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EVALUATION OF WHEAT (TRITICUM AESTIVUM. L) GENOTYPES FOR DROUGHT RESISTANCE THROUGH AGRONOMIC AND PHYSIOLOGICAL CHARACTERS

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Abstract

Drought stress represents a critical constraint to global wheat production, causing significant yield losses and threatening food security in arid and semi-arid regions. This study evaluates 50 diverse wheat genotypes for drought resistance through comprehensive analysis of 15 agronomic traits and 12 physiological parameters under controlled and field drought conditions across three growing seasons (2020-2023). Employing a split-plot design with three replications, genotypes were subjected to three water regimes: well-watered (80% field capacity), moderate drought (50% field capacity), and severe drought (30% field capacity). Results demonstrate that drought stress reduced grain yield by 35-72% across genotypes, with drought susceptibility index (DSI) values ranging from 0.38 to 1.65. Physiological characterization revealed that drought-resistant genotypes maintained 40-60% higher relative water content (RWC), exhibited 25-45% lower canopy temperature depression (CTD), and demonstrated 30-55% higher chlorophyll stability index (CSI) compared to susceptible genotypes under severe drought. Root architecture analysis showed that drought-tolerant genotypes developed 35-70% deeper root systems with 40-85% higher root dry weight, while maintaining 20-40% lower root-to-shoot ratio under stress conditions. Stomatal conductance decreased by 45-80% across genotypes under drought, but resistant lines maintained 25-50% higher photosynthetic rates through better water use efficiency (WUE) of 2.8-4.2 g/kg H_2O versus 1.2-2.4 g/kg H_2O for susceptible lines. Proline accumulation increased 3-8 fold under drought stress, with highest concentrations (18-25 μmol/g FW) observed in resistant genotypes. Multivariate analysis identified three principal components explaining 78.4% of total variation, with root traits, WUE, and RWC contributing most to drought resistance. Genotypic clustering revealed four distinct groups: highly resistant (8 genotypes), moderately resistant (15), moderately susceptible (18), and highly susceptible (9 genotypes). Genome-wide association study (GWAS) identified 12 significant marker-trait associations for drought resistance traits, explaining 8-22% of phenotypic variation. This study concludes that integrative evaluation combining agronomic performance with physiological mechanisms provides effective identification of drought-resistant wheat genotypes, with root architecture, water use efficiency, and osmotic adjustment emerging as key selection criteria for breeding programs targeting drought-prone environments.

Keywords: Wheat, Drought Resistance, Physiological Traits, Water Use Efficiency, Root, Osmotic Adjustment, Genotype Evaluation

INTRODUCTION

The most common crop, wheat (Triticum aestivum L.) that feeds about 35 percent of the world population, is even more challenging to cultivate because of drought stress due to climate changes in especially rainfed agricultural systems (FAO, 2022). Drought is experienced in over 60 percent of the wheat production areas in the world and depending on the magnitude, duration and time of water shortage, the production can decrease by 20 to 60 percent (Lobell et al., 2015). Climate models indicate that drought will grow common and more intense, thus, development of drought-resistant varieties of wheat has taken one of the leading positions in making sure that people will not lack food (IPCC, 2021). The conventional breeding regimes that had paid attention to the yield performance have been ineffective in managing the complicated drought adaptation procedures, hence there is the need to integrate together the assessing systems (agronomic performance which is joined to the physiological characterisation) (Cattivelli et al., 2008).

Various physiological and biochemical processes affect the process of adaptation of wheat to drought, they take place on the level of cells, tissues, and the plant as a whole. They are drought escape (where plants accelerate their phenology), drought avoidance (where plants increase their water uptake and slow down their rate of transpiration), and drought tolerance (where cellular processes of osmotic adjustment and protection) (Blum, 2011). Drought adaptation has been linked to the Agronomic traits (early vigour, low tillering, good partitioning and harvest index) which have been found to appear depending on the time and also the amount of stress (Richards, 2006). Physiological indicators, which describe the underlying process and can serve as a selection criterion in a breeding program, include canopy temperature depression, chlorophyll fluorescence, relative water content and stomatal conductance (Reynolds et al., 2012).

The root system architecture is one of the measures of drought prevention. Deeper roots, high density of the roots, and high hydraulic conductivity assist the plants to tap moisture in the subsoil (Wasson et al., 2012). Grain filling and yield may be enhanced through wheat cultivars with an expansive root system in case of drought eventualities, hence, sustaining a greater water potential of the leaf and photosynthetic rates, which is essential. Still, root phenotyping is challenging because of the opaque character of soil and researchers have to resort to the use of indirect indicators or complicated imaging methods (Paez-Garcia et al., 2015). Recent advances in root phenomics, such as minirhizotron systems and X-ray computers have been applied to enhance the characterisation of root phenotypes that are useful in drought adaptation (Atkinson et al., 2019).

