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Original Research

Ascertaining the Robust Drought Tolerant Wheat Germplasm for Sustainable Agriculture

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Abstract

This study aims to discover and assess how various wheat genotypes respond to abiotic stress, such as drought, which can result in considerable yield losses in wheat production. A serious global challenge to food security is the depletion of water resources brought on by excessive irrigation use and climate change. Therefore, this study was conducted using morphological characteristics to assess drought tolerance. To investigate wheat genotypes' tolerance to drought. A total of 50 wheat genotypes were sown in the field using a Randomized Complete Block Design (RCBD) with 3 replications of normal and drought stress conditions. Principal component analysis (PCA), genotypic and phenotypic associations, analysis of variance, and reduction percentage computation were all used in this investigation. Results showed that significant variability was present. Based on the performance, there were notable differences in the number of tillers, plant height, chlorophyll content, number of spikelets per spike, peduncle length, flag leaf area, biomass, main spike weight, main spike grain weight, yield per plant, and thousand-grain weight. A significant positive link between grain yield, thousand-grain weight, and the number of grains per spike was found using correlation analysis. The five genotypes G7, G16, G24, G38, and G45 fared well, while the genotypes G11, G23, G32, G41, and G49 did poorly. Out of 12 principal components (PCs), the first five PCs showed significant genetic variation under both conditions. The first five PCs showed 0.75% and 0.72% cumulative genetic variation under normal and drought conditions, respectively. Other characters' performances were improved by the selection made based on these characteristics. According to the results, the highest performing germplasm under

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drought stress may be a desirable genotype for upcoming breeding projects and early selection criteria for producing high yields.

Keywords: bread, wheat, drought, chlorophyll, yield

Introduction

Wheat, being the second most important staple food of the human population, is adapted to a wide range of eco-climatic conditions on six continents of the world. The demand for wheat is rising in tandem with the ongoing population growth and is predicted to increase by 40% by 2030. Thus, in order to maintain long-term food security, wheat production must be drastically increased [1]. Low yields can be caused by a variety of factors, such as low-quality seed, improper weed removal techniques, delayed planting, poor soil management, uneven fertilizer application, diseases, a lack of water, heat and drought stress brought on by climate change, and more [2]. Wheat's status is crucial among cereal crops due to its high consumption and nutritional value. Wheat scientists now face more problems in breeding wheat varieties with increased yield, quality, and resilience to both biotic and abiotic stressors due to the world's population growth and improved lifestyle. A diet high in wheat contains more fiber than a diet high in meat [3]. However, research has demonstrated that wheat proteins lack important amino acids like lysine and threonine [4]. Developing new and improved varieties of wheat that can yield more and perform better under various agro-climatic conditions might lead to an increase in wheat output and quality [5]. Drought is one of the many obstacles compromising wheat production. Low rainfall and unpredictable fluctuations in precipitation are the main causes of drought [6]. Water shortages reportedly cause 17% to 70% of yield losses. 50% to 90% less wheat was produced than could have been under irrigation in emerging nations as a result of a water shortage. During the stages of tillering, jointing, booting, anthesis, and filling, wheat plants exhibit a significant response to water deficiency stress. The crucial stage of tillering is when the wheat plant produces its florets, spikelets, primodia, and tillers [7]. At this point, water deficit stress can result in a 46% reduction in wheat production overall. The process of drought resistance is complicated and depends on a number of parameters, including crop type, drought intensity, duration, and plant development stages. Under drought stress, a plant must rely on many systems at once to survive [8]. Recurrent drought is the leading abiotic stress causing reduced production and productivity of wheat, especially in low altitude regions [9].

Vigorous seedlings are a key indicator of a plant's ability to produce large amounts of food quickly [8, 10]. The amount of chlorophyll in leaves serves as a proxy for the photosynthetic capacity of plant tissues. In situations of drought, the concentration of chlorophyll pigments changes. Plant resilience to drought stress is dynamically influenced by carotenoid levels. Conditions lacking in water prevent the synthesis of chlorophyll a and b, lower the quantity of binding-related proteins, and decrease the amount of pigment-related proteins that are necessary for light harvesting and other proteins related to photosystem II. Various techniques were developed to screen wheat genotypes for drought tolerance during the seedling stage. Relative water content and the root-to-shoot ratio were proposed by [11] as selection criteria for drought resistance in wheat. Relative water content (RWC) is a useful factor for choosing drought-tolerant wheat types when the seedling stage is approaching. The relationship between RWC and cell volume can accurately depict the equilibrium between water absorbed by the plant and water released by transpiration [12].

There are still relatively few cultivars with stable drought tolerance expressed in a variety of environmental conditions, despite the fact that breeding for drought tolerance is acknowledged widely as an important strategy. The identification of superior genotypes and environmental conditions that impact its expression complicate the polygenic characteristic of drought tolerance. Additionally, the identification of superior genotypes under fluctuating moisture conditions is complicated by the unexpected nature of drought manifestation and the various methods that plants have chosen to cope with drought stress. For drought tolerance, field-based empirical selection is still frequently employed [13, 14].

Therefore, considering the aforementioned facts, the current investigation aimed to predict the performance of wheat lines/varieties for grain yield and yield-related parameters under normal and drought-related stress conditions.

