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Genotypic Performance and Selection Criteria for Enhancing Drought Tolerance in Hexaploid Wheat

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ABSTRACT Wheat is a staple food in many developing countries like Pakistan with a passage of time population of Pakistan increase therefore, it creates food security issues, to overcome on these types of issues, it is necessary to develop such verities of wheat that have potential to meet challenges environmental changes like water scarcity etc. An experiment was conducted to investigate the response of 50 wheat genotypes at maturity stage under drought conditions having three environments (Normal and Drought D1, D2) by using Randomized Completely Block Design (RCBD). The ANOVA showed highly significant differences among the genotypes in all traits under studied. The genotypic and phenotypic correlation showed positive correlation under normal and both drought condition except peduncle length both in normal and drought (D1, D2) conditions. The genotypes G-5(AZRC-1), G-17 (Faisalabad 2008), G-12 (Inqilab), G-26 (Khirman), and G-31(Hashim-8) showed tolerance against drought in current experiment. Selection based on these characteristics and improved the performance of other characters. Because of these findings, selection based on these qualities is not appropriate for drought tolerance. The best performing germplasm under drought stress can be a desirable genotype for future breeding programs and early selection criteria for generating high yielding, according to the findings.

Keywords: Wheat; Grain; Yield; Genotypic; Phenotypic; Correlation

INTRODUCTION A member of the poaceae family Triticum aestivum L is main source of staple foods in the country of Pakistan. It is significant as a staple food since it provides dieters, energy, proteins, and carbohydrates. One of the most important staple crops for global food security is wheat, which meets 20% of the world's protein and calorie demands and produces 730 million tons of grain annually from an area of around 2.1 million km2 worldwide. Worldwide, wheat accounts for 41 percent of the grain calories consumed, with developing countries accounting for thirty-five percent and developed nations accounting for 74%, correspondingly (Anwaar et al., 2020). Wheat, one of the grains, is a significant essential crop that is primarily farmed in semi-arid and dry locations around the globe. A key part of Pakistan's economy is agriculture, semi-arid areas contribute for twenty-six percent of gross domestic product and this industry indirectly sustains the nation's people. Cotton, wheat, rice, sugarcane, fruits,

and vegetables are some of the most important crops for agriculture. Compared with other grain crops, wheat-based goods have higher levels of carbohydrates and nutrients (Adrees et al., 2020).

Wheat production decreases of as much as 21 percent have apparently been documented globally because of severe drought (Lesk and Anderson, 2021, Zeng et al., 2024, Saeed et al., 2024). The most extensively adaptable crop in the globe is wheat provides about half of the dietary protein and more than 50% of the daily calories for a third of the global population (Dhakal, 2021). Crop development, nitrogen and water relationships, the process of photosynthesis and assimilate partitioning are all affected by stress from drought, which eventually results in a considerable decrease in the yield of crops for over a third of the globe's humanity for food in grains. It provides calories to the

worldwide diet because it contains more protein than any other cereal crop (Bukhari et al., 2021).

Drought is one of the main environmental factors restricting agricultural productivity worldwide (Guo et al., 2017). These changes depend on the effected plants' genotype among the major grain crops cultivated in dry areas where drought-related damage has a big impact on productivity, is wheat. Over a billion individuals are thought to be suffering from food insecurity that number is expected to treble (Dorostkar et al., 2015). Nourishing the people and supplying the water needed for growing food in a society undergoing high population expansion at a period characterized by worldwide environmental change is the biggest challenges facing economies and societies (Dorostkar et al., 2015). Flowering, poor grains set, and growth are impacted by terminal drought in wheat at the anthesis and the grain-filling period (Zahra et al., 2021). Under drought stress, at maturity spike length, spike weight, grains per spike, and 1000-grain weight all dramatically decreased. Due to the adverse effect on the number of spikelet's and the spikelet's per spike, a second ridge is the anthesis phase of development that is most important to water deficiency in terms of yield. Lack of water affects the thesis and grain-filling phase, lowering grain production. It is generally known that plant height, biomass, and yield, as compared to the number of spikes and grain weight, are includes that are more susceptible to water deficiency (Peymaninia et al., 2012, Rashid et al., 2024, Mushtaq et al., 2024). All stages of wheat growth are hindered by drought, but the reproductive stage, which includes the blooming and grain-filling phases (terminal drought), is particularly problematic and causes significant output reductions (Zahra et al., 2021, Li et al., 2024, Khan et al., 2024).

