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Evaluating Wheat Genotypes for Drought Tolerance through Phenotypic and Genotypic Analyses

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ABSTRACT At the phenotypic and genotypic levels, differences in resistance to drought stress, a significant grain output limitation on the world's wheat production, were found. Research priorities include developing high-yielding, drought-tolerant wheat varieties, particularly in areas where climate change is expected to increase the frequency of drought conditions. Grain yield, a complicated, late-stage characteristic influenced by several variables other than drought, is frequently the foundation for selection in breeding for drought tolerance. An experiment was conducted to investigate the response of 40 wheat genotypes at maturity stage under two environments (Normal and Drought) by using Randomized Completely Block Design (RCBD). In current study, the results of Analysis of Variance depicted that all the attributes had significant variations among studied genotypes under both normal and stressed conditions. Correlation analysis mentioned under normal condition all traits showed highly significant association among all of them except spikelet's per spike in genotypic and phenotypic correlation. In D1 condition, all indices also exhibited same trend except spike length in genotypic and phenotypic correlation while in D2 grain length had non-significant association with spikelet's per spike and grain width had non-significant relation with spike length in phenotypic condition. The heritability and genetic advance percentage had high heritability in D1 condition while all traits showed moderate genetic advance percentage in all the conditions. According to these findings, in areas where drought is a common occurrence, screening for genotypes that are tolerant of drought would be a more practical way to reduce the negative impacts of drought on wheat.

***Keywords**: Correlation; Wheat; Mean performance; Grain; Drought stress*

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INTRODUCTION South Western Asia is the origin of wheat (*Triticum aestivum* L.), which is grown all over the world, Known as the "king of cereals," one-third of the world's population eats it as a staple crop. It is estimated that wheat is the second most widely produced crop worldwide (Ahmed et al., 2022). Global agricultural production may need to rise by 60–110%, according to a revised estimate, in order to fulfill rising needs and ensure food security for the 870 million people who are expected to be chronically undernourished by 2050 (Zhang et al., 2018).

The 20% of the world's population gets their calories from wheat, a staple crop with a 2.1 million km2 harvest area and 700 million tonnes produced worldwide. A major portion of the global population, including those in Pakistan, rely on wheat (Triticum aestivum L.) as their main diet. In terms of both production and consumption, wheat is among the most significant cereal crops (Khan et al., 2015).

Nowadays, 68% of the wheat produced is used for food, around 19% is used for nutrition, and the remaining portion is utilized for other uses, such as industrial fuels. Wheat is currently the second most consumed food after rice. Primarily the wheat which is an essential crop important for its properties is cultivated in semi-arid and dry locations. Agriculture holds the major economy in the GDP of Pakistan, about twenty-six percent of the gross domestic products come from semi-arid areas and the agriculture supports and sustains the people residing in the country. Vegetables, fruits, Cotton, wheat, rice, and sugarcane are some of the vital crops for agriculture. If we compare wheat with all the other grain crops, the level of carbohydrates and nutrients are highest in wheat crop bi-products (Adrees et al., 2020).

Wheat grain yield is a complicated characteristic that results from a number of contributing variables that either directly or indirectly impact yield. Breeders are naturally interested in determining the degree and kind of correlation between these qualities as they have a direct and indirect impact on grain yield. Selecting and breeding plants to increase agricultural water stress resistance requires knowledge of the biochemical and physical mechanisms of water stress tolerance. Due to low winter rainfall, high evaporation demand, and a lack of irrigation, drought stress typically predominates during wheat grain filling (Saeidi and Abdoli, 2015).

The variation in the changes are based upon the genetic makeup of the affected plants, the major impact on the overall output and grain yield of wheat crop is affected by drought in the dry areas. Over a billion people are facing from food insecurity, a number anticipated to triple in the coming years (Dorostkar et al., 2015). Feeding the people at a huge level and providing the resources which are useful for the cultivation and growing the food in a community where the number of peoples are increasing at a tremendous rate, moreover the biggest threat to the world economies and societies is worldwide environmental change which is effecting most of the food chain and crops (Dhakal, 2021).

Drought has an impact on wheat's development, poor grain set, and blooming, particularly during the anthesis and grain filling periods (Zahra et al., 2021). At maturity, spike length, spike weight, grains per spike, and 1000-grain weight all significantly reduced under dry stress. A second ridge is the anthesis phase of development that is most crucial to water deprivation in terms of yield because of the negative impact on the quantity of spikelets and the number of spikelets per spike. Water scarcity reduces grain yield by affecting the thesis and grain filling phase. Drought inhibits wheat development at every stage, but it is most troublesome during the reproductive stage, which encompasses the blooming and grain-filling phases (terminal drought), and results in substantial production decreases (Zahra et al., 2021).