Materials and Methods

Experimental Location and Site

The experiment was carried out in the field of the Department of Plant Breeding and Genetics (PBG), Islamia University of Bahawalpur. In this work, 50 genotypes were grown and assessed for physio-morphological characteristics at maturity under both normal and drought-stressed conditions using a Randomized Complete Block Design (RCBD) in a triplicate fashion. The analysis revealed that the soil was sandy clay loam with a pH of 7.6 and 0.85%

organic matter. The seeds of 50 wheat genotypes were collected and arranged for sowing purposes. In the beginning, seeds of each genotype were sown in a 2 m long row for each replication under normal and drought conditions. Plant-to-plant and row-to-row distances were maintained at 6 inches and 12 inches, respectively. The experiment included standard agronomic and cultural procedures, with two seeds per hill being sown with the aid of a dibbler. To maintain the plant population, seedlings were thinned to one seedling per hill after they were established. In the normal experiment, recommended irrigation was applied at three critical stages, i.e., at (1) tillering (35 days after sowing, DAS), (2) booting (85 DAS), and (3) milking (112 DAS [15]). In the stressed experiment, drought stress was applied at the tillering stage by upholding (missing) the irrigation treatment. One set of genotypes was irrigated at all three critical stages, while the other set of the same wheat genotype was kept under drought stress, missing the irrigation at the first (tillering) critical stage at 35 DAS. At the time of maturity, from each replication, 5 healthy plants randomly selected for each genotype were grown under normal and drought experimental conditions. The data was collected from tagged plants for yield and yield related traits, namely: No of tillers**,** Spikelets per spike, Chlorophyll Content, Flag Leaf Area (cm), Plant Height (cm), Peduncle Length (cm), Spike Length (cm), Biomass (g), Main Spike Weight (g), Grain Yield per Spike (g), Yield per plant (g), and 1000 grain weight (g). The analysis of variance (ANOVA) was performed on the scoring data of variance (ANOVA) using statistics 8.1 [16]. Genotypic and phenotypic correlation analyses were conducted using R Studio. For correlation analysis significance levels, = 0.01 was used for highly significant effects and =0.05 was used for significant effects. Principle component analysis (PCA) was performed using the Minitab software to ascertain the relationship between traits and genotypes under drought-stricken conditions [17]. The following formula was used to calculate the reduction percentage:

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

Results and Discussion

Analysis of Variance

Analysis of variance revealed the existence of highly significant differences among different wheat genotypes for grain yield and quality-related traits under both normal and drought conditions (Table 1). All the studied characteristics, including NT, SPS, CC, PH, PL, FLA, BM, MSW, MSGW, YPP, and TGW, exhibit highly significant variations among wheat genotypes, according to the conducted analysis. The accessions that showed variance in performance in comparison to the genotypes investigated for the researched qualities under drought conditions were indicated by the mean variability of different seedling traits; those with the best performance were thought to be drought-tolerant (Table 1). In this study, the relationship between genotype and phenotype varies significantly among different genotypes. There were identical results published by Fouad et al. [18].

The mean values of spikelets per spike changed significantly, ranging from 3.14 to 4.66 under drought. The genotypes G45 (3.14), G7 (4.16), G24 (4.27), G38 (4.43), and G16 (4.66) performed best under drought conditions, and the genotypes G49 (16.07), G11 (16.95), G41 (16.96), G23 (17.43), and G32 (19.35) performed poorly under drought conditions, as shown in Table 2. Under drought duress, the characteristics of the shoot and root significantly declined. The decline in shoot characteristics was significantly greater than that of root characteristics. In addition, under drought stress, shoot length, fresh weight, and dry weight all decreased. Jager et. Al. also [19] also reported identical outcomes. One essential characteristic of wheat plants that is affected by water scarcity is their shoot length. Any trait's phenotypic response results from the interaction of environment and genotype [20]. Under normal circumstances, the mean values for shoot length ranged from 3.08 to 3.98 cm, while under conditions of stress, their dimensions were 11.00 to 25.19 cm.

Under drought circumstances, the genotypes that showed the highest quality of biomass were G45 (-8.04), G24 (-1.27), G16 (3.85), G38 (4.30), and G7 (4.34), while the low quality of biomass was shown by the genotypes G11 (20.29), G32 (21.25), G49 (23.52), G41 (25.03), and G23 (33.03), as shown in Table 2. According to [21], all

Table 1. Analysis of variance (ANOVA) for grain yield and related traits under normal and drought stress conditions.

Source	DF	NT	SPS	CC	SL	PH	PL	FLA	BM	MSGW	YPP	TGW
REP	2	10.97	18.91	1.71	6.90	1.74	7.11	14.85	14.83	36.06	3.86	78.80
GEN	49	6.16	14.37	32.20	8.65	143.72	20.66	138.07	224.34	0.99	55.90	72.12
TRT	1	218.62	284.58	234.25	142.79	603.51	167.69	6919.07	1326.87	153.87	551.19	173.38
GEN*TRT	49	2.85	3.59	14.31	3.22	41.43	3.27	37.27	11.08	0.24	1.95	86.27
Error	198	1.33	1.30	1.25	0.67	1.10	1.15	2.15	3.82	0.14	1.30	28.58
Total	299											

Table 2. Reduction percentage under drought stress condition.