Therefore, it is crucial to assess the manufacturing methods and modify them to fit these circumstances. The results demonstrated that drought decreased the agronomic traits in wheat among various growth stages. The best option for improving wheat production under limited water supply is to develop tolerant genotype for the drought prone areas. The objectives of this research works is: To develop the drought tolerant genotypes, improving grain yield under drought stress condition. To assess the performance of different wheat Genotypes under normal and drought condition based on some yield related traits and Assessment of correlation between these studied traits was an objective of this investigation. From this study, we will be able to find some promising performance genotypes that can be used in future breeding programs.

MATERIALS AND METHODS
The experiment was carried out on November 2021 to find the ability of wheat genotypes to tolerate the drought conditions based on morphological attributes. Experiment was conducted in the experimental area of department of Plant Breeding and Genetics Faculty of Agriculture and Environment; The Islamia University of Bahawalpur (IUB) by using Randomized Complete Block Design having three treatments Normal, D1 and D2 respectively and each treatment has three replications. Normal irrigation was given to the normal treatment while in D1 irrigation was skipped at tillering stage and in D2 irrigation was skipped at the anthesis

stage. 10 seeds of each genotype were sown having plant-to-plant distance of 6 inch and row-to-row distance of 12 inch. Five plants were selected from each genotype. Thinning was done to keep one plant per hole. All the agronomic practices were done as recommended. The following indices were studied: Plant height (PH), Flag leaf Area (FLA), No of Tillers (NTP), Peduncle length (PDL), Biological Yield (BY), Spike Weight (SW), Grain Weight Per Spike (GWS), 1000 Grain Weight (TGW), and Grain Yield per plant (GY). Five plants were selected from each line and were tagged for data collection data were collected from those plants that were tagged for all the traits and data were averaged for statistical analysis. The following the formula described by (Muller, 1991) used to calculate the flag leaf area.

Flag leaf area = Flag leaf length $\times$ Flag leaf Width $\times$ 0.75

Analysis of variance (ANOVA) was performed (Steel et al., 1997) using statistics 8.1. Phenotypic and genotypic correlation was also performed by using R studio. Mean reduction was performed by using the following formula:

Mean Reduction= (normal traits mean-drought trait mean)/normal trait mean)*100

RESULTS
Significant differences were observed among studied genotypes and treatments in response to normal and drought stress conditions for all evaluated indices, demonstrating the presence of substantial genetic diversity as mentioned in Table 1.

Performance of genotypes based on Reduction Percentage
Plant Height (PH)
Wheat genotypes G5(50.81), G17(48.81), G12(55.27), G26(51.1) observed low value of reduction percentage in plant height, it means these genotypes were performed best in normal and drought stress 1 condition. The genotypes G11(13.11), G15(25), G35(18.18), G40(-25) had high value reduction percentage these genotypes were performing worst in normal and drought D1 condition. Under drought condition D2, the genotypes G12(50.81), G31(48.81), G5(55.27), G17(51.1) performed best because they showed low values of reduction percentage. While genotypes G47(-13.11), G11(-25), G35(18.18), G40(-25)observed high values of reduction percentage which mean these genotypes were not performed best for plant height in drought stress condition 2 respectively as shown in Table 2

Flag leaf area (FLA)
The genotypes observed low value of reduction percentage were G5(50.81), G17(48.81), G12(55.27), G26(51.1) that were the best performer in normal and drought condition 1. The genotypes G11(-13.11), G47(-25), G35(18.18), G40(-25) had high values of reduction percentage which shows these genotypes were not performing best in drought stress 1 and normal respectively. The genotypes G26(50.81), G12(48.81), G31(55.27), G5(51.1) had low values of reduction percentage which shows these genotypes were performing best in drought stress condition. The reduction percentage of genotypes G40(-13.11), G15(-25),G35(-18.18), G11(-25) revealed maximum reduction percentage values which performed worst in drought stress 2 condition respectively as shown Table 2.