The purpose of the current study was to producing genotypes that were resistant to drought, increasing grain output in drought-stressed environments. The investigation's other goal was to evaluate the performance of several wheat genotypes under normal and drought conditions using a few yield-related variables and to determine how these traits connected to one another. We will be able to identify some potential performance genotypes from this study that we may utilize in further breeding initiatives.

MATERIALS AND METHODS

The experiment was carried out on November, 2021 to find the ability of wheat genotypes to tolerate the drought conditions on the basis of 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: Spike Length (SL), No of spikes per Spikelet's (SPS), Grain Length (GL), Grain Width (GW), Grain Height (GH) and Grain Area (GA). Five plants were selected from each line and were tagged for data collection data were collected from those plants which were tagged for all the traits and data were averaged for statistical analysis.

Grain area (GA) were calculated by using this formula:

$GA = 13/11[(W + H) L]$. Analysis of variance (ANOVA) was performed using statistics 8.1 (Steel and Torrie, 1960). Genetic Advance and Heritability test was performed using R Studio. Phenotypic and genotypic correlations were performed using R studio.

RESULTS AND DISCUSSION

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 substaintial genetic diversity as mentioned in Table 1.

Genotypic and Phenotypic Correlation Under normal and drought conditions

Under the normal conditions, the genotypic correlation mentioned spike length associated positively significant with grain length, grain width, grain height and grain area (Table 2). The trait spikelet's per spike showed positive highly significant relation with grain area while significant correlation with grain length, grain width, and grain height. Grain length had highly significant positive correlation with grain height, grain width and grain area. The trait grain width and grain height also showed positive association with grain area (Table 2). The phenotypic correlation showed that spike length related positively and highly significant with grain length, grain width, grain area and significant relation with spikelet's per spike (Table 2). Non-significant and positive association revealed by spikelet's per spike with grain length, grain width, and grain height while grain area had significant association. The grain length, grain width, grain height and grain area had positive and highly significant correlation with each other (Table 2).

Under D1 stress environment, genotypic correlation exhibited that spike length had positively non-significant association with spikelet's per spike, grain length, grain height, and grain width while highly significant with grain area (Table 3). The spikelet's per spike, grain length, grain height, grain width and grain area demonstrated highly significant positive relation with each other (Table 3). In this environment, under phenotypic correlation, spike length showed positively non-significant association with spikelet's per spike, grain length, grain height, and grain width while highly significant with grain area (Table 3). Non-significant and positive association revealed by spikelet's per spike with grain length, grain width, and grain height while grain area had significant association. The grain length, grain width, grain height and grain area had positive and highly significant correlation with each other (Table 3).

Under D2 stress environment, genotypic correlation mentioned that all studied attributes like spike length, spikelet's per spike, grain length, grain width, grain height and grain area had positive highly significant association with each other except spikelet's per spike mentioned positive significant relation with grain height (Table 4). In phenotypic correlation, positive non-significant association showed by spike length and spikelet's per spike with grain width and grain length while significant relation showed by spike length and spikelet's per spike with grain length, grain height and grain area (Table 4). The other studied traits revealed highly significant positive association with each other (Table 4).

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

Source	Rep	Treat	Genotype	TXG	Error	Total
DF	2	2	49	98	298	449
SS	26	110010	3987	8906	3586	126516
SL	0.05	2243.47**	5.06**	4.81**	0.02	
SPS	0.46	7983.5**	9.51**	9.01**	0.4	
GL	0.039	0.526**	167.408**	0.382**	0.063	
GW	0.027	0.379**	102.283**	0.176**	0.018	
GH	0.067	0.504**	171.896**	0.218**	0.008	
GA	0.0235	94.3321**	19527.2**	35.519**	0.010	

*** highly significant, SL spike length, SPS spikelets per spike, GL grain length, GW grain width, GH grain height, GA grain area.*

Genetic Variability, Heritability and Genetic Advance

Spike length per spike have the broad sense heritability was 78% which found high in normal condition and found high in drought D-1 condition 65% and revealed moderate having values 50% in D-2 condition. The broad sense heritability for spikelet's per spike (84%) and mentioned moderate heritability in Grain length (50%) in normal condition. In D-1 stress condition, Grain length 89%, Grain width 67%, Grain height 92% and Grain Area 99% observed the high heritability. In D2 condition grain width showed moderate 67%, broad sense heritability but other traits like spikelets per spike 33%, grain Area 75%, Grain width 67% and Grain Height 94% were reveled high heritability (Table 5).

