Research Article

Field and AI Based Screening Against Drought Stress With Morpho-Physiological Assisted Characterization of Bread Wheat Genotypes

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Abstract | Bread wheat (*Triticum aestivum* L.), is staple food for human in various regions across the globe. Variations in average rain fall, frequency and pattern are limiting factors for wheat yield and growth. A field trail was conducted to evaluate ffifty genotypes of wheat on the basis of morphological and physiological characteristics. The images of morphological traits of the plants were fed to neural network to explore the role of artificial intelligence (AI) in screening. The experiment was laid out in randomized complete block design (RCBD) with two factors water stress (50% of field capacity) and well-irrigated (100% of field capacity) factorial arrangements. Reduction percentage was calculated among the genotypes to evaluate the performances of genotypes. The genotypes G8 (SHALKOT-14), G22 (JANBAZ-10) and G43 (GOLD-16) performed best in both normal and water deficit condition while genotypes G28 (204088), G13 (BENAZIR) and G38 (204164) had lowest performances in both conditions. Pearson's Correlation exhibited that most of the studied indices had significant association with each other in both environments. Principal component analysis revealed only two PCs being significant out of eight with cumulative variation of 78.0% and 77.2% under normal and drought stress conditions respectively. Cluster heat map displayed different values by a color-coding scheme. Neural Network categorized images into drought tolerant and susceptible classes. The model exhibited 100% of the accuracy. The proposed method provides a key starting point for drought tolerance lines, reducing the need for extension agents or experienced farmers. It will support farmers to determine and explore drought tolerance lines in breeding programs.

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Introduction

The accessibility of nutritious foods is seriously threatened by the enormous increase in the world's population, which is predicted to reach approximately 9.8 billion people by 2050 (FAO, 2023). There is a need to increase the overall global production of wheat by at least 60% in order to fulfill the required demand

(Kradetskaya *et al*., 2024). This makes it even more difficult to achieve, considering the drastic effects of climate change, especially drought, being one of the most notable abiotic stressors reducing wheat yield worldwide. In addition to serving as an important source of protein from plants, wheat offers a variety of vital vitamins and minerals and makes up a significant amount of the world's daily calorie intake. Dietary fibre, B-complex vitamins, and essential minerals like iron, magnesium, and zinc are all abundant in whole grain wheat (Ray *et al*., 2013; Hamzah *et al*., 2024).

Wheat farming has a significant part in the global economy in terms of farmed area as well as food supply, feeding, and trade. Climate change has increased the number of frequency and intensity of the drought events in the wheat grown regions such as arid and semi-arid regions. For example, drought has led up to 50% decrease in wheat yield. To further increase water-use efficiency, future tactics may combine synthetic biology techniques with micro biome-assisted breeding. In light of growing aridity and climate unpredictability, scientists want to ensure global food production by utilizing wheat's genetic variety and state-of-the-art breeding methods (Khan *et al*., 2025).

Drought stress shows up as diverse patterns and intensities at different stages of crop growth. A crucial component of stable wheat yield is the ability to tolerate drought, which is a very complex trait. Drought stress negatively impacts the physio-morphological traits of wheat crops, including shoot and root lengths, relative water content, chlorophyll content, and leaf area. The capacity of plant tissues to photosynthesize is indicated by the amount of chlorophyll in their leaves. The concentration of chlorophyll pigments varies during drought. It is one of the most common causes of crop loss worldwide, reducing the average yield of agricultural plants by around 50% (Ahmed *et al*., 2022; Nassima *et al*., 2024).

The incidence of drought stress limits wheat productivity more than any other environmental factor. Drought has a detrimental effect on plant establishment, which in turn affects growth and development. Cell development and assimilation partitioning are hindered by the water deficit (Saihood *et al*., 2024). Drought during the reproductive stage is more harmful to plant metabolic systems than it is during the vegetative development stage. This is because under stressful conditions, photosynthesis, reproductive development, and eventually grain output at anthesis are all markedly reduced (Raza *et al*., 2019).

Genetic diversity is used comprehensively to increase yield, disease resistance, and stress tolerance (Mir *et al*., 2012). The genetic diversity of modern wheat cultivars has remarkably dropped as a result of rigorous selection for high yield and uniformity during the Green Revolution (Shan and Osborne, 2024). This has led to reduced potential for further enhancements in the context of abiotic stress tolerance. The precision agriculture is the demand of current world. The role of AI cannot be denied in agricultural productivity. Neural network has shown remarkable results in classification problems (Qureshi *et al*., 2025; Nafees *et al*., 2013). Screening of germplasm using AI tools is reliable and less time consuming (Qureshi *et al*., 2024; Ahmad *et al*., 2013).