No. of Tillers per Plant (NTP)

The genotypes G5(50.81), G17(48.81), G12(55.27), G26(51.1) depicted maximum values for reduction percentage, it means these genotypes were worst performed in irrigated and drought stress condition 1 as mentioned in Table 2. Whereas the minimum reduction was observed for G11(-13.11), G40(-25), G35(-18.18), G15(-25) it means these genotypes were performed well in this environment D1. The genotypes G17(50.81), G31(48.81), G12(55.27), G26(51.1) showed the low value of reduction percentage it means these genotypes performed best in environment D2. Whereas genotypes G40(-13.11), G15(-25), G35(-18.18), G11(-25) highly effected showed highest reduction percentage in no of tillers per plant respectively.

Peduncle Length (PDL)
Peduncle length indicated that genotypes do not performing best in drought and irrigated environment were G11(-13.11), G35(-25), G15(18.18), G40(-25) has more reduction, it means these genotypes were not show tolerance against the water stress. The genotypes G5 50.81), G17(48.81), G12(55.27), G26(51.1) showed the low value of reduction percentage followed by 50 bread wheat genotypes in the irrigated and drought 1 condition respectively. The genotypes G26(50.81), G31(48.81), G12(55.27), G5(51.1) performed best because they have low values of reduction percentage in peduncle length while genotypes G47(-13.11), G15(-25), G35(-18.18), G40(-25) had high values of reduction percentage which shows these genotypes were not performing best in drought stress condition 2 respectively as shown in Table 2.

Biological Yield per Plant (BY)
The genotypes G5 (50.81), G17(48.81), G12(55.27), G26(51.1) that were the best performer in irrigated and drought condition 1 because they had low values of reduction percentage. The genotypes G15(-13.11), G11(-25), G35(-18.18), G40(-25) had high values of reduction percentage which shows these genotypes were not performing best in both drought stress 1 and normal condition. The genotypes G17(50.81), G31(48.81), G12(55.27), G5(51.1) had low values of reduction percentage which shows these genotypes were performing best whereas the reduction percentage of genotypes G47(-13.11), G15(-25), G35(-18.18), G11(-23.88) revealed maximum reduction percentage values which performed worst in drought stress condition 2 respectively as shown Table 2.

Main Spike weight (MSW)
The genotypes observed low value of reduction percentage of spike weight were G5(50.81), G17(48.81), G12(55.27), G26(51.1)that were the best performer in irrigated and drought condition. The genotypes G11(-13.11), G35(-25), G15(-18.18), G40(-25) had high values of reduction percentage which shows these genotypes were not performing best in both drought stress 1 and normal condition. The genotypes G31(50.81), G26(48.81), G12(55.27), G17(51.1) had low values of reduction percentage which shows these genotypes were performing best whereas the reduction percentage of genotypesG47(-13.11), G15(-25), G35(-18.18), G40(-25) revealed maximum reduction percentage values which performed worst in drought stress condition 2 respectively as shown Table 2.

Grain Weight per Spike (GWS)

Under the drought stress 1, the genotypes G5(50.81), G17(48.81), G12(55.27), G26(51.1) that were the best performer in irrigated and drought condition. The genotypes G11(-13.11), G40(-25), G35(-18.18), G15(-25) had high values of reduction percentage which shows these genotypes were not performing best in both drought stress 1 and normal condition. The genotypes G31(50.81), G26(48.81), G12(55.27), G17(51.1) had low values of reduction percentage which shows these genotypes were performing best whereas the reduction percentage of genotypes G15(-13.11), G11(-25), G35(-18.18), G40(-25) revealed maximum reduction percentage values which performed worst in drought stress condition 2 respectively as shown Table 2.

Thousands Grain weight (TGW)
The genotypes observed low value of reduction percentage were G5(50.81), G17(48.81), G12(55.27), G26(51.1) that they were the best performer for thousand grain weight in irrigated and drought condition. The genotypes G11(-13.11), G15(-25), G35(-18.18), G40(-25) had high values of reduction percentage which shows these genotypes were not performing best in both drought stress 1 and normal condition. The genotypes have low values of reduction percentage which shows these genotypesG17(50.81), G5(48.81), G12(55.27), G26(51.1) were performing best whereas the reduction percentage of genotypes G35(-13.11), G11(-25), G15(-18.18), G40(-25) revealed maximum reduction percentage values which performed worst in drought stress condition 2 respectively as shown Table 2.