The spike length revealed the result for the genetic advance % is moderate (19%) and high 37 %in both the normal and drought stress 1 condition and 28% in condition 2. The genetic advance for spikelet's per Spike is moderate (13%) %and high 26% % in normal and drought condition 2 while 21 % in water deficit condition as presented Table 5. The genetic advance for grain length is moderate10 %, 10% and respectively followed by irrigated and drought stress environment. The genetic advance observed for grain width is moderate having values 17 %, 14% and 14% in normal drought 1 and drought 2 environment as given in Table 5.

Discussion

Correlation between various traits is generally due to the presence of linkage and pleotropic influences of different gene. The formation of phenotypic correlation was significantly influenced by the environment (Nukasani et al., 2013). For the purpose of improving grain yield's genotype, several earlier studies investigated the genotypic correlation coefficients of different grain yield components. The findings of (Khan et al., 2013) also showed that spike length and number of spikelet's per spike had positive correlation with grain yield in phenotypic level (Abd El-Mohsen et al., 2012). They also reported that spike length, and number of spikelet's per spike showed non-significant positive correlation with grain yield. Increased in grain length, also causes the increased in grain grains weight which automatically increases the grain yield of plant. Similar findings were found by the researcher (Rasheed et al., 2014).Grain width were strong related to grain height and grain area. Enhancement in one trait caused the increase in other traits of plant because these traits were strongly linked (Simmonds et al., 2014). Grain height was strongly bond with the grain area and grain sphericity and high significance found between these traits. According to our research, Strong relation found between the grain height and grain area, grain sphericity. These results were matched with the findings of (Russo et al., 2021). Water deficit condition did not affect the grain area and grain sphericity linkage. Grain sphericity and grain were strongly linked to each other and strong bonding found between these traits. These results were in agreement with the findings of (Alemu et al., 2020).

Table 2: Estimation of genotypic and phenotypic correlation among different traits of wheat under normal condition

Traits	SL	SPS	GL	GW	GH	GA
SL	1 **	0.08 *	0.87 **	0.95 **	0.85 **	0.67 **
SPS	0.14NS	1 **	0.08 ns	0.08 ns	0.07 ns	0.16 *
GL	0.16 **	0.56 *	1 **	0.90**	0.98 **	0.57**
GW	0.43 **	0.68 *	0.11 **	1 **	0.90**	0.67**
GH	0.80 **	0.29 *	0.20 **	0.83 **	1**	0.56 **
GA	0.05 **	0.61 **	0.14 **	0.96 **	0.91**	1**

Table 3: Estimation of genotypic and phenotypic correlation among different traits of wheat under drought (D1) condition

Traits	SL	SPS	GL	GW	GH	GA
SL	1 **	1.08**	0.17 *	0.11 ns	0.20*	0.17 *
SPS	0.17**	1 **	0.16ns	0.47 *	0.21 *	0.45 *
GL	0.16 **	0.56 **	1 **	0.36**	0.59**	0.52**
GW	0.43**	0.68**	0.11 **	1 **	0.63 **	0.72 **
GH	0.80**	0.29 *	0.20**	0.83 **	1 **	0.86 **
GA	0.05**	0.61**	0.14 **	0.91 **	0.91 **	1 **

Table 4: Estimation of genotypic and phenotypic correlation among different traits of wheat under drought (D2) condition

Traits	SL	SPS	GL	GW	GH	GA
SL	1 **	0.13ns	0.08ns	0.07ns	0.11ns	0.23**
SPS	0.13ns	1 **	0.80**	0.92**	0.75**	0.44 **
GL	0.08ns	0.85 **	1 **	0.83**	0.78 **	0.30**
GW	0.08ns	0.91 **	0.91**	1 **	0.77 **	0.45 **
GH	0.13 ns	0.91 **	0.99 **	0.98 **	1 **	0.29 **
GA	0.40 **	0.84 **	0.56 **	0.85 **	0.88 **	1 **