Genotypes	NTP	SPS	CC	SL	PH	PL	FLA	BM	MSW	MSGW	YPP	TGW
G1	15.84	4.82	10.88	10.20	5.73	11.38	17.89	8.42	22.69	19.73	19.59	4.21
G2	23.97	9.92	9.54	5.31	2.85	6.73	17.62	7.78	16.24	11.82	12.53	3.75
G3	22.74	8.52	6.52	6.52	2.02	14.66	20.69	8.30	16.80	14.67	13.32	4.27
G4	4.43	10.82	5.34	10.64	1.87	12.44	28.28	9.70	19.81	16.70	10.76	5.24
G5	25.36	12.83	12.15	8.61	2.63	7.12	28.55	5.68	22.12	24.75	15.28	5.05
G6	24.98	10.23	8.46	4.00	4.00	8.09	27.96	8.97	15.57	20.45	19.62	4.47
G7	3.00	4.16	5.15	3.72	2.25	5.62	6.23	4.34	14.94	6.78	4.46	2.91
G8	5.86	9.29	19.43	9.99	5.91	7.10	16.99	8.36	15.80	9.48	24.83	7.00
G9	24.51	8.60	8.93	6.67	3.65	11.83	6.79	10.37	18.07	22.45	14.93	4.70
G10	13.10	13.02	10.41	4.78	3.69	10.96	17.27	10.85	18.94	21.97	21.50	6.19
G11	39.89	16.95	20.75	14.73	13.30	24.24	40.45	20.29	26.38	34.26	23.11	7.58
G12	33.03	15.09	15.86	4.58	3.41	20.72	30.09	5.77	18.35	16.79	18.31	4.26
G13	24.66	8.55	11.56	11.67	5.87	9.23	32.57	8.92	21.47	21.98	12.19	6.35
G14	18.14	10.48	7.32	6.32	2.43	8.06	16.01	7.04	17.10	20.55	13.08	4.98
G15	9.19	8.54	6.53	7.99	2.28	14.22	25.48	8.75	20.91	25.39	15.77	7.05
G16	2.36	4.66	5.05	3.98	3.14	6.60	3.25	3.85	14.93	2.78	9.51	3.29
G17	20.82	7.21	6.59	7.93	2.24	10.21	7.84	12.86	16.15	18.69	16.13	5.55
G18	24.59	4.74	13.55	10.40	10.41	9.55	30.98	14.40	21.91	22.19	21.89	3.89
G19	10.11	8.28	13.34	7.57	3.04	11.79	25.76	12.82	16.68	17.80	21.86	4.25
G20	17.32	8.28	11.75	12.35	3.23	10.32	15.78	13.44	18.19	13.67	15.98	4.67
G21	33.39	7.05	6.06	5.81	2.36	8.60	12.50	12.41	19.71	20.91	17.64	5.73
G22	23.46	9.48	7.75	11.31	3.02	15.43	24.36	17.54	22.90	19.10	20.65	3.88
G23	41.47	17.43	20.55	14.57	9.72	23.17	38.75	33.03	23.20	28.87	28.50	8.70
G24	2.66	4.27	4.63	3.48	2.82	5.36	5.35	6.27	13.81	5.69	9.67	1.69
G25	23.57	7.30	7.58	7.38	3.53	9.88	14.51	8.96	18.21	22.66	14.49	5.60
G26	33.16	7.34	9.78	6.15	3.28	10.25	28.62	15.97	16.88	15.78	22.56	4.34
G27	33.65	14.21	15.22	10.53	1.79	9.05	35.88	9.28	16.22	11.67	20.33	5.23
G28	15.52	14.41	9.27	9.98	3.03	14.80	8.73	10.03	21.78	15.30	15.49	5.87
G29	18.00	6.83	16.05	10.27	3.60	10.46	7.22	17.97	16.97	26.74	17.99	4.13
G30	20.24	11.76	15.54	13.81	4.05	9.26	34.34	8.43	15.10	12.23	11.00	5.57
G31	26.18	13.08	11.47	14.22	2.49	7.32	29.22	9.64	18.01	11.61	20.49	5.61
G32	33.85	19.35	26.00	14.41	2.41	20.44	37.96	21.25	26.17	26.76	30.89	7.14
G33	30.14	12.84	7.14	11.23	4.01	12.03	35.20	15.02	18.05	16.04	18.41	4.29
G34	21.04	7.02	16.03	13.00	3.70	17.18	33.13	11.20	20.86	17.02	19.48	4.56
G35	17.73	8.10	7.20	7.22	4.01	9.71	33.79	7.40	18.94	7.41	14.26	5.58
G36	32.64	8.78	19.53	8.69	2.04	18.68	21.93	11.12	22.23	23.84	16.84	4.32
G37	15.39	7.07	13.58	11.92	2.75	16.15	19.94	9.30	18.40	11.32	13.26	3.41
G38	3.88	4.43	3.56	3.08	2.95	3.31	4.44	4.30	14.49	1.70	10.22	3.25
G39	32.41	6.41	7.60	10.37	2.74	17.64	12.07	8.65	19.16	19.83	10.47	4.38
G40	18.46	6.47	6.37	12.78	1.38	11.75	10.32	13.28	19.51	26.06	21.45	4.79

Table 2. Continued.