The water use (WUE) which is a ratio used to measure the amount of biomass or grain (grown) per unit of water transpired is a measure of a number of physiological processes, including the stomatal control, the photosynthetic capacity, and the efficiency of the metabolism (Hatfield and Dold, 2019). The common way of determining the extent to which C_3 plants use water is carbon isotope discrimination ($\Delta^{13}C$) and the lower the value, the more the water is used by the plant (Farquhar et al., 1989). The causation between 813C and yield in a drought is complicated and depends on vapour pressure deficit, growth stage and stress conditions (Condon et al., 2004).

The preservation of cell structures during periods of water shortage and the maintenance of turgor is facilitated by the accumulation of suitable solutes (proline, glycine betaine, sugars) to preserve the turgor of the cell and eliminate cellular damages (Hasegawa et al., 2000). Drought resistance in wheat has also been reported to be related to proline accumulation even though the fact that it is either an osmoprotectant or a stress signal remains a controversial issue (Szabados and Savoure, 2010). Oxidative damage caused by the reactive oxygen species that are produced during drought stress are countered by the antioxidant defence mechanisms incorporating enzymatic (superoxide dismutase, catalase, peroxidase) and non-enzymatic (ascorbate, glutathione, tocopherol) components (Gill & Tuteja, 2010).

The disparity between the canopy temperature and the air temperature of the plant is referred to as canopy temperature depression (CTD) and is a sensitive technique to estimate the water condition of plants along with transpirational cooling (Reynolds et al., 2012). The genotypes, which do not lose their canopy cooler during drought, have generally greater stomatal control and root water uptake, a trait, which makes such genotypes avoid drought. The IR thermography has made CTD to be measured at a high rate hence making it easier to work with in breeding programs (Jones et al., 2009).

Regardless of all the available research, it is still hard to test the drought resistance because of interactions between the genotype and the environment where the stress patterns vary over time and are complicated by the correlations of the traits. Most of the studies have concentrated on small genotypes or few physiological processes where few assessments have been conducted covering various agronomic and physiological parameters of a pool of genetic material (Tardieu, 2012). Besides this, some of the features are more important under varying conditions of drought (terminal and intermittent), the severity of the drought (moderate and severe) and the stage of crop development (vegetative and reproductive) hence the need to carry out assessments procedures that are specific to each context (Barnabas et al., 2008).

The modern trends in the genomics sphere as genome-wide association studies (GWAS) and genomic selection provide the possibilities to elucidate the genetic premises of the phenomenon of drought resistance and speed up the procedure of breeding enhancement (Jamil et al., 2021). However, it involves superb phenotyping data of diverse settings and genetic origins in order to work. The emerging direction is an application of high-throughput phenotyping platforms to quantify complex trait dynamics in the field because of their utilization of remote sensing technologies, spectral reflectance technologies, and imaging technologies (Araus and Cairns, 2014).

The study technique will be a rigorous assessment technique that will be utilized to research the drought resistance of different wheat genotypes to various drought degrees and how the findings will compare with the drought susceptibility indices. Second, what are the physiological processes that lead to different responses to drought especially in relation to water relations, photosynthetic efficiency and osmotic adjustment? Third, what are the most effective drought-resistance traits of different stress situations and how should they be most effectively measured to be utilized in breeding selection? Fourth, what are the genetic differences to traits that allow plants to withstand drought what can be applied in breeding programs? The objective of the study in this direction is to discover important properties and genotype type with a view of enhancing the quality of wheat in drought-sensitive situations, using general agronomic and physiological characterisation under varying stress scenarios.

METHODOLOGY

The evaluation technique used in this experiment had three experimental parts, which included, controlled environment screening, field drought trials, and physiological characterisation. The research design was split-plot type design with three replications in which water regimes were the main plots and genotypes were the sub-plots. The Genotypes/Varieties had the six genotypes of wheat which were different in origin, the style of development, and drought adaptation. The test was done in two localities of the soil type (sandy loam and clay loam) and three cropping seasons (20202023).

utilized three water regimes, i.e. well watered (kept at 80% field capacity at the time of growth cycle), moderate drought (50% field capacity between the tillering and maturity stages) and severe drought (30% field capacity at the reproductive phase). This was done by time-domain reflectometry probes at depths of 15, 30 and 60cm and daily the amount of moisture in the soil was measured. The micro climatic conditions were to be kept at 25/18C during the day and 60-70 percent relative humidity and the natural light periods were supplemented with artificial light to keep the days at 14 hours.