Grain yield per plant (GYP)
The genotypes observed low value of reduction percentage of grain yield per plant that were G31 (50.81), G17 (48.81), G12 (55.27), G26(51.1) the best performer in irrigated and drought condition. The genotypes G11(-13.11), G15(-25), G35(-18.18), G40(-25) had high values of reduction percentage which shows these genotypes were not performing best in both drought stress 1 and normal condition. The genotypes G5(50.81), G31(48.81), G12(55.27), G26(51.1) had low values of reduction percentage which shows these genotypes were performing best whereas the reduction percentage of genotypes G15(-13.11), G47(-25), G35(-18.18), G40(-25) revealed maximum reduction percentage values which performed worst in drought stress condition 2 respectively as shown Table 2.

Genotypic and Phenotypic Correlation Under normal and drought conditions
The genotypic correlation Table 3 depicts that differences among the breeding material for no of tillers to Plant height (0.12**), Spike weight (0.85**), Spike Grain weight (0.96**), Biological yield (0.78**), 1000-grain weight (0.97**) and grain yield/ plant (0.82**) had highly significant genotypic correlation. But another trait like Flag leaf area (-0.02ns) mentioned non-significant correlation with Plant height (0.99**) and peduncle length (0.86**) under normal condition. Table 4 further shows that number of tillers per plant (0.84**) had positive genotypic correlation with grain yield plant (0.97**) under drought (D1) condition. Plant height (0.84**), Flag leaf Area (0.99**), Spike Grain weight (0.99**), main spike weight (0.86**), 1000-grain weight (0.97**), biological yield (0.79**) had also significant positive genotypic correlation with grain yield plant per plant.

Grain yield per plant would increase if the genotype having greater number of tillers per plant and longer maturation period in maturity would be selected. Another trait like peduncle length (0.08**) had non-significant genotypic correlation with Plant height (0.05ns). Number of tillers plant had significant genotypic correlation with all other traits. This trait had non-significant correlations with peduncle length under drought stress (D1) condition. Under drought d2 condition in (Table 5) no of tillers per plant have positive and highly significant association with traits like peduncle length (0.63**), plant height (0.84**), Spike weight (0.82**), Spike grain weight (0.68**), Biological Yield (0.83**), Thousand Grain weight (0.29**) and Grain Yield (0.82**). Grain weight (-0.17ns) but 1000 grain weight (0.50**) had significant genotypic correlation with Grain yield per plant. Similarly Biological yield had also highly significant genotypic correlations with thousand Grain weight (0.08**) and negative but significant association shows with (-0.30*) Grain Yield per plant. Genotypic association is important in determine how closely key yield-contributing factors are connected to grain yield /plant using genotypic association.

The phenotypic correlation for no of tillers to plant height (0.95**), Spike weight (0.89**), Spike Grain weight (0.95**), Biological yield (0.98**), 1000-grain weight (0.96**) and grain yield/plant (0.96**) were highly significant phenotypic correlation but another trait like peduncle length (-0.06ns) had negative non-significant correlation with no of tillers per plant under normal condition as shown in (Table 3). This table further revealed that peduncle length (0.01ns) had non-significant correlation with plant height under normal condition. Plant height (0.63**), Flag leaf Area (0.84**), spike Grain weight (0.82**), main spike weight (0.68**), 1000-grain weight (0.83**), biological Yield (0.29**) had also significant positive phenotypic correlation with grain yield plant per plant. An- other trait peduncle length had non-significant phenotypic correlation with Plant height (0.07ns). Under drought condition no of tillers per plant had positive and highly significant association with traits like Biological Yield (0.17**), plant height (0.09**), Spike weight (0.02**), Spike grain weight (0.03**), Thousand Grain weight (0.13**) and Grain Yield (0.03**). But another traits like Peduncle length (0.05ns), Flag leaf area (0.1ns) had non-significant phenotypic correlation with no of tillers per plant as shown in Table 4. The phenotypic correlations of Flag leaf area had non-significant either negative or positive correlation with peduncle length (0.04ns) but it had negative highly significant correlation with grain yield per plant. Similarly, Biological yield had also highly significant phenotypic correlations with thousand grain weight (0.53**) and negative but significant associated (-0.61*) with Grain Yield per plant as shown in Table 5.