G41	39.69	16.96	23.82	14.35	1.02	18.75	36.58	25.03	25.08	27.17	22.99	11.06
G42	26.55	14.67	6.38	12.48	2.77	9.17	25.30	18.44	21.05	18.13	12.20	3.84
G43	28.91	11.06	15.75	11.72	2.98	10.02	32.16	13.28	20.63	17.92	12.39	4.47
G44	17.00	8.18	18.98	13.10	2.34	17.79	22.31	8.19	20.80	8.23	12.86	6.30
G45	19.78	12.69	7.18	10.42	3.25	14.21	16.04	11.92	21.10	19.71	15.99	4.45
G46	15.53	14.96	12.54	10.98	2.35	12.90	27.84	13.54	22.87	12.36	10.70	4.21
G47	3.60	3.14	5.31	3.75	0.91	6.59	6.38	8.04	14.94	3.63	10.19	3.39
G48	22.74	7.56	6.93	11.46	1.04	8.30	12.12	7.50	18.05	18.86	19.76	5.50
G49	34.14	16.07	25.63	15.40	3.24	19.26	35.99	23.92	24.21	29.20	23.56	7.56
G50	19.70	8.53	17.57	11.45	2.26	15.09	29.28	6.88	20.05	19.08	17.31	4.87

NT = No of tillers, SPS = Spikelets per spike, CC = Chlorophyll Content, SL = Spike Length, PH = Plant Height, PL = Peduncle Length, FLA = Flag Leaf Area, BM = Biomass, MSW = Main Spike Weight, MSGW = Grain Yield per Spike, YPP = Yield per plant, TGW = 1000 grain weight

genotypes exhibited highly significant differences in wheat yield, plant height, and thousand grain weight. Wheat breeders [22] published identical results for agromorphological characteristics and cereal yield under stress and non-stress conditions. The genotypes that showed superlative performance for YPP were G7 (4.46), G16 (9.51), G24 (9.67), G45 (10.19), and G38 (10.22). On the other hand, the genotypes that showed poor performance were G11 (23.11), G49 (23.56), G41 (24.83), G23 (28.50), and G32 (30.89), as shown in Table 2. G24 (13.81), G7 (14.49), G16 (14.93), G45 (14.94), and G38 (14.94) are those genotypes that showed the best under drought conditions for main spike weight, and G24 (1.69), G7 (2.91), G38 (3.25), G16 (3.29), and G45 (3.39) showed the best for 1000 grain weight.

Table 3. Best and worst genotypes under drought stress conditions.

Traits	Best	Worst
NT	G16 (2.36), G24 (2.66), G7 (3.00), G45 (3.60), G38 (3.88)	G32 (33.85), G49 (34.14), G41 (39.69), G11 (39.89), G23 (41.47)
SPS	G45 (3.14), G7 (4.16), G24 (4.27), G38 (4.43), G16 (4.66)	G49 (16.07), G11 (16.95), G41 (16.96), G23 (17.43), G32 (19.35)
CC	G7 (5.15), G16 (5.65), G38 (3.56), G24 (4.65), G45 (5.31)	G23 (20.55), G11 (20.75), G41 (23,82), G49 (25.63), G32 (26.00)
SL	G38 (3.08), G24 (3.48), G7 (3.72), G45 (3.75), G16 (3.98)	G41 (14.35), G32 (14.41), G23 (14.57), G11 (14.73), G49 (15.40)
PH	G45 (0.91), G38 (1.02), G16 (1.38), G24 (1.79), G7 (1.87)	G41 (5.73), G32 (5.87), 23 (9.72), G49 (10.41), G11 (13.30)
PL	G38 (3.31), G24 (5.36), G7 (5.62), G45 (6.59), G16 (6.60)	G41 (18.75), G49 (19.26), G32 (20.44), G23 (23.17) , G11 (24.24)
FLA	G16 (3.25), G38 (4.44), G24 (5.35), G7 (6.23), G45 (6.38)	G49 (35.99), G41 (36.58), G32 (37.96), G23 (38.75) , G11 (40.45)
BM	G47 (8.04), G24 (6.27), G16 (3.85), G38 (4.30), G7 (4.34)	G11 (20.29), G32 (21.25), G49 (23.52), G41 (25.03), G23 (33.03)
MSW	G24 (13.81), G7 (14.49), G16 (14.93), G45 (14.94), G38 (14.94)	G23 (23.20), G49 (24.21), G41 (25.08), G11 (26.17) , G32 (26.38)
MSGW	G16 (1.70), G38 (2.78), G7 (3.63), G24 (5.69), G45 (6.78)	G32 (26.76), G41 (27.17), G11 (28.87), G49 (29.20) , G23 (34.26)
YPP	G7 (4.46), G16 (9.51), G24 (9.67), G45 (10.19), G38 (10.22)	G11 (23.11), G49 (23.56), G41 (24.83), G23 (28.50), G32 (30.89)
TGW	G24 (1.69), G7 (2.91), G38 (3.25), G16 (3.29), G45 (3.39)	G32 (7.14), G49 (7.56), G11 (7.58), G23 (8.70), G41 (11.06)

Photosynthesis is the primary process in plant cells that controls the low concentration of water culture media [23]. More chlorophyll will result in more effective photosynthesis mechanisms. The genotypes G7 (-53.15), G16 (-28.65), G38 (3.56), G24 (4.65), and G45 (5.31) showed the best performance under drought conditions, and the genotypes G23 (20.55), G11 (20.75), G41 (23, 82), G49 (25.63), and G32 (26.00) performed poorly under drought conditions, as shown in Table 3. Similar results were observed by wheat scientists [24, 25], who reported that drought stress substantially affects chlorophyll and causes leaves to turn yellow rather than green.

