-1137 tolerated drought conditions better. These highly tolerant genotypes showed no drastic reduction in morphological characteristics at mild and severe drought stress as compared to control (Khalid *et al.*, 2021). Group II, containing moderately tolerant genotypes P1543/2567600, YSC-15, FH-949 and FH-949 showed less decrease in growth parameters under mild drought conditions (70% field capacity), but severe reduction was observed under high drought conditions (40% field capacity). The genotypes FH-922, FH-985, FH-949 and FH-1257 were considered drought sensitive because they showed significant reduction both at mild and severe drought stress as compared to control conditions. It has earlier been reported that drought stress during the vegetative phase of growth reduces the plant growth and development (Jaleel *et al.*, 2009) that has mainly been attributed to greater leaf senescence and reduction in cell enlargement accompanied by disturbance in other essential metabolic pathways (Manivannan *et al.*, 2007).

## Conclusion

Drought stress significantly altered growth, physiological and molecular responses of studied genotypes. Cluster analysis yielded useful information on the drought tolerance potential of maize genotypes. Some genotypes grouped together because of their better performance and were considered drought tolerant (Yousafwala hybrid, P3164w/2403481 and FH-1137) while others as drought sensitive (FH-922, FH-985, FH-949 and FH-1257) as they showed drastic reduction in growth even under mild drought conditions. Moreover, the genotypes P1543/2567600, YSC-15, FH-949 and FH-949 were considered moderately tolerant as their

growth was slightly affected under mild drought conditions but significantly affected under severe drought. The promising genotypes (Yousafwala hybrid, P3164w/ 2403481 and FH-1137) can be used in further breeding programs for developing drought tolerant genotypes and can be cultivated in regions with limited water resources in order to increase cultivated area and production efficiency.

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