DISCUSSION

The analysis of variance observed the variation among the studied traits in all the environments. The researchers satated that these variations were helpful in selection crieteria. In wheat, genotype with high plant height is more sensitive to lodging. Grain weight decreased because genotypes with high plant height require more energy to transfer the solute to the seed as, a result grain yield

decreased (Khadka et al., 2020). In wheat, larger flag leaf area is responsible for greater photosynthesis level. It was reported by water deficit condition decreased half flag leaf area. In wheat tillers has a major contribution in yield potential of wheat. Genotype and environmental setting significantly influence it. It is reported that tillers add 35% to 50% in plant yield (Pang et al., 2020, Ali et al., 2024, Ahmed et al., 2024). Peduncle length can be measured from the end of spike to the first node of plant (Pour-Aboughadareh et al., 2020). The lowest biological yield occurred during the stage of grain development and under conditions of greatest drought stress.

This variation may be the result of different cultivars' decreased capacity for assimilation, composition, and transmission of nutrients because of water scarcity, which lowers biological yield. The expansion of leaf surface and/or its higher durability, which results in a larger biological yield by generating an effective physiological source for absorbing more light, may be the cause of the rise in biological production of plants under favorable irrigation (Frantová et al., 2022). Drought stress at flowering stage reduces the amount of floret sterility and leads to a reduction in grains spike (Frantová et al., 2022). No of grains/ Spike have direct effect on grain yield is decreased because of drought stress during the grain formation stage. The decrease in grain weight may be caused by a decrease in the availability of propagating grain material. Of course, slower material transfer rates and shorter grain formation times can result in greater grain weight decrease (Hussain et al., 2018). The 1000-grain weight is one of the most significant factors that is impacted by a shortage of moisture at the conclusion of the growing season and following pollination. They added that during the grain production stage, drought-related stresses mostly influences and decreases the weight of 1000 grains (Hussain et al., 2020).

Correlation between various traits is generally due to the presence of linkage and pleotropic influences of different gene. The environment (Nukasani et al., 2013) significantly influenced the formation of phenotypic correlation). It also shows that in the genetic material under research, choosing long duration genotypes would result in larger 1000-grain weights than short duration genotypes. Only the genotypic relationship among spike length and spike weight in grains was negative. If the genotype had a protracted maturation, it would be lower (Bernhardt et al., 2020). For improving grain yield's genotype, several earlier studies investigated the genotypic correlation coefficients of different grain yield components. According to several researchers, grain yield and 1000-grain weight are positive associated (Singh et al., 2023). The researchers concluded that the development of grain yield was highly influenced by yield components such as tillers per plant. They also concluded that spike grain weight and thousand-grain weight are main contributors to grain yield in wheat. (Dabi et al., 2019) reported that grain yield had positive significant correlation with plant height, spike grain weight, thousand grain weight, biological yield, and no of tillers per plant both at genotypic and phenotypic levels, which agree with the findings of the current studies. Non-significant positive correlations were observed between grain yield with spike length and number of tillers per plant at both

genotypic and phenotypic level. Furthermore, (Anjum et al., 2021) reported that grain yield showed significant positive correlation with no of tillers per plant. If challenges like drought stress are expected, negative correlations show an inverse association between earliness characters and grain yield which is desirable (Baye et al., 2020).

Table 1. The Analysis of variance (ANOVA) for studied indices

Source	Replication	Treat	Genotype	treat*genotype	Error	Total
DF	2	2	49	98	298	449
SS	26	110010	3987	8906	3586	126516
PH	13.2	5505.2**	81.4**	90.9**	12	
FLA	0.035	19.75**	3.06**	2.161**	0.0297	
NTP	0.1	11.32**	1.88**	1.89**	0.02	
PDL	0.02	3612.41**	5.31**	3.67**	0.01	
BY	0.00312	10179.5**	10.3165**	15.0937**	0.0525	
MSY	0.0295	65.853**	0.2529**	0.3868**	0.008	
GWS	0.0006	0.1213**	31.6803**	0.1263**	0.0007	
TGW	5.18	15.26**	2675.07**	6.55**	3.52	
GYP	0.01509	41.629**	11005.5**	34.2326**	0.00546	