This current investigation aims to address these gaps by conducting a comprehensive Field and AI based screening of germplasm against drought tolerance with morpho-physiological assisted characterization of different bread wheat genotypes. By integrating multiple approaches, this study seeks to identify promising genotypes with superior drought tolerance, which can be utilized in breeding programs to develop drought-resilient wheat varieties.

Materials and Methods

To assess the drought tolerance of wheat genotypes, fifty genotypes were assessed in the field based on their morphological and physiological characteristics (Table 1). The experiment was carried out in the Department of Plant Breeding and Genetics' experimental field at the Faculty of Agriculture and Environment, the Islamia University of Bahawalpur (IUB) in November 2024-2025 using a randomized complete block design (RCBD), each with three replications. Two drought treatment variables were included in the experiment: water stress (50% of field capacity) and well-irrigated (100% of field capacity). Ten seeds of each genotype were sown in rows, maintaining plant into plant distance of 06 inches and row into row distance of 12 inches respectively. Three critical growth stages—tillering (35 days after sowing, or DAS), booting (85 DAS), and milking (112 DAS)—were irrigated during the normal treatment. Water stress emerged in the drought-stressed treatment by skipping irrigation at milking stage. From each genotype, five seeds per genotype were sown. To maintain one plant per hole, thinning was done. All agronomic practices were carried out according to the guidelines. Data of following traits were recorded, Number of Tillers per plant (NTP), Spikelets per spike (SPS), Flag Leaf Area (FLA) (cm^2), Relative Water Content (RWC), Chlorophyll Contents (CC), Grain yield per plant (GYP) (g), Thousand grain weight (TGW) (g) and Plant height (PH) (cm). The images of morphological traits of studied lines showing drought tolerance and intolerance were collected at maturity to feed to neural network. Flag leaf area was calculated using the formula provided by (Müller, 1991).

Table 1: *Names of 50 bread wheat genotypes used in the experiment along with their codes*

No.	Variety names	No.	Variety names
G1	IHSAN16	G26	BWP-97
G2	JAUHAR16	G27	Pakistan 20
G3	NIFA AMAN	G28	204088
G4	NN GANDAM I	G29	Akbar-19
G5	SINDHU16	G30	ANAJ-17
G6	ZINCOL 2016	G31	166
G7	BORLAUG 2016	G32	AS-021
G8	SHALKOT-14	G33	PAK-13
G9	AZRC-1	G34	AROOJ
G10	LALMA-13	G35	15-STRN-NAWAB
G11	PIRSABAK-2013	G36	178
G12	SHAHKAR-2013	G37	204171
G13	BENAZIR	G38	204164
G14	HAMAL-FAQIR	G39	SADIQ-15-STRN
G15	NIFA-LALMA	G40	214313
G16	NIA SAARANG	G41	10-SATY
G17	MILLAT-2011	G42	HTYT-9
G18	DHARABI-2011	G43	GOLD-16
G19	PUNJAB-2011	G44	ASS-15-STRN
G20	AARI-2011	G45	SILVER-BLUE
G21	NIFA-BARSAT-10	G46	TD-01
G22	JANBAZ-10	G47	FSD-08
G23	SIRAN-2007	G48	NISHAN-E-BAKHAR
G24	ATA HABIB 2010	G49	SEHER-6
G25	KT 2009	G50	SHAHFAQ 2006

Flag leaf area = Flag leaf length × Flag leaf Width × 0.74

(Barrs and Weatherley, 1962) employed the following formula to determine the relative water content:

RWC (%) = ((Fresh Weight − Dry Weight)/(Turgid Weight − Dry Weight)) × 100

The following formula was used to quantify the amounts of chlorophyll a and b (Lichtenthaler and Wellburn, 1983);(Lohithaswa *et al*., 2014):

Chl a (mg g–1) = [12.7×(OD663)–2.69×(OD645)] ×V/1000×W

Chl b (mg g–1) = [22.9×(OD645)– 4.68×(OD663)]× V/1000×W

where

W, weight of fresh leaves; OD, optimal density; and V, volume of extract.