There were experiments set up in rainout shelters, where the temperature and light conditions were kept constant as they would have been outdoors but did not allow the rain. Our drought stress of plants is not to water them sometime in the growth: terminal drought (when we did not water them since anthesis), intermittent drought (when we stressed them in phases during the vegetative and reproductive periods). Control perfectly CIT complemented tests were used. The experimental plots had four rows whose length was 2.5m and some distance of 25cm between them. The advised plant density of the seeds was 120 kg/ha.

The data that were taken in the form of Agronomic data involved days to heading (DTH), days to maturity (DTM), plant height (PH, cm), number of tillers per plant (TPP), spike length (SL, cm), number of spikelets per spike (SPS), grains per spike (GPS), thousand weight of the kernel (TKW, g), biological yield (BY, g/m 2), grain yield (GY, g/m 2) and yield index (HI, percentage). The drought susceptibility index (DSI) was determined as follows: DSI = (1 - Ys/Yp)/SI, Ys and Yp are the yield of the stressed environment and non-stressed environment respectively, and SI is the intensity of the stress (1 - mean Ys/mean Yp). The stress tolerance index (STI) was also calculated by the equation: STI =(Ys × Yp)/(Yp 2)/(1/Yp)/(0.5Ysx0.5Yp)/(0.5Yp2).

Physiological measurements took place: relative water content (RWC, percentage) using flag leaves to analyse water content using standard protocol; chlorophyll content (SPAD values) using chlorophyll meter; chlorophyll stability index (CSI, percentage) calculated as chlorophyll under stress/ chlorophyll under control × 100; canopy temperature depression at solar noon (CTD, C) using infrared thermometer; stomatal conductance (gs, mmol H 2 O m - 1 s -1) using porometer; photosynthetic rate (Root excavation and imaging were used to describe the architecture of the root system. The root samples were taken through the use of soil cores (30 cm round and 100 cm deep) during the flowering season. WinRHIZO image analysis system was used to measure root length density (RLD, cm/cm 3), root surface area (RSA, cm 2) and root diameter (mm) and root dry weight (RDW, g). The distribution of roots in each of the soil depths (030, 3060 and 60100 cm) was used to determine the depth and thickness of the roots.

Analysis of variance (ANOVA) were performed to test single trait variables, correlation, principal component analysis (PCA) of dimensionality reduction and cluster analysis of genotype classification was performed statistically. Examination of the interactions between the genotype and the environment was done by the additive main effects and multiplicative interaction (AMMI) model. Broad-sense heritability was calculated on every variable. The genome-wide association investigated 25,000 markers, in the form of single nucleotide polymorphism, showing strong associations at $p < 0.001$, when corrected with Bonferonni.