*** highly significant, PH plant height, FLA flag leaf area, NTP number of tillers per plant, PDL peduncle length, BY biological yield, MSY main spike weight, GWS grain weight per spike, TGW thousand grain weight, GYP grain yield per plant.*

Table 2. Comparisons of best performing and worst performing genotypes under drought D1 and D2 conditions

		Best Performing Genotypes	Worst Performing Genotypes
PH	D-1	G5(50.81), G17(48.81), G12(55.27), G26(51.1)	G11(13.11),G15(25),G35(18.18),G40(-25)
	D-2	G12 (50.81), G31(48.81), G5(55.27), G17(51.1)	G47(-13.11), G11(-25), G35(18.18), G40(-25)
FLA	D-1	G5(50.81), G17(48.81), G12(55.27), G26(51.1)	G11(-13.11), G47(-25), G35(18.18), G40(-25)
	D-2	G26(50.81), G12(48.81), G31(55.27), G5(51.1)	G40(-13.11), G15(-25),G35(-18.18), G11(-25)
NTP	D-1	G5(50.81), G17(48.81), G12(55.27), G26(51.1)	G11(-13.11), G40(-25), G35(-18.18), G15(-25)
	D-2	G17(50.81), G31(48.81), G12(55.27), G26(51.1)	G40(-13.11), G15(-25), G35(-18.18), G11(-25)
PDL	D-1	G5 50.81), G17(48.81), G12(55.27), G26(51.1)	G11(-13.11), G35(-25), G15(18.15), G40(-25)
	D-2	G26(50.81), G31(48.81), G12(55.27), G5(51.1)	G47(-13.11), G15(-25), G35(-18.18), G40(-25)
BY	D-1	G5(50.81), G17(48.81), G12(55.27), G26(51.1)	G15(-13.11), G11(-25), G35(-18.18), G40(-25)
	D-2	G17(50.81), G31(48.81), G12(55.27), G5(51.1)	G47(-13.11), G15(-25), G35(-18.18), G11(-23.88)
MSW	D-1	G5(50.81), G17(48.81), G12(55.27), G26(51.1)	G11(-13.11), G35(-25), G15(-18.18), G40(-25)
	D-2	G31(50.81), G26(48.81), G12(55.27), G17(51.1)	G47(-13.11), G15(-25), G35(-18.18), G40(-25)
GWS	D-1	G5(50.81), G17(48.81), G12(55.27), G26(51.1)	G11(-13.11), G40(-25), G35(-18.18), G15(-25)
	D-2	G31(50.81), G26(48.81), G12(55.27), G17(51.1)	G15(-13.11), G11(-25), G35(-18.18), G40(-25)
TGW	D-1	G5(50.81), G17(48.81), G12(55.27), G26(51.1)	G11(-13.11), G15(-25), G35(-18.18), G40(-25)
	D-2	G17(50.81), G5(48.81), G12(55.27), G26(51.1)	G35(-13.11), G11(-25), G15(-18.18), G40(-25)
GYP	D-1	G31(50.81), G17(48.81), G12(55.27), G26(51.1)	G11(-13.11), G15(-25), G35(-18.18), G40(-25)
	D-2	G5(50.81), G31(48.81), G12(55.27), G26(51.1)	G15(-13.11), G47(-25), G35(-18.18), G40(-25)

Table 3. Estimation of genotypic and phenotypic correlation among different traits of wheat under normal condition

Traits	NTP	FLA	PL	PH	MSW	SGW	BY	TGW	GY
NTP	1**	-0.06 NS	0.95**	0.97 **	0.95 **	0.89 **	0.96 **	0.98 **	0.96**
FLA	0.12**	* 1 **	0.01 NS	-0.08NS	-0.07**	-0.01**	-0.09**	-0.11**	-0.06**
PDL	0.86**	-0.02 NS	1 **	0.93**	0.97 **	0.89 **	0.93**	0.94 **	0.94**
PH	0.99**	0.73**	0.47 **	1 **	0.95 **	0.89 **	0.98 **	0.98 **	0.94 **
MSW	0.85**	-0.74 **	0.71 **	0.03 **	1 **	0.96 **	0.96**	0.96**	0.92 **
SGW	0.96**	-0.71 **	0.23 **	0.85**	1.01 **	1 **	0.93	0.91**	0.85**
BY	0.78**	0.71 **	0.57 **	0.07**	-0.46 **	-0.28*	1 **	0.97**	0.91**
TGW	0.97**	0.58 **	0.02 **	0.73**	-0.76 **	-0.41**	0.08 **	1 **	0.93**