Using Statistix 8.1, collected data on seedling characteristics were subjected to the ANOVA technique (Steel and Torrie, 1960). Software called MiniTab was used to perform multivariate analysis and summarize the obtained data (Ahmed *et al*., 2019). Cluster heat maps were performed by using RStudio. Correlation Pearson was also done by using RStudio. Characters that showed notable variations across the genotypes under study were further examined for analysis and correlation using following Pearson formula for correlation.

$$r = \frac{n(\sum xy) - (\sum x)(\sum y)}{\sqrt{[n\sum x^2 - (\sum x)^2][n\sum y^2 - (\sum y)^2]}}$$

Reduction/change in morph-physiological traits under drought as compared to normal was calculated using the following formula;x^2

$$\text{Reduction in trait (\%)} = \left(1 - \frac{\text{Performance under drought condition}}{\text{Performance under normal condition}}\right) \times 100$$

In object recognition research, the right dataset is crucial from training to testing. The required images were acquired using an Android phone camera. The images of tolerant and susceptible plants were collected. Plants were divided into two groups by experience farmers and extension workers which served as a benchmark for developing neural network model. The image pixel values served as the source for model training and testing. Smartphone images have different resolutions and sizes. These features require uniform adjustment for better pattern extraction. This preprocessing is also crucial for obtaining consistent results from deep neural networks. Furthermore, the image preprocessing procedure involves cropping and images with the highest resolution are suitable for use in the dataset. Image resizing also minimizes model training time. This process divides the dataset into training, validation, and testing sets. The training set is used for model training, validation set for hyperparameters tuning and test set for actual performance respectively. 80% and 20% of data set were used for training and testing respectively. The model accuracy results were set as a standard to check model performance.

Table 2: *Eigenvalues, variability (%) and cumulative (%) values under normal (N) and water deficit conditions (WD)*

SOV	ENV	PC1	PC2	PC3	PC4	PC5
Eigen-value	N	4.7144	1.5268	0.8321	0.3617	0.3385
Eigen-value	WD	4.8064	1.3662	0.7528	0.5409	0.2723
Propor-tion	N	0.589	0.191	0.104	0.045	0.042
Propor-tion	WD	0.601	0.171	0.094	0.068	0.034
Cumu-lative	N	0.589	0.78	0.884	0.929	0.972
Cumu-lative	WD	0.601	0.772	0.866	0.933	0.967

Results

Assessment of genetic variation under normal and drought stress conditions

Under both normal irrigation and drought stress, analysis of variance was performed for the genotypes, environment, and their interactions. All the studied components revealed the significant variations among them. The results were shown in Table S1. The genotypes G8 (-1.9), G22 (-4.3) and G43 (-1.1) had minimum values of reduction percentage (RP) for plant height. These genotypes had best performing ability in this attribute, while the genotypes G13 (13.9), G28 (13.6) and G38 (13.6) had maximum value of RP and having low ability to perform in stress environment as mentioned in Table S2. The average performances of genotypes were also present in Figure 1. In number of tillers under given conditions, the genotypes G43 (-6.7), G22 (-27.3) and G8 (-12.5) had lowest value of reduction percentage and performed best in given environment. In comparison with the best performing genotypes, the genotypes G38 (124.6), G28 (124.6) and G13 (161.2) had high value of reduction percentage and had low ability to performed in stress environment as showed in Table S2. The average performances of genotypes were also present in Figure 1. The genotypes G22 (-4.9) followed by G43 (-4.7) and G8 (-9.4) had low values of reduction percentage in spikelets per spike. The genotypes G28 (76.4), G13 (72.1) and G38 (66.0) had high value of reduction percentage in said trait, so it means that these genotypes had poor performance for spikelets per spike in the stress condition as represented in Table S2. Flag leaf area revealed that in both condition, the higher performance observed by genotypes were G8 (18.5), G43 (26.4) and G22 (19.8). So, these genotypes had minimum values for reduction percentage in such condition. While the genotypes that showed lower performance were G13 (91.5), G38 (90.9) and G28 (112.8) had maximum values for reduction percentage which means their performance were low in condition as displayed in Table S2. The average performances of genotypes were also present in Figure 1. Under normal and stress conditions, the genotypes G22 (16.2), G43 (14.5) and G8 (1.54) had less value of reduction percentage as compared to all other genotypes in this trait while the genotypes G28 (37.7), G38 (16.8) and G13 (35.0) had maximum value of reduction percentage for relative water content. The genotypes G8 (-15800) followed by G22 (-2953.8) and G43 (-5810) had low value of reduction percentage in chlorophyll contents. So, the genotypes G8, G22 and G43 had desirable chlorophyll contents in normal and water deficit condition. The genotypes G28 (2142.8), G13 (1763.8) and G38 (2218.7) had high value of reduction percentage in trait, so it means that these genotypes had poor performance for chlorophyll contents in the stress condition as represented in Table S2. In grain yield per plant under given conditions, the genotypes G43 (20.8), G22 (23.2) and G8 (22.4) had lowest value of reduction percentage and performed best in given environment. In comparison with the best performing genotypes, the genotypes G38 (52.3), G28 (46.8) and G13 (52.3) had high value of reduction percentage. This trait revealed that in both condition, the higher performance observed by genotypes were G8 (-11.7), G43 (-3.0) and G22 (-5.4). So, these genotypes had minimum values for reduction percentage in such condition. While the genotypes that showed