Correlation Analysis

The correlation analysis indicated strong positive correlations for most of the traits within the same experiment. In this experiment, evidence of both genotypic and phenotypic correlations of different traits in normal and stress conditions may help advance strategies for the assortment of required varieties with preferred traits (Table 4). According to genotypic correlation, positive and highly significant correlations were found between the number of spikelets per spike (r = 0.56**) with plant height, main spike weight, chlorophyll content, spike length, yield per plant, and thousand grain weights [18]. In addition to a positive and highly significant genotypic correlation with thousand-grain weight (r = 0.70**), there was a positive and statistically significant genotypic correlation with peduncle length, flag leaf area, biomass, main spike grain weight, and yield per plant. Yield per plant (r = 0.70**) showed a positive and significant phenotypic association with thousand-grain weight, as shown in Table 4. However, a positive and statistically significant genotypic connection was found between the area of the flag leaf and the chlorophyll content. Plant biomass (r=0.88**) was positively and statistically significantly associated with main spike weight, main spike grain weight, and plant yields. Javed et al. [26] also found a strong positive link between biomass output, plant height, 1000-grain weight, and grain yield in their investigation of advanced wheat genotypes. The thousand-grain weight (r = 0.06NS), flag leaf area, and peduncle length were shown to have a positive but not statistically significant phenotypic correlation under drought (Table 5). According to Ali et al. [27], there is a strong positive correlation between plant height and grain weight. In the current study, the relationship between genotype and phenotype varies significantly for each genotype. Main spike grain weight (-0.15^{ns}) was found to have a negative and minor phenotypic connection to thousand-grain weight, but a positive and substantial phenotypic connection to yield per plant. Both Javed et al. [28] and Baye et al. [26] showed similar results under drought conditions, which are negative but statistically significant.

Principal Component Analysis

Principal component analysis (PCA) was used to examine the wheat genotypes to characterize the variety of the germplasm and the relationship between the wheat seedling indices under both normal and drought stress conditions. PCA based on the correlation matrix. The statistically significant principal components (PCs) were selected based on the eigenvalues' importance, as determined by Kaiser [29]. The PCs classified as significant were limited to those with eigenvalues greater than one. Multivariate statistical analysis, known as principal component (PC) analysis, is used to examine and deconstruct big and complicated datasets. The results of Kamel [12, 30] showed that this analysis

Table 4. Genotypic correlation and phenotypic correlations under normal conditions.

	NT	SPS	CC	SL	PH	PL	FLA	BM	MSW	MSGW	YPP	TGW
NT	1**	0.40**	0.33**	0.13^{ns}	0.29**	0.42**	0.27**	0.63**	0.40**	0.28**	0.70**	0.22**
SPS	0.56**	1**	0.32**	0.23**	0.58**	0.26**	0.14^{ns}	0.26**	0.37**	0.21**	0.42**	0.26**
CC	0.42**	0.39**	1**	0.16^{ns}	0.24**	0.55**	0.39**	0.40**	0.19*	0.40**	0.42**	0.10^{ns}
SL	0.17^{ns}	0.36**	0.21^{ns}	1**	0.42**	0.25**	0.17*	0.08^{ns}	0.50**	0.27**	0.13^{ns}	0.09^{ns}
PH	0.32*	0.66**	0.26^{ns}	0.54**	1**	0.33**	0.35**	0.29**	0.38**	0.22**	0.33**	0.14^{ns}
PL	0.47**	0.3*	0.62**	0.32*	0.34*	1**	0.42**	0.34**	0.39**	0.29**	0.40**	0.05^{ns}
FLA	0.31*	0.17**	0.42**	0.23^{ns}	0.35*	0.42**	1**	0.33**	0.31**	0.24**	0.34**	0.02^{ns}
BM	0.7**	0.31*	0.43**	0.10^{ns}	0.29*	0.35*	0.33*	1**	0.25**	0.15^{ns}	0.82**	0.18*
MSW	0.57**	0.46**	0.28*	0.62**	0.48**	0.50**	0.42**	0.34*	1**	0.32**	0.31**	0.16^{ns}
MSGW	0.4**	0.28*	0.61**	0.31*	0.33*	0.45**	0.34*	0.20^{ns}	0.51**	1**	0.20*	0.15^{ns}
YPP	0.79**	0.5**	0.47**	0.18^{ns}	0.34*	0.41**	0.35*	0.83**	0.40**	0.31*	1**	0.18*
TGW	0.7**	0.1**	0.61**	0.47**	0.47**	0.15^{ns}	0.06^{ns}	0.61**	0.60**	0.27^{ns}	0.57**	1**

reduces the number of associated variables from a bigger one to a smaller one.

Of the twelve main components (Table 6), four showed substantial fluctuation during drought circumstances, and the first five showed Eigenvalues of more than one (significant) under normal conditions. Under normal and stress conditions, the first three PCs showed 0.75% and 0.72% total variation, respectively, in the studied germplasm. Under normal circumstances, the first PC explained 0.24% of the variation, the second, 0.20%, the third, 0.11%, and the fifth, 0.9%. Under drought conditions, as shown in Table 6, the first PC contributed 0.21% of the total variance, the second contributed 0.20%, the third contributed 0.11%, the fourth contributed 0.10%, and the fifth contributed 0.10%.

The PC1 was highly related to spike length (0.48) and main spike weight (0.46) under normal conditions, while under stress conditions It was highly related to peduncle length and chlorophyll content (Table 6). There is a negative association between PC4 and SPS, which suggests that SPS has a major impact on this factor in typical settings. On the other hand, PC2, PC4, and PC5 were found to have unfavorable associations. The fact that PL is positively correlated with both PC3 and PC4 demonstrates that it has an effect on those variables. The fact that YPP is positively correlated with both PC2 and PC4 demonstrates its effect on those subsystems. TGW had a positive connection with PC5 that was statistically significant. Table 7 showed that TGW has a small effect on PC1, PC2, PC3, and PC4 under typical settings, as indicated by the small correlations between these variables.