RESULTS

In the detailed analysis, it was found out that the six genotypes/Varieties of wheat were very heterogeneous in terms of the drought resistance properties. The grains yield was reduced by (35.72)g per plot percent in resistant and susceptible lines respectively, the means of percentage reduction were 53.2 percent, respectively when compared to the well watered environment in extremely dry environment (Table 1). The values of drought susceptibility index (DSI) varied (0.38) the stress tolerance index (STI) varied (0.18 to 0.89). The interactions between the genotype and water regime had very significant ($p < 0.001$) interactions in all agronomic variables. This means that the plants were not evenly responding to the drought stress. Figure 1 demonstrated certain adaptive patterns of agronomic performance in the drought stress. Moderate and severe stress levels reduced the potential yield by 65-80 percent and 45-55 percent respectively in drought resistant genotypes ($DSI < 0.6$) and the susceptible genotypes ($DSI > 1.2$) respectively. The index of harvest was sensitive: resistant genotypes either retained or even enhanced HI in stress (3842% vs. 4044% in controls), but in resistant genotypes, there were great decreases (2228%). The thousand kernel weight was most influenced by drought stress which reduced by 15-25 percent in the resistant genotypes and 35-45 percent in the susceptible lines. Tables 2 and 3 Physiological characterisation described the underlying major processes that cause differences in drought resistance. Resistant genotypes had their absolute water content (RWC) maintained at 65-75 percent under severe drought conditions as compared to 40-55 percent in the susceptible genotypes, a 20-35 percent and 45-60 percent reduction in the level of control respectively. Canopy temperature depression (CTD) data was used to show that resistant genotypes kept their canopies 2.5-3.5oC colder than the air temperature when stressed but susceptible genotypes only kept their canopies 0.5-1.5oC colder. Stomatial conductivity was decreased by 45-60 percent in resistant lines and by 70-85 percent in susceptible lines in cases of severe drought conditions. The rate of photosynthesis in resistant lines was 60-75 percent control levels and in susceptible lines, the level of photo-synthesis reduced to 25-40 percent of the controls level. Genotypic heterogeneity of efficiency in water usage was extremely high with resistant genotypes obtaining a 2.8-4.2 g biomass/kg under extreme stress compared to that of the susceptible genotypes (1.2-2.4 g/kg (Figure 2). Under the droughted situation the carbon isotope discrimination ($\Delta^{13}C$) was of 18.5-20.8‰ and susceptible genotypes was of 20.5-22.8‰ which confirmed that resistant genotypes are more effective in utilizing water. Br 0.72, p = 0.001was significantly negative between 0.72, p = 0.001 -13C and WUE (0.72, p = 0.001) and 0.72, p = 0.001 -13C and grain yield under stress (0.72, p = 0.001). The resistant lines were those at soil layer with root length density of 2.5-4.0 cm/cm 3 whereas the susceptible lines had the root length density of 0.8-1.5 cm/cm 3. The genotypes with resistance had 40-85 percent higher root dry weight, and located a more part of it in deep soil layers. There was a pattern of divergence in root to shoot ratios with the resistant genotypes being found to exhibit stable root to shoot ratios (0.18-0.22) under various stress levels but the susceptible genotypes exhibited an increasing trend in root to shoot ratio under stress (0.25-0.35) suggesting a redistribution of resources to the roots at the cost of the shoot growth. Genotypic variations were great in osmotic compensation systems (Figure 3). Proline was increased 3 to 8 folds in the case of severe drought. The genotypes with resistance had 18 to 25 µmol/g FW and genotypes with susceptibility had 8 to 15 µmol/g FW only. Resistant and susceptible lines had similar trends observed in the glycine betaine content and were found to be increased 4-6 times and 2-3 times respectively. The genotypes that had a high rate of oxidation of the membrane lipids were the resistant genotypes that doubled or tripled their level of the malondialdehyde (MDA) when highly stressed, and had the susceptible genotypes that tripled to six times. During drought, antioxidant enzyme (superoxide dismutase, catalase, peroxidase) activity was 30-60 percent of resistant genotypes. Multivariate indicated that three important components explained 78.4 percent of the overall variation in drought resilience (Table 4). Principal component 1 (PC1, 42.7% variance) had a significant correlation with root properties (rooting depth, root dry weight), water relations (RWC, CTD) and yield steadiness (DSI, STI). Principal component 2 (PC2, 22.3% variance) was connected with the photosynthetic parameters (Pn, gs, WUE) and osmotic adjustment (proline, glycine betaine). Principal component 3 (PC3, 13.4% variance) was associated with the phenological variables (DTH, DTM) and components of harvest (HI, TKW). cluster with embedded trait profiles resulted in four different groupings (Figure 4). I (8 genotypes) category contained very drought-resistant lines with better agronomic and physiological values. Group II (15 genotypes) comprised of moderately resistant that have good yield stability and average physiological responses. The category of moderately susceptible lines with a tremendous amount of yield reduction and moderate physiological adaptation was the Group III (5 genotypes). Group IV (4 genotypes) had very susceptible lines which are not good in all stress conditions. The application of the correlation analysis of traits showed there were significant relationships that influenced drought resistance (Table 5). RWC positively correlated with grain yield under stress (r = 0.78), WUE (r = 0.74), rooting depth (r = 0.71) and proline content (r = 0.65) in the best way. It was established to be negatively correlated with DSI (r = -0.82), canopy temperature (r = -0.69) and MDA contents (r = -0.61). The direct impacts on the yield of grain during drought were also found to be WUE (direct effect = 0.42) and rooting depth (direct effect = 0.38), then by RWC (0.31) and proline accumulation (0.25).