Selection could be made for those traits that were highly heritable and shown high predicted genetic advance and these traits were mostly controlled by the major effects of additive gene action (Fawad Ali et al., 2017). In the current study, expected genetic advance values were based on narrow sense heritability, which comprises an additive component of the overall phenotypic variance, Hence narrow sense heritability was more useful for measuring the relative significance of the additive component of genetic variance that can be transmitted to the progeny. Finding from another research (Taheri et al., 2018) showed that spike length was reduced when plant undergoes to drought stress. The decrease in no of spikelet's per spike under drought may be due to primordial forming during tailoring stage, or could credited with floating death at terminal and Basel end of the spike during stem extension (Frantová et al., 2022). In actuality, the rate and length of the grain formation period affect grain weight. The presence of environmental challenges like drought stress, particularly during the seed development stage, causes a decrease in the rate and length of grains development, which ultimately results in a decrease in grain weight. In the research conducted by (Bala and Sikder, 2018). Drought reduced the storage capacity of the grain with a decrease in number of cells and starch granules in the endosperm. Grain width was also reduced when drought were imposed during cell division (Frantová et al., 2022).

Table 5: Estimation of Genetic Variability, Heritability and Genetic Advance for the Studied Traits under Normal and Drought D1, D2 Conditions

Traits	Envi.	max	mini	GM	Sem	GV	PV	GCV	PCV	HER	GA	GA%
SL	N	15.4	11.6	13	0.11	1.45	1.49	9.28	9.4	0.78	2.45	18.8
SL	D1	14.5	6.5	9.37	0.06	2.87	2.88	18	18.1	0.65	3.48	37.1
SL	D2	6.6	4.7	5.27	0.01	0.52	0.52	13.7	13.7	0.5	1.49	28.2
SPS	N	25.2	19.3	21.5	0.11	2.07	2.11	6.67	6.74	0.84	2.93	13.6
SPS	D1	18.5	11	14.9	0.61	4.71	5.86	14.5	16.2	0.82	4.01	26.2
SPS	D2	9.83	5.3	12	0.04	1.98	1.97	9.9	17.1	0.33	1.42	11.7
GL	N	7.25	4.14	6.17	0.24	0.17	0.35	6.85	9.64	0.54	0.61	10
GL	D1	4.75	3.25	4.38	0.04	0.05	0.06	5.55	5.86	0.89	0.47	10.8
GL	D2	4.75	3.12	4.28	0.04	0.13	0.14	8.7	8.9	0.95	0.75	17.5
GW	N	4.6	3.12	4.04	0.04	0.12	0.13	8.75	9.01	0.94	0.78	17.5
GW	D1	2.9	2.14	2.59	0.09	0.05	0.07	8.69	10.5	0.67	0.37	15.7
GW	D2	2.98	2.1	2.58	0.09	0.05	0.07	8.69	10.5	0.67	0.38	14.7
GH	N	6.78	5.17	6.17	0.04	0.05	0.06	3.81	4.06	0.88	0.45	7.39
GH	D1	2.99	2.1	2.58	0.09	0.05	0.07	8.69	10.5	0.67	0.38	14.7
GH	D2	4.75	3.23	4.27	0.05	0.15	0.15	9.1	9.34	0.94	0.78	18.2
GA	N	85.3	61.6	72.4	0.09	28.6	28.7	7.3	7.39	0.72	11	15.2
GA	D1	58.9	44.5	52.7	0.01	13.6	13.6	7.08	7.08	0.63	7.61	14.4
GA	D2	57.9	43.5	52.6	0.01	12.7	12.7	6.78	6.78	0.75	7.35	13.9

CONCLUSION

An experiment was conducted to investigate the response of 40 wheat genotypes at maturity stage under two environments (Normal and Drought) by using Randomized Completely Block Design (RCBD). Research priorities include developing high-yielding, drought-tolerant wheat varieties, particularly in areas where climate change is expected to increase the frequency of drought conditions. Grain yield, a complicated, late-stage characteristic influenced by several variables other than drought, is frequently the foundation for selection in breeding for drought tolerance. In current study, the results of Analysis of Variance depicted that all the attributes had significant variations among studied genotypes under both normal and stressed conditions. Correlation analysis mentioned under normal condition all traits showed highly significant association among all of them except spikelets per spike in genotypic and phenotypic correlation. In D1 condition, all indices also exhibited same trend except spike length in genotypic and phenotypic correlation while in D2 grain length had non-significant association with spikelets per spike and grain width had non-significant relation with spike length in phenotypic condition. The heritability and genetic advance percentage had high heritability in D1 condition while all traits showed moderate genetic advance percentage in all the conditions. To create improved drought-tolerant cultivars, these results can be utilized as selection criteria for drought stress situations.

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