The PCA extracted twelve principal components (PCs) to assess drought tolerance in the wheat genotypes based on their key morphological and yield related traits (Table 6). Among these 12 PCs, only five had an eigenvalue greater than 1, having variations up to 0.72% of the overall data under drought stress conditions (Table 6 and Fig. 1).

This (Table 7) is a principal component analysis loading plot (PCA). Principle component analysis (PCA) is a statistical method that creates new variables known as principle components (PCs) from the original variables in order to minimize the dimensionality of a data collection. The majority of the variance

Table 5. Genotypic correlation and phenotypic correlation under drought stress conditions.

	NT	SPS	CC	SL	PH	PL	FLA	BM	MSW	MSGW	YPP	TGW
NT	1**	0.33**	0.39**	0.47**	0.44**	0.36**	0.44**	0.69**	0.43**	0.36**	0.61**	0.17**
SPS	0.40**	1**	0.35**	0.46**	0.53**	0.13 ns	0.35**	0.34**	0.30**	0.21**	0.43**	0.26**
CC	0.47**	0.42**	1**	0.36**	0.38**	0.40**	0.33**	0.48**	0.38**	0.37**	0.44**	0.16 ns
SL	0.58**	0.63**	0.43**	1**	0.56**	0.47**	0.47**	0.52**	0.35**	0.31**	0.47**	0.10 ns
PH	0.53**	0.61**	0.40**	0.66**	1**	0.32**	0.38**	0.46**	0.28**	0.29**	0.34**	0.11 ns
PL	0.44**	0.15 ns	0.45**	0.56**	0.34**	1**	0.34**	0.39**	0.35**	0.20**	0.29**	0.01 ns
FLA	0.55**	0.41**	0.36**	0.57**	0.39**	0.36**	1**	0.48**	0.47**	0.40**	0.55**	0.01 ns
BM	0.81**	0.39**	0.51**	0.61**	0.46**	0.41**	0.49**	1**	0.36**	0.23**	0.76**	0.18**
MSW	0.65**	0.35**	0.50**	0.53**	0.35**	0.45**	0.59**	0.46**	1**	0.60**	0.28**	0.01 ns
MSGW	0.46**	0.28**	0.54**	0.49**	0.42*	0.31*	0.58**	0.33*	0.82**	1**	0.21**	-0.15 ns
YPP	0.72**	0.48**	0.46**	0.55**	0.35*	0.31*	0.57**	0.77**	0.35*	0.29*	1**	0.16 ns
TGW	0.69**	0.90**	0.76**	0.33*	0.34*	0.08 ns	-0.02 ns	0.66**	-0.14 ns	-0.27 ns	0.52**	1**

Table 6. Variability under normal and drought conditions.

Variability	Environments	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
Eigenvalue	Normal	2.93	2.40	1.32	1.30	1.09	0.9	0.88	0.56	0.28	0.16	0.13	0.05
	Drought	2.54	2.42	1.32	1.23	1.14	0.82	0.75	0.53	0.41	0.33	0.32	0.21
Proportion (%)	Normal	0.24	0.20	0.11	0.11	0.09	0.08	0.07	0.05	0.02	0.01	0.01	0.0
	Drought	0.21	0.20	0.11	0.10	0.1	0.07	0.06	0.04	0.03	0.03	0.03	0.0
Cumulative (%)	Normal	0.24	0.44	0.55	0.66	0.75	0.83	0.9	0.95	0.97	0.99	1.00	1.00
	Drought	0.21	0.41	0.52	0.63	0.72	0.79	0.85	0.9	0.93	0.96	0.98	1.00

in the data is captured by the PCs, which are simply linear combinations of the original variables. The loading plot displays the relative importance of each original variable on each PC. The graph has two plots, one for the data under drought conditions and one for the data under normal conditions. Each plot has two axes, PC1 and PC2, which are the first and second principal components. The lines in the plots represent the original variables,

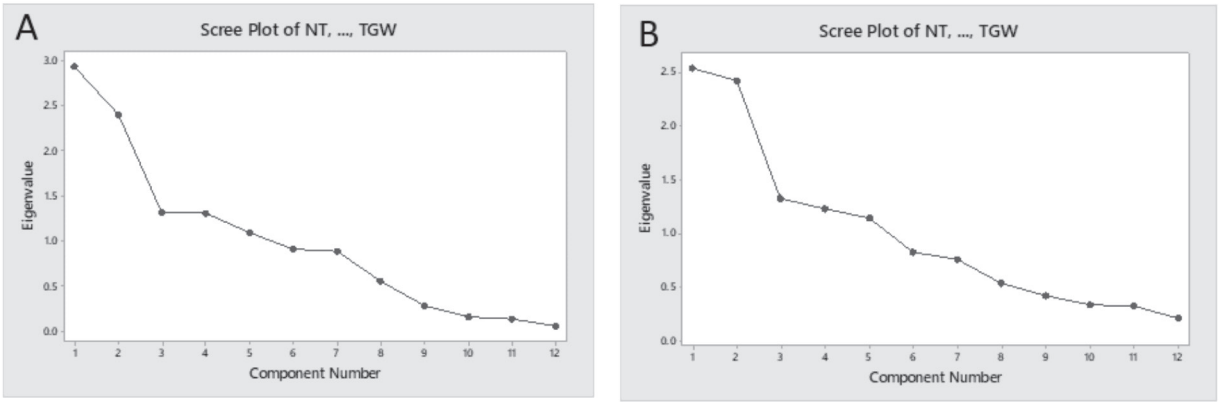

Fig. 1. (A) Scree plot graph under normal conditions (B) Scree plot graph under drought conditions.