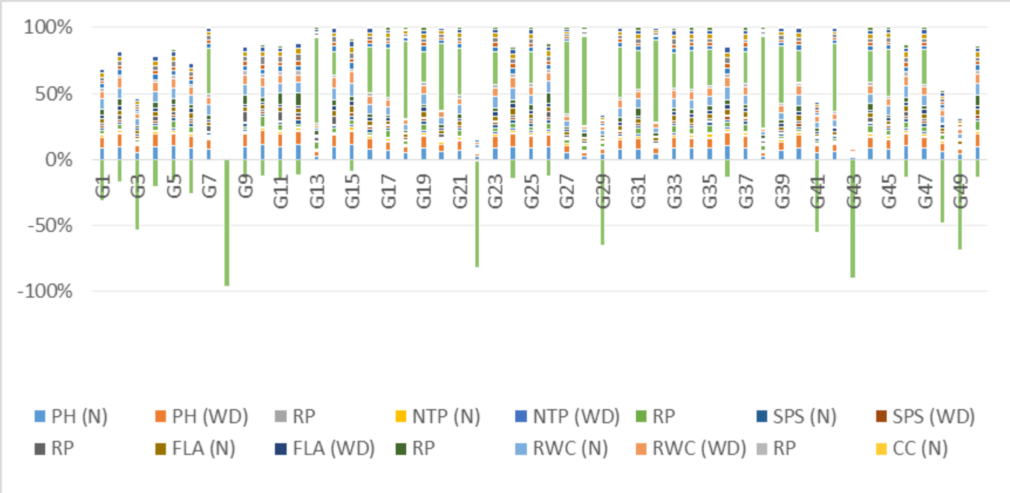

Figure 1: *Reduction percentage of attributes in non-stressed (N) and water deficit (WD) conditions*

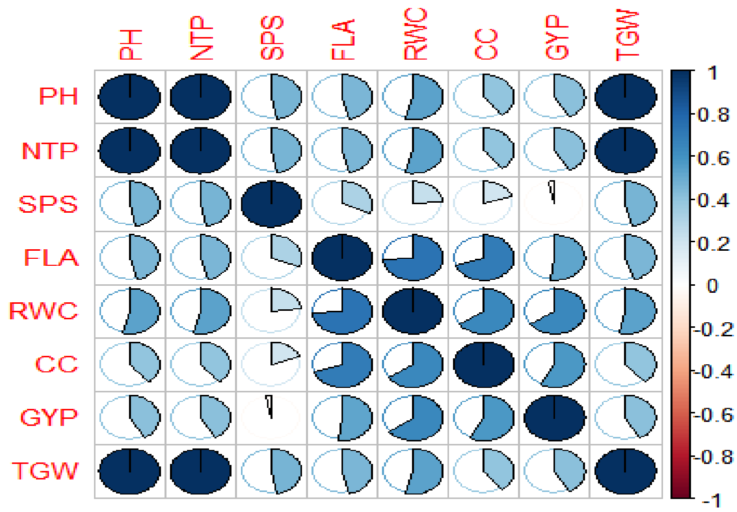

Figure 2: *Correlation among studied indices under non-stressed condition*

lower performance were G13 (44.5), G38 (41.2) and G28 (41.24) had maximum values for reduction percentage which means their performance were low in condition as displayed in Table S2. The average performance of genotypes was also present in Figure 1. The neural network model showed 100% accuracy in the classification of tolerance/intolerance lines.

Correlation studies

Under non-stressed normal irrigated condition, the associations among studied attributes were observed as exhibited in Figure 2. Plant height associated positively and highly significantly with number of tillers, spikelets per spike, flag leaf area, relative water content, chlorophyll content, grain yield per plant and thousand grain weight. A highly significant and positive relation was observed between number of tillers and spikelets per spike (0.4624**), flag leaf area (0.458**), relative water content (0.5377**), chlorophyll content (0.3927**), grain yield per plant (0.418**) and thousand grain weight (0.998**). The trait spikelets per spike revealed positively highly significant association with thousand grain weight (0.4644**) and significant relation with flag leaf area (0.3114*) while non-significantly associated with relative water content (0.2324ns) and chlorophyll content (0.1921ns). A negative and non-significant correlation displayed between spikelets per spike and grain yield per plant (-0.0289ns). Flag leaf area had positive and highly significant association with relative water content (0.7349**), chlorophyll content (0.6931**), grain yield per plant (0.5204**) and thousand grain weight (0.458**). The attribute relative water content mentioned highly significant and positive relation with chlorophyll content (0.65**), grain yield per plant (0.6464**) and thousand grain weight (0.5367**). Chlorophyll content associated positively and highly significantly with grain yield per plant (0.572**) and thousand grain weight (0.3918**). A positive and highly significant correlation revealed

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by grain yield per plant with thousand grain weight (0.4182**).