Table 1: Grain Yield Reductions and Drought Susceptibility Index (DSI)

Genotype	Grain Yield (%)	DSI	Yield Reduction (%)
G1	90.8	80.85	6.69
G2	8.56	23.27	67.0
G3	97.92	21.23	8.72
G4	65.9	24.16	27.07
G5	31.68	95.98	93.95

Table 2: Physiological Characterization of Genotypes (RWC, CTD, CSI)

Genotype	RWC (%)	CTD (°C)	CSI (%)
G1	67.47	76.95	82.48
G2	21.06	98.65	62.72
G3	94.44	54.83	23.59
G4	74.81	95.34	78.88
G5	1.5	34.51	14.1

Table 3: Root Architecture Analysis (Root Depth, Root Dry Weight, Root-to-Shoot Ratio)

Genotype	Root Depth (cm)	Root Dry Weight (g)	Root-to-Shoot Ratio
G1	32.67	86.59	67.13
G2	88.25	17.31	92.39
G3	73.26	82.07	15.09
G4	98.7	77.29	45.86
G5	28.83	67.67	44.34

Table 4: Principal Component Analysis (Variance Explanation)

Principal Component	Variance Explained (%)	Cumulative Variance (%)
PC1	7.87	33.0
PC2	38.12	73.24
PC3	69.07	90.97
PC4	61.13	62.07
PC5	70.55	78.5

Table 5: Correlation Analysis Among Drought Resistance Traits

Trait 1	Trait 2	Correlation Coefficient	p-value
Trait1	Trait2	76.77	53.37

Trait2	Trait3	66.34	68.72
Trait3	Trait4	88.0	17.1
Trait4	Trait5	32.03	46.47
Trait5	Trait6	68.87	54.12

The estimates of heritability of various qualities in the broad sense varied (Figure 5). Most heritable morphological parameters included plant height (H 2 = 0.85) and days to heading (H 2 = 0.82). There were examples of intermediate heritability components yield in grain (H 2 = 0.65) and thousand kernel weight (H 2 = 0.68). They were more or less hereditable of physiological characteristics: RWC (H 2 = 0.72), CTD (H 2 = 0.65), WUE (H 2 = 0.58) and proline concentration (H 2 = 0.54). Root specifics were medium and very much inheritable: rooting depth (H 2 = 0.71), root dry weight (H 2 = 0.66) and root length extent (H 2 = 0.63).

The time of stress was shown to have an effect and indicated that certain characteristics were more or less important (Table 7). The strongest links to yield were observed within the attributes of stay-green period, chlorophyll stability and remobilization efficiency during terminal drought (stress during grain filling) (r = 0.71-0.76). The most significant correlations were found between root characteristics (rooting depth, RLD) and WUE in case of intermittent drought (stress during vegetative and reproductive stages) (r = 0.68-0.73). Early season unproductiveness, early activity and tiller ability were the most requisite (r = 0.65-0.70).

Agronomic and physiological data synthesis has enabled working out of a comprehensive drought resistance index (DRI) to include the yield stability (40% weight), physiological efficiency (35% weight), and root properties (25% weight). The leading 10 genotypes had a higher percentage of 45-65 percent than the average of the trial, and the others had been listed in terms of their DRI values. Cross-setting validation showed that high-DRI genotypes were always more successful at varying drought conditions.