Table 7. Loading factor of significant variables under normal drought conditions.

Variable	Environments	PC1	PC2	PC3	PC4	PC5
NT	Normal	0.27	0.47	0.12	-0.1	-0.27
	Drought	0.12	-0.51	0.2	0.15	0.12
SPS	Normal	0.31	0.24	0.05	-0.54	-0.31
	Drought	-0.05	-0.4	0.55	-.0.05	-0.16
CC	Normal	-0.03	-0.08	0.7	-0.2	0.03
	Drought	0.2	-0.21	0.26	-0.59	0.19
SL	Normal	0.48	-0.3	-0.09	0.17	0.07
	Drought	0.37	-0.08	-0.22	0.23	-0.37
PH	Normal	0.4	-0.22	0.02	-0.28	-0.02
	Drought	0.43	-0.08	0.21	0.16	-0.41
PL	Normal	0.13	-0.12	0.58	0.4	-0.26
	Drought	0.33	-0.01	-.0.21	-0.09	0.43
FLA	Normal	0	-0.05	-0.37	0.08	-0.56
	Drought	-0.23	-0.19	0.01	0.58	0.01
BM	Normal	0.19	0.42	0.04	0.37	0.23
	Drought	0.13	-0.41	-0.51	-0.07	0.14
MSW	Normal	0.46	-0.34	-0.06	0.01	-0.02
	Drought	0.51	0.14	0.16	0.05	0.05
MSGW	Normal	0.27	-0.1	-0.08	0.35	0.06
	Drought	0.42	0.15	-0.01	0.25	0.21
YPP	Normal	0.27	0.5	-0.05	0.2	0.06
	Drought	-0.05	-0.53	-0.29	0.01	0
TGW	Normal	0.17	0.06	-0.06	-0.28	0.62
	Drought	0.04	0.01	-0.29	-0.37	-0.61

such as P1, P2, P3, etc. The length and direction of each line indicate how much each variable contributes to t he PCs. We can see that P1 has a higher loading on PC1 under drought conditions than under normal conditions, which means that P1 explains more variation in the data when there is drought, as shown in Fig. 2.

When choosing parents from a variety of backgrounds for hybridization and other plant breeding techniques, principal component analysis can be useful [31]. The selection of the various parent groups benefited from the genotype projection on PC1 and PC2. The expected pattern of genotypes on the two PCs indicated

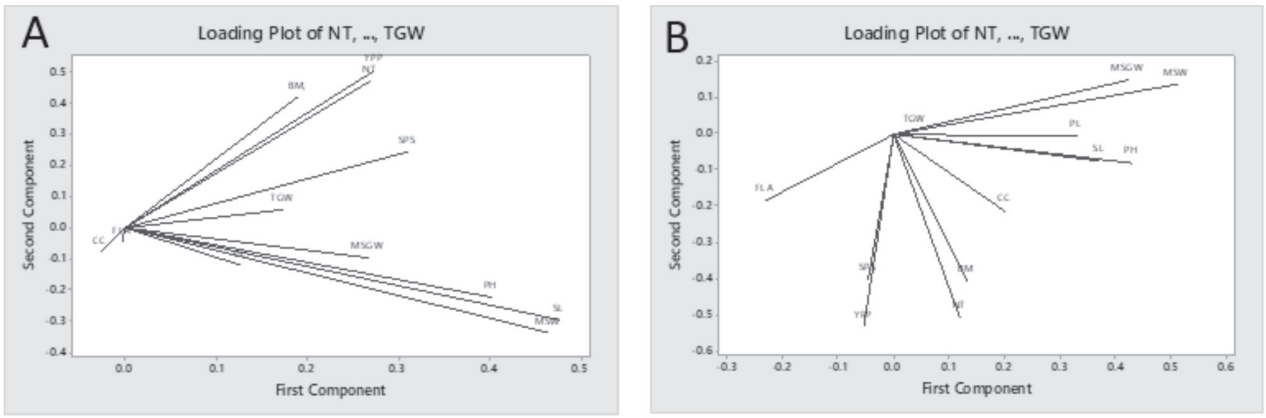

Fig. 2. (A) Principal component (PC) loading plot (projection of variables) of Fig. 2a Principal component (PC) loading plot of seedling traits under normal conditions. (B) Principal component loading plot of seedling traits under drought conditions.