Under stressed water deficit condition, the associations among studied attributes were observed as exhibited in Figure 3. Plant height associated positively and highly significantly with number of tillers (1**), spikelets per spike (0.3649**), flag leaf area (0.4992**), relative water content (0.4989**), chlorophyll content (0.3738**), grain yield per plant (0.4725**) and thousand grain weight (1**). A highly significant and positive relation was observed between number of tillers and spikelets per spike (0.365**), flag leaf area (0.499**), relative water content (0.4999**), chlorophyll content (0.374**), grain yield per plant (0.473**) and thousand grain weight (0.996**). The trait spikelets per spike revealed positively highly significant association with flag leaf area (0.5486**), relative water content (0.3557**) and thousand grain weight (0.3649**) and significant relation with chlorophyll content (0.3328*). Flag leaf area had positive and highly significant association with relative water content (0.6934**), chlorophyll content (0.6099**), grain yield per plant (0.6448**) and thousand grain weight (0.4992**) as displayed in Figure 3. The attribute relative water content mentioned highly significant and positive relation with chlorophyll content (0.6882**), grain yield per plant (0.6446**) and thousand grain weight (0.4989**). Chlorophyll content associated positively and highly significantly with grain yield per plant (0.4488**) and thousand grain weight (0.3738**). A positive and highly significant correlation revealed by grain yield per plant with thousand grain weight (0.4725**).

Principal component analysis (PCA)

In current investigation, under both conditions, two PCs revealed significant values out of eight PCs. The eigenvalues accounted for first PC was (4.7144) and for second PC was (1.5268) under the normal condition while under water deficit drought condition there values were 4.8064 and 1.3662. According to Table 2, the first PC contributed 0.589% to this variance, whereas the second PC contributed around 0.191% in normal irrigated condition while in water deficit condition, the first PC contributed 0.601% to this variance, whereas the second PC contributed around 0.171%.Under normal environment, in PC1 the attribute plant height (4.12) was highly related followed by number of tillers (4.12), thousand grain weight (4.12), relative water content (0.368), flag leaf area (0.344), chlorophyll content (0.316), grain yield per plant (0.298) and spikelets per spike (0.22). PC2 showed that grain yield per plant (0.413) was highly related to flag leaf area (0.324), relative water content (0.316), chlorophyll contents (0.41), spikelets per spike (-0.388), thousand grain weight (-0.32), number of tillers (-0.32) and plant height (-0.32). Under drought environment, in PC1 the attribute plant height (0.399) was highly related followed by number of tillers (0.399), thousand grain weight (0.399), flag leaf area (0.363), relative water content (0.355), chlorophyll content (0.299), grain yield per plant (0.33) and spikelets per spike (0.258). PC2 showed that chlorophyll contents (0.395) was highly related to flag leaf area (0.341), relative water content (0.326), grain yield per plant

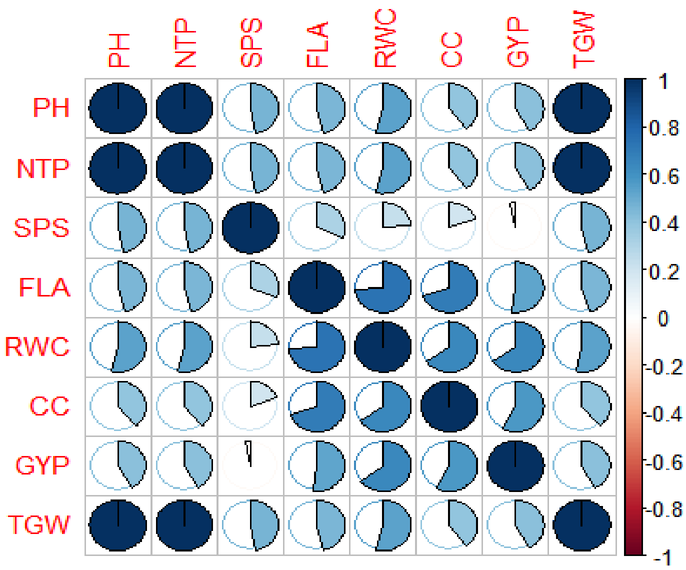

Figure 3: *Correlation among studied indices under water deficit condition*

(0.258), spikelets per spike (0.204), thousand grain weight (-0.414), number of tillers (-0.414) and plant height (-0.414). Additionally, Figures S1 and S2 displayed the projection of the important features in all conditions. PCA may be able to see patterns and correlations in the dataset. The projections of the genotypes were presented in Figure 4 and Figure 5. In these Figures, the diversity among genotypes was observed. Some of the genotypes had positive association with each other while some other genotypes exhibited negative association between them. With PCA, results from other statistical analyses can be enhanced and validated.