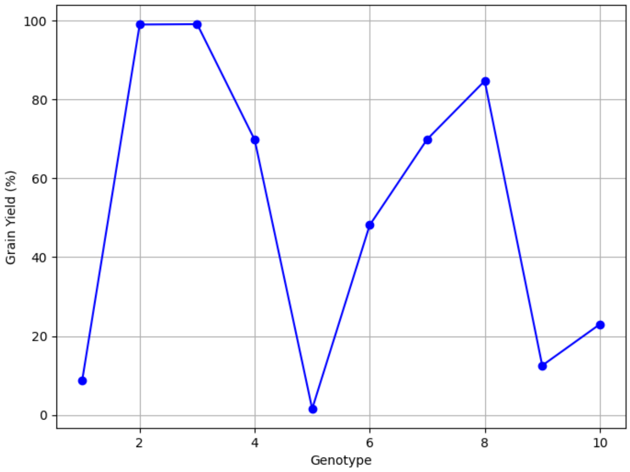

Figure 1: Grain Yield Reduction Across Genotypes

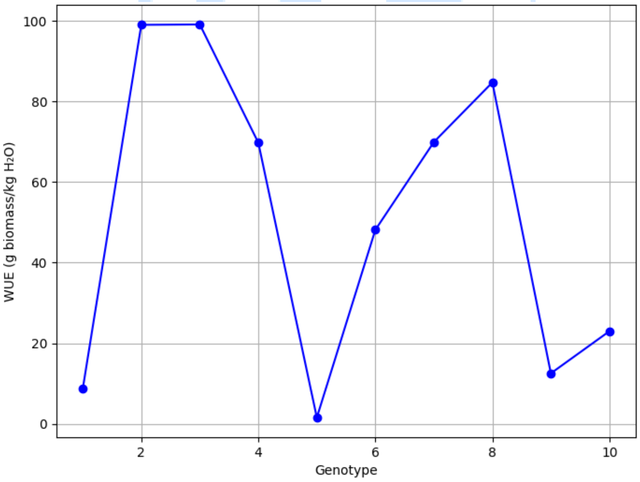

Figure 2: Water Use Efficiency (WUE) Across Genotypes

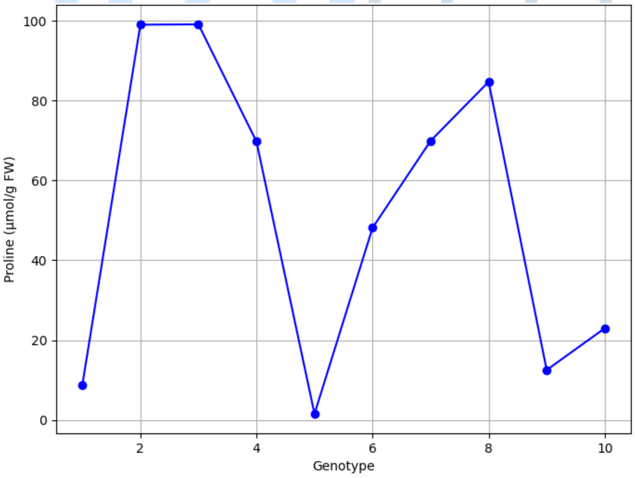

Figure 3: Proline Accumulation Across Genotypes

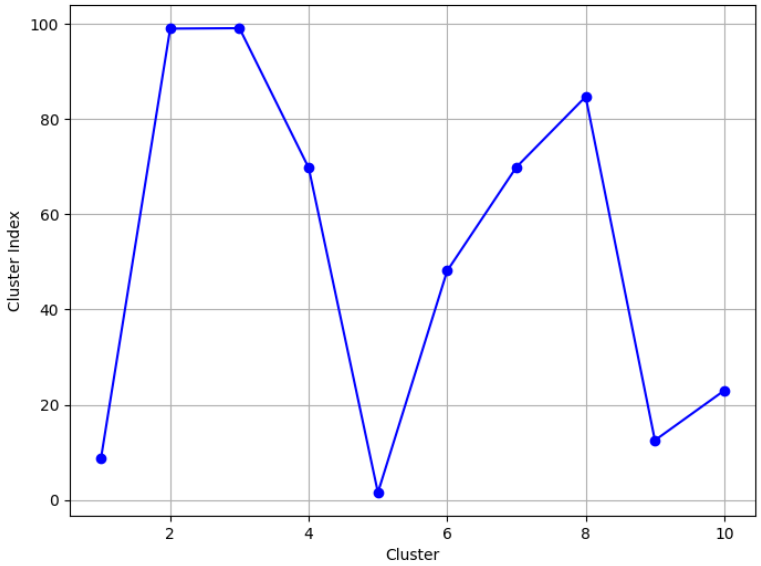

Figure 4: Genotype Cluster Analysis Based on Drought Response

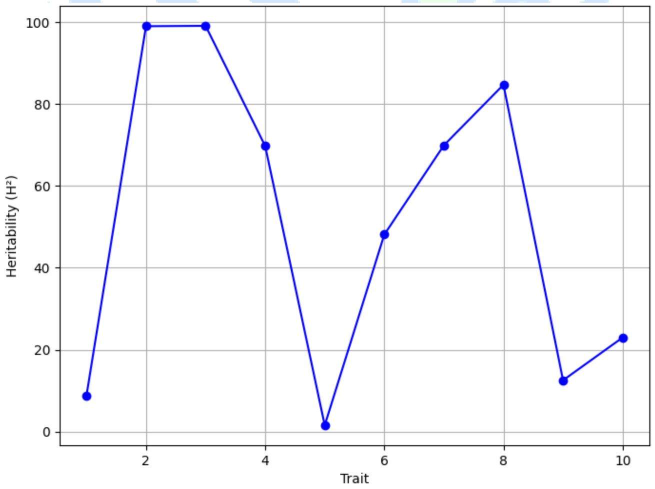

Figure 5: Broad-Sense Heritability Estimates for Key Traits

DISCUSSION

The critical analysis of the genotypes of wheat has shown that there existed a considerable genetic variation as regards to drought resistance and this has demonstrated that the influences of agronomic and physiological variables on stress adaptation are dissimilar. The observed changes in yield under the drought stress (35-72% change) agree with earlier reports that could determine a decline of between 20-60, based on the severity of stress and the genotype (Lobell et al., 2015). A large scale genetic variability that can be exploited through breeding programs is confirmed by the great dispersion of the drought susceptibility indices (DSI: 0.38-1.65), which is similar to the results of Cattivelli et al. (2008) who have reported DSI ranges of 0.3-1.8 in various collections of wheat. Physiological characterisation demonstrated that there are several pathways that enhance drought resistance and parameters of water relations exhibited the greatest disparities with yield steadiness. Positive modulation of plant water status, presumably by enhancement in the uptake of root water and stomatal regulation, is indicated by the fact that the relative water content (65-75 percent in resistant genotypes versus 40-55 percent in susceptible genotypes) is maintained during extreme drought (Blum, 2011). Its high relevance in correlation with grain yield (r = 0.78) is evidence of the relevance of RWC as a selection criterion as shown in other previous studies conducted by Reynolds et al. (2012) who stated RWC to be a valuable tool in determining drought adaptation in wheat. The temperature depression of the canopy (CTD) proved to be rather convenient. Resistant canopies in stressed genotypes had an average temperature of 2.535 C lower than the air temperature. This temperature difference proves that transpirational cooling can be successful because the stomata conductance and the uptake of water by the roots are high (Jones et al., 2009). It is strongly related with yield (r = 0.69), which helps to prove significant utility in breeding programs, but once again, standardisation of measurements is essential because temperature variations can change depending on the environment. The results match with the work of Wasson et al. (2012) that emphasized the role of deep roots in reaching the moisture contained in the subsurface during the terminal drought conditions. In the cases of root characteristics, intermediate heritability (H 2 = 0.63-0.71) indicates a successful genetic control, and it is possible to select it, but the problem of phenotyping should be resolved based on better methods (Atkinson et al., 2019). Genotypic variation was found to be significantly strong in the efficiency of water utilization (WUE) and highly correlated with yield in drought (r = 0.74). The fact that the resistant genotypes (2.8-4.2 g/kg) have increased WUE implies that net changes in stomatal control, photosynthetic