| GY | 0.82** | -0.61 ** | 0.27 ** | 0.81 ** | 1.15 ** | 1.04 ** | -0.30* | 0.58** | 1** |

Table 4. Estimation of genotypic and phenotypic correlation among different traits of wheat under drought (D1) condition

Traits	NTP	PDL	PH	FLA	SGW	MSW	TGW	BY	GY
NTP	1 **	-0.11NS	0.63 **	0.84**	0.82 **	0.68 **	0.83 **	0.29**	0.82 **
PDL	-0.12NS	1 **	0.07 NS	-0.07 NS	-0.06NS	-0.01NS	-0.062NS	0.08**	-0.05NS
PH	0.84 **	0.08 NS	1 **	0.69**	0.67 **	0.52**	0.70 **	0.30 **	0.66 **
FLA	0.99 **	0.07 NS	0.82**	1 **	0.89 **	0.75 **	0.96 **	0.41**	0.94**
SGW	0.99 **	0.06 NS	0.83 **	0.92 **	1 **	0.86 **	0.89 **	0.43 **	0.87 **
MSW	0.86 **	0.01NS	0.71 **	0.81 **	0.95 **	1**	0.74**	0.44**	0.74 **
TGW	0.97 **	0.05 NS	0.83 **	0.97 **	0.92 **	0.83**	1**	0.41 **	0.89 **
BY	0.79**	0.19 NS	0.74 **	0.88 **	0.96 **	0.07**	0.92 **	1*	0.42 **
GY	0.97 **	-0.04NS	0.77 **	0.95 **	0.90 **	0.81**	0.91 **	0.91 **	1**

Table 5. Estimation of genotypic and phenotypic correlation among different traits of wheat under drought (D2) condition

Traits	NTP	FLA	PDL	PH	MSW	SGW	BY	TGW	GY
NTP	1 **	0.14NS	0.05NS	0.09**	0.02**	0.03**	0.17**	0.13**	0.03**
FLA	0.15NS	1 **	0.04NS	0.09**	0.02NS	0.04NS	0.27**	0.15 NS	-0.03 NS
PDL	0.63 **	-0.02NS	1**	0.06**	0.02NS	0.07**	0.08 NS	0.04 NS	0.06**
PH	0.84 **	-0.32*	0.47 **	1 **	0.55 **	0.81**	-0.08**	-0.08NS	0.77**
MSW	0.82**	-0.74**	0.71 **	0.03 **	1 **	0.62 **	-0.16 *	-0.13NS	0.65 **
SGW	0.68 **	-0.71 **	0.26 **	0.85 **	0.01 **	1 **	-0.16 *	-0.15 NS	0.82**
BY	0.83 **	0.71 **	0.57 **	-0.07 NS	-0.46**	-0.28*	1 **	0.53 **	-0.16 *
TGW	0.29 **	0.58**	0.02 **	-0.25 NS	-0.76 **	-0.41**	0.08 **	1 **	-0.08 NS
GY	0.82 **	-0.61**	0.27**	0.81**	0.15**	0.04 **	-0.30 *	-0.50**	1**

CONCLUSION

Results has showed that genotypes performed best in both the normal and drought conditions are G-5(AZRC-1), G-17(Faisalabad 2008), G-12(Inqilab), G-26(Khirman),and G-31(Hashim-8). These genotypes performed best in drought and normal because these genotypes screened as drought resistance because they have lowest reduction percentage. The genotypes that do not performed better in both stressed and non-stress condition were G-47, G-30, G-15, and G-35. They were drought susceptible because they had highest reduction percentage. The genotypic and phenotypic correlation showed positive correlation under normal and both drought condition except peduncle length in both normal and drought D1, D2 condition. The best performing germplasm under drought stress can be a desirable genotype for future breeding programs and early selection criteria for generating high yielding according to the findings.

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