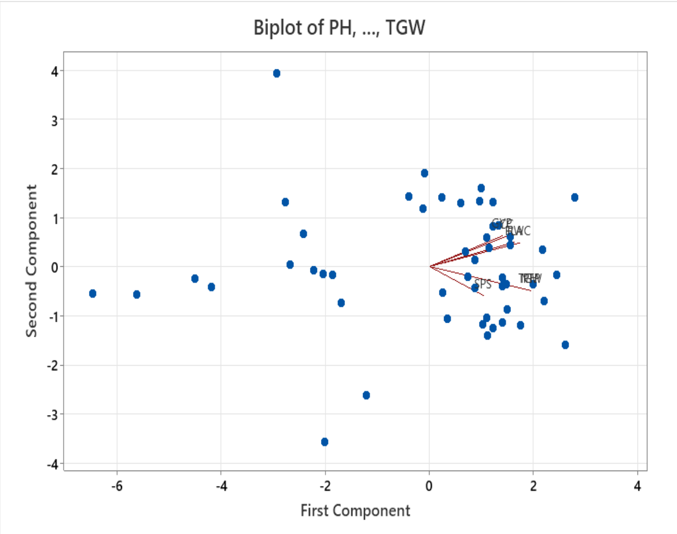

Figure 4: *Projection of genotypes on biplot under non-stressed condition*

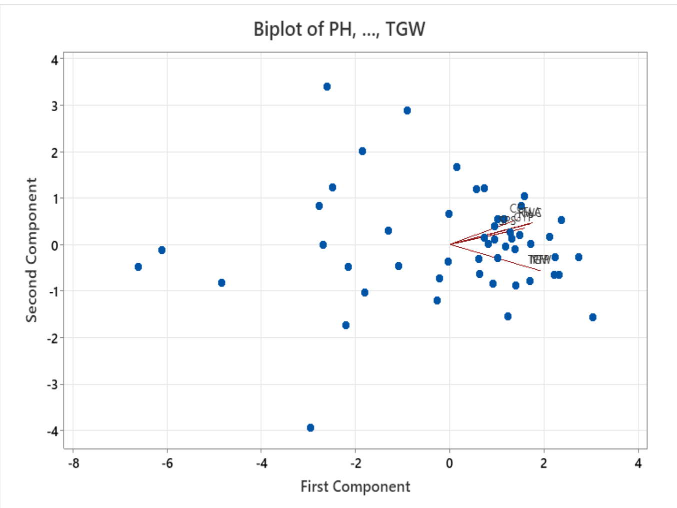

Figure 5: *Projection of genotypes on biplot under stressed condition*

Cluster heat map

A heat map is a type of data visualization where different values are shown by a color-coding scheme. In both conditions, each row presented the genotypes, likely from different populations as presented in Figure 6 and Figure 7. The columns displayed the traits studied in this research. The gradient in this heat map is yellow-to-red, with increasing intensity (from yellow to dark red) signifying an increase in the magnitude of the characteristic. Genotypes that exhibit similar phenotypic characteristics across the evaluated criteria and are closely grouped together in the row dendrogram demonstrate a degree of genetic or functional similarity. But the elements that cluster together in the column dendrogram, such as flag leaf area (FLA) and grain yield per plant (GYP), are most likely positively associated, indicating that increases in one characteristic could be related to improvements in the other. Genotypes with deep red coloration in the plant height (PH) or relative water content (RWC) columns are most likely higher or have better water retention abilities. Conversely, those who appear pale yellow in these columns usually have lower trait evaluations, indicating their performance was poorer in those regions. According to this map, the darker color represented the best performance of genotypes which means genotypes G8, G9, G14 and G12 were the best performer for chlorophyll content, relative water content, flag leaf area and grain yield potential while genotypes G23, G21, G43 and G49 were performed worst in normal condition. Under water deficit condition, the genotypes G12, G11, G13, G44, G41 and G20 showed maximum performance for chlorophyll content, relative water content, flag leaf area and grain yield potential while genotypes G39, G43, G30, G16 and G40 performed minimum.