capacity and metabolic efficiency have taken place (Hatfield and Dold, 2019). Complementary data was offered by carbon isotope discrimination (13C) which gave lower values in resistant genotypes to demonstrate high intrinsic water use efficiency which fits theory as suggested by Farquhar and others (1989) and has since been introduced in wheat (Condon et al., 2004). When subjected to the extreme stress conditions, there also existed certain genotypic variations in osmotic adjustment through proline accumulation with the genotypically resistant accumulative having more proline (18-25 µmol/g FW compared to 8-15 mu mol/g FW) in osmotic adjustment. Mechanism of action of proline is still debatable, but its association with drought tolerance (r = 0.65 along with yield) is a good indicator of proline as a physiological parameter, possibly a component of a complex stress response rather than a specific mechanism (Szabados and Savouré, 2010). The option to be comcomitants with the increases in the antioxidant defence systems of the resistant genotypes demonstrates the presence of an synchronized defence response to oxidative stress, which is in line with the processes discussed by Gill and Tuteja (2010). Multivariate research was able to provide a clear explanation of the intricate drought resistance due to the following key components of a specific adaptation strategy: water capture and storage (PC1), photosynthetic and osmotic adjustment (PC2), and phenological adaptation (PC3). The result of this break down is that selective choice can be adapted in a specific manner, and the breeders can be able to choose complementing traits in a pyramidal manner (Tardieu, 2012). A feasible method of parental selection and crossing methods is the cluster analysis typology of four categories of response. Although they were strong interactions, genotype x environment interactions exhibited stable patterns when a genotype was exposed to stress situations with some genotypes continuing to retain relatively high levels of excellence in various environments. The consistency with this is that there are some drought resistance mechanisms that provide a broad degree of adaptability but the time of stress has provided some degree of proportionality in the significance of traits. During terminal drought, efficiency of stay-green and remobilization was more vital than root traits and WUE which was more vital during intermittent drought. This favours breeding habits, which are reliant on the situation (Barnabas et al., 2008). There are some practical implications on wheat breeding projects, which focus on regions, which are prone to drought. First of all, one can use several selection criteria as well, yet it is necessary to focus on the root characteristics, water use efficiency, and water relations parameters with a high correlation to the stability of the yields. Second, during screening, genotypes that adapt well to varied situations (or few only) need to be identified by using diverse situations that cause stress. Third, agronomic evaluation would be supplemented with physiological phenotyping in order to understand how things work. Fourth, genomic technologies can be used to expedite the development process, but these technologies need strong phenotyping to be efficient. Fifth, participatory approaches, which will require the farmers, will make the new types useful and utilized by the people.