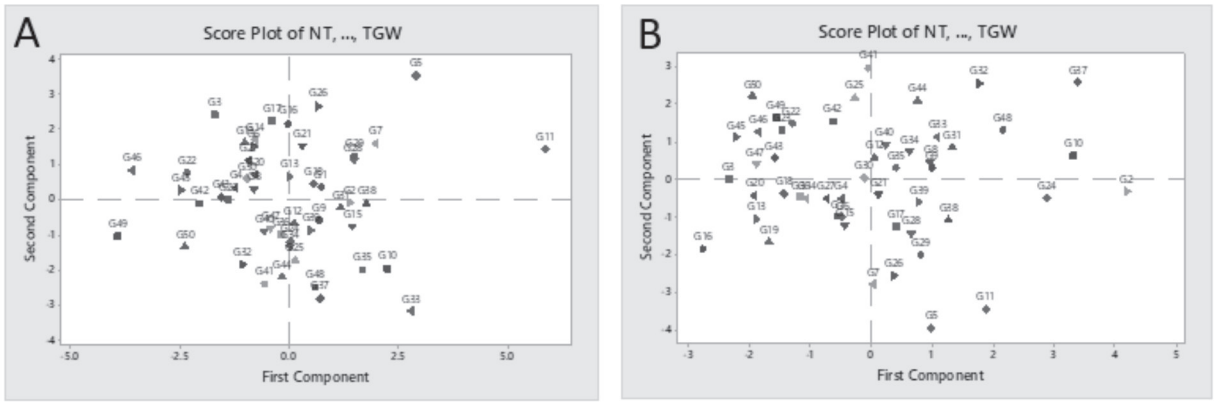

Fig. 3. (A) Two-dimensional score plot of wheat genotypes on PC1 and PC2 under normal conditions. (B) Two-dimensional score plot of wheat genotypes on PC1 and PC2 under drought conditions.

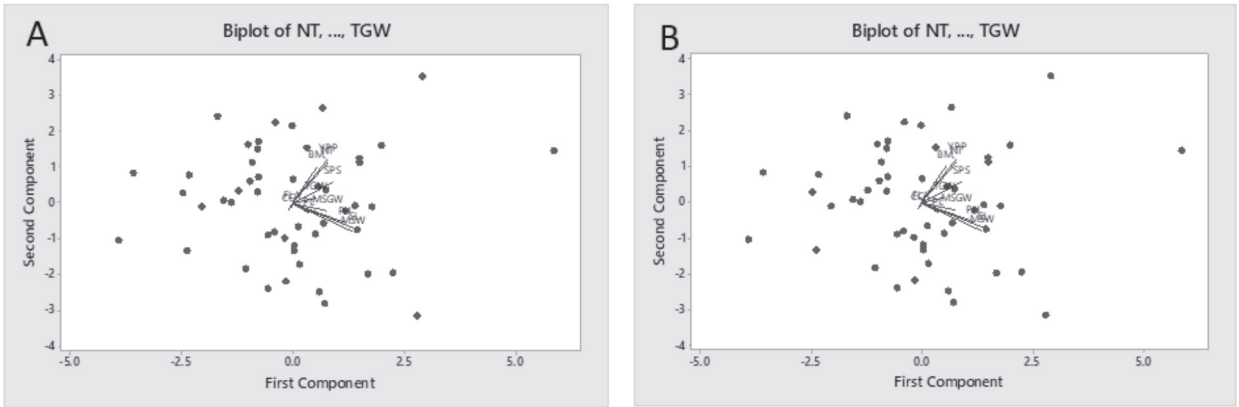

Fig. 4. (A) Biplot graphs under normal conditions (B) Biplot graphs under drought conditions.

the population structure under normal and drought conditions. The genotypes appearing in the same square box in Figs. 3a) and b), had the same performance, while those appearing in different squared boxes showed differing performance. Under normal conditions, G5, G11, G26, and 38 were opposite to G49 and G50. Genotypes G3 and G44 were opposite to genotype G10, while G33 and G17 were opposite to each other and showed clear diversity among all genotypes (Fig. 3a). There was a clear difference between drought-tolerant and drought-susceptible genotypes. Under drought conditions, the genotypes G10 and G37 were opposite to G16, G19, and G32, while G50 was opposite to G11 and G24. Genotype G44 and genotype G10 showed clear diversity from G16 and G20 (Fig. 3b).

None of the interventions resulted in statistically significant alterations in the PCA. It is a powerful statistical method for reducing the number of dimensions in a dataset and extracting actionable, fact-based feedback from a complex one [32]. The angle between the cosines of the trait vectors is used in the PCA Biplot to approximately depict the correlation between traits. An angle less than 90 degrees indicates independence between the features, whereas an angle greater than 90 degrees indicates a positive link. Our findings, however, demonstrated unequivocally that the contributions of a trait pair to the Biplot for PCA and the correlations between a trait pair were well-coordinated with the approximate vector angles (Figs. 3, 4). Other researchers have utilized PCA Biplot analysis to successfully screen drought-tolerant wheat cultivars [33]. So it is likely that it is useful here as well.

Conclusion

In this study, a total of 50 wheat genotypes were used to investigate the response of each genotype to drought stress. There are two different sets of plots (one with normal conditions and the other with drought stress). According to the results of this study, five genotypes (G7, G16, G24, G38, and G45) performed best in both normal and drought conditions. The genotypes G11, G23, G32, G41, and G49 did not perform better under both stressful and non-stress conditions due to their high decline in reduction percentage. Among these spring wheat genotypes, those that did better under both conditions were deemed drought-tolerant, and those that performed the worst were deemed drought-susceptible. Under normal conditions, PC1 exhibited 0.24%, whereas PC1 exhibited 0.21% under drought conditions. In order to develop wheat germplasm that is tolerant to drought stress, this study found favorable features under drought stress that might be used in wheat breeding programs. As a result, by utilizing contemporary breeding techniques, these genotypes will be essential in the future development of drought tolerance.

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Conflict of Interest

The authors declare no conflict of interest.

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