Discussion

A totally randomized factorial design was used to screen 50 spring wheat genotypes in the field. For every parameter under study, there were very significant changes between accessions under normal and drought circumstances. Research on wheat has yielded comparable results, with scientists noting that water stress causes a considerable decrease in chlorophyll levels and leads to yellowing of leaves (Qadeer *et al*., 2023). The number of tillers produced by each plant is another important characteristic of wheat. Based on the climate, the quantity of tillers affects the grain yield of the crop (Rafay *et al*., 2014). It is important to clarify the two main components of grain number in wheat: the number of spikes per plant (influenced by crop density and the number of tillers per plant) and the number of grains per spike (determined by

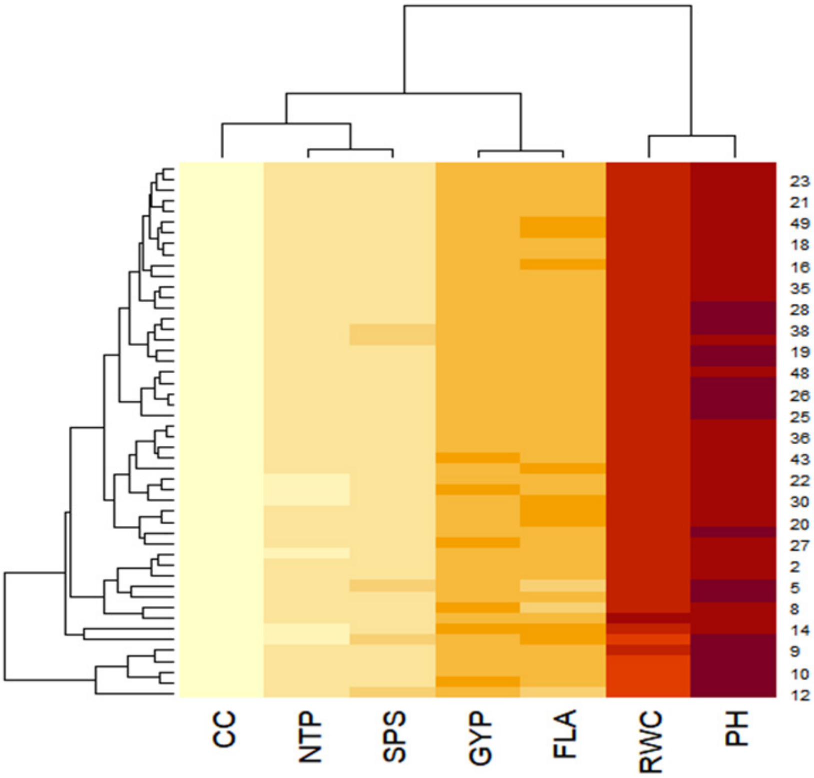

Figure 6: *Cluster heat map under normal irrigated condition*

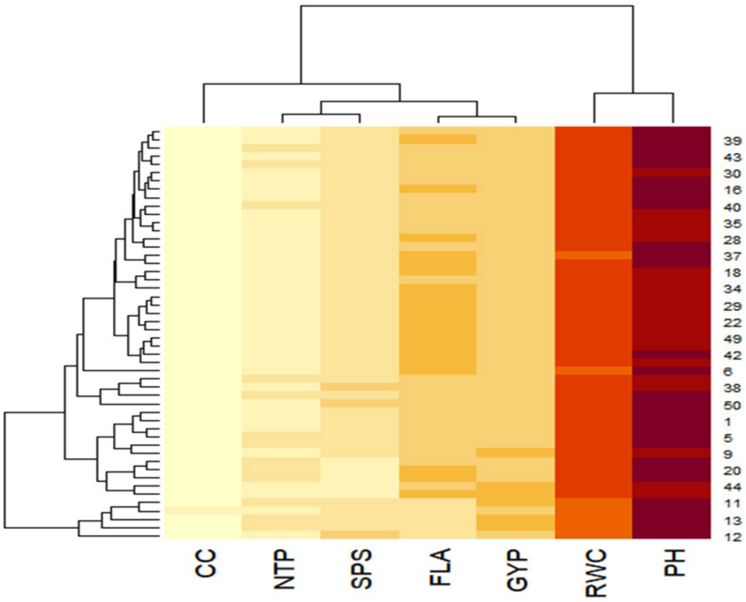

Figure 7: *Cluster heat map under water deficit condition*

floret fertility, grain set, and the number of spikelets per spike (Ahmed *et al*., 2023). According to (Mickky *et al*., 2020) comparable research has shown that while all cultivars experienced a decline in leaf succulence, stomatal opening area, shoot biomass, density, and dispersion due to the water-stressed environment, the extent of this decline varied. Evidence has previously connected higher RWC to drought tolerance in several wheat varieties, explaining that drought-tolerant types maintained higher water contents when water supply was limited (Wasaya *et al*., 2021). Photosynthesis is the primary mechanism in plant cells that regulates the low concentration of water culture medium. More efficient photosynthesis will result from higher chlorophyll levels. Research on wheat has produced comparable results, with scientists observing that water stress causes a considerable decrease in chlorophyll levels and leads to yellowing of leaves (Qadeer *et al*., 2023). Studies of historical yields have demonstrated that enhancements in grain production always coincide with increases in the amount of grains. As a result, it may be necessary to enhance the grain number further to boost future yield outputs. According to (Al Aboud *et al*., 2025), during the young microspore stage of pollen production, which is a specific phase of early reproductive development, cereals that self-fertilize are particularly susceptible to abiotic stress. The weight of 1000 grains has dropped as a result of the water deficit in bread wheat; nevertheless, there have also been reports of a considerable fall in 1000-grain weight in wheat. It is imperative that breeders focus on balancing these qualities through genetic exploitation (Stallmann *et al*., 2022).

Correlation analysis, which provides a mathematical framework for understanding how traits differ among wheat genotypes, is a crucial part of the research. Its use enhances the findings by offering valuable data that supports objectives, guides breeding strategies, and expands our knowledge of the genetic and phenotypic environment in field. Wheat breeding initiatives have a data-driven foundation for decision-making thanks to the links made by the study. By using this information to rank genotypes with desirable trait combinations, breeders can improve the efficacy of selection procedures (Siddiq and Vemireddy, 2021). Furthermore, (Rafay *et al*., 2014) found a positive correlation between the number of tillers per plant and various factors: plant height, productive grain weight per spike, number of grains per spike, spikelets per spike, and thousand grain weight. According to (Zahra *et al*., 2021; Ali *et al*., 2024), the number of tillers was negatively associated with the 1000 grain weight, but positively correlated with all other parameters in both normal