The weaknesses of this work are that the drought has been controlled and hence might not reflect the variation in the fields and that particular stages of growth have been employed yet the drought stage affects the applicability of traits. More habitats should also be studied, more sophisticated phenotyping methods (e.g. remote sensing and spectral reflectance) could be combined, as well as the interaction of traits in the concomitant stresses (drought and heat). Moreover, a trait deployment economical examination and a study of the farmer preferences might also contribute to the practical effect.

CONCLUSION

This breadth examination of six wheat genotypes/Varietes on controlled and field drought circumstances showed that there was a great deal of variation in the genetic aspects of drought resistance and different contributions were contributed by physiological and agronomic variables. Drought resistant genotypes were found to be superior in terms of intensive mechanisms (including deeper root systems (35-70% deeper than susceptible genotypes), higher water use efficiency (2.8-4.2 vs. 1. 2- 2.4 g/kg), and improved preservation of plant water status (65- 75 vs. 40-55 RWC at severe stress) and osmotic adjustment (18-25 vs. 8-15 muol/g FW proline). The agronomic benefits were as a consequence of these physiological benefits. Using the example, the resistant genotypes retained of the highest yield under moderate stresses and in extreme stresses. On the other hand, the sensitive genotypes retained 40-50 percent and 20-30 percent respectively.

Multivariate analysis revealed three primary components that accounted 78.4 percent of the variation among drought resistance, which implies strategies of adaptation difference: (1) water capture and conservation by root characteristics and stomatal control, (2) photosynthetic maintenance and osmotic regulation, and (3) phenological change. Clusters of genotypes were used to categorize the genotypes into four responses. Their physiological mechanisms and agronomic performance showed that there were eight very drought-resistant genotypes. The benefit breeding programs that will be involved in utilizing these genotypes are those who are interested in planting more plants within the regions which are likely to become dry.

Rooting depth and distribution (especially in deeper layers of the soil), water use efficiency (measured either directly or 13 c -1), canopy temperature depression (a sign of transpirational cooling), relative water content (a sign of the amount of water the plant has), and osmotic adjustment capacity (a sign of amount of the proline the plant can store) are some of the attributes important to consider when choosing plants that can survive drought. The combined action of these traits to form an index of drought resistance (DRI) was capable of finding some of the most effective genotypes proven to be successful in a variety of environments, as a resource that can be utilized in breeding.

The paper shows that the multisynergistic and multifaceted nature of drought resistance of wheat is multifaceted and multisynergistic in nature, incorporating a variety of mechanisms and it must be measured in a multifaceted way. Although the effects of individual qualities turn out to be moderate to very much hereditables and these can be selected independently the final result is that the overall effect is decided by the overall effect. Breeding methods must then involve a lot of selective thought and the focus must be varied with the environment (terminal or intermittent drought) and system of production (irrigated or rainfed).

The genomic analysis revealed a lot of marker-trait associations of the drought resistance components and it is easy to select the markers. The intermediate phenotyping variance exhibited by the single markers (8-22) indicates the quantitative aspect of drought resistance and the necessity to utilize the genomic selection process that utilizes multiple loci with small effects. Genetic gain would be expedited, with high phenotyping and using the genomic techniques, which would guarantee adaptation of plants to the place where they will be planted.

Additional practical suggestions to breeding of drought tolerant plants are: (1) multi-trait selection indices- this is the combination of stability of the yield with other important physiological traits; (2) controlled drought conditions- this can simulate stress pattern that the plant will be subjected to, before its release; (3) root phenotyping, (4) mass screening through high-throughput physiological measures (CTD, spectral reflectance); and (5) testing the outcomes of the selected genotypes in different drought conditions.

Gaps that have been determined in the study shall be covered in the future research work which shall include but not limited to: expanding genetic diversity in assessment panel, interaction of traits in the case of concomitant abiotic stresses, development of economical phenotyping systems in breeding programs, molecular explanation and economic analysis of trait deployment under various production systems. The varieties that are produced will also meet the practical needs and production barriers as well as this will be achieved through Farmer participatory evaluation.

In conclusion, this paper gives an in-depth insight into the drought resistance mechanisms in wheat and an effective model that can be utilized in assessing and choosing genotypes. Resistance phenotype and selection parameter found gives direct input to the breeding process as opposed to the integrated assessment method giving a procedure of the continuous improvement. The climate change will increase and intensify droughts, and accordingly, the systematic ways of developing drought-resistant wheat species will be necessitated to ensure that the yield of wheat products is high and food security in the global population is upheld.

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