and drought conditions. In conditions of drought stress, there was a highly significant correlation between the number of spikelets per spike and both plant height and spike length. Under normal conditions, grain yield showed a considerable positive correlation. The number of tillers and spikelets per spike also showed a positive relationship, while the 1000-grain weight demonstrated a negative correlation (Zahra *et al*., 2021). A positive and statistically significant genotypic correlation was found between the chlorophyll content and the area of the flag leaf (Javed *et al*., 2022). Due to the fact that greater RWC guarantees improved hydration of leaf tissues, encourages chlorophyll production, and preserves photosynthetic efficiency, a positive correlation is usually noted. The relationship, while currently robust, may diminish due to reduced water availability and chlorophyll degeneration caused by oxidative stress (Pour-Aboughadareh *et al*., 2021). It demonstrated a positive and significant correlation with the qualities under study in both stress and non-stress situations. Nonetheless, a favorable and statistically significant genotypic connection between the chlorophyll concentration and the grain yield was discovered (Ahmed *et al*., 2020).

PCA allows phenotypic variation to be separated into genetic and environmental components for the purpose of quantifying trait heritability (Xiao *et al*., 2018). By visually inspecting the genotype distribution in the reduced-dimensional space, researchers may confirm that the patterns they observe align with the natural structure of the data. The assessment of genetic diversity is strengthened by taking this step (Asif *et al*., 2018). PCA is a helpful technique for reducing the dimensionality of the dataset. Given that multiple qualities are being assessed across a broad spectrum of wheat genotypes, the original data set is most likely high-dimensional (Christina *et al*., 2021). PCA may be able to see patterns and correlations in the dataset. The PCA scores and loading show how different genotypes are positioned in relation to each other based on the evaluated features (Wang *et al*., 2022). PCA provides a graphic representation of the association between numerous factors and how they all contribute to the overall genetic diversity. This approach is helpful in determining the relationships between yield parameters and offers insights into the complex genetic architecture governing these agronomically important factors (Ahmad *et al*., 2023).

Clustered heat maps, which combine the two primary techniques of heat mapping and hierarchical clustering, are powerful visualization tools that draw attention to connections and patterns in complex datasets that may not be readily apparent through other forms of analysis. In his study, (Ahmad *et al*., 2022) described how various genotypes of wheat (*Triticum aestivum* L.) responded to drought circumstances in terms of yield and yield-related parameters. The resistant genotypes under drought are shown by a darker hue and a positive region on the heat map in relation to the color scale. Darker regions on the negative spectrum represent genotypes that are vulnerable to drought. The heat map provided further visual representation of the genetic grouping. 100% accuracy of AI model endorsed the finding of Imran *et al*. (2024) who got same accuracy during classification problem.

Conclusions and Recommendations

Fifty wheat (*Triticum aestivum* L.) genotypes were evaluated in the field based on their morphological and physiological characteristics. The analysis of variance mentioned significant variation among the studied genotypes. Reduction percentage was calculated among the genotypes to evaluate the performances of genotypes. The genotypes G8, G22 and G43 performed best in both normal and water deficit condition while genotypes G28, G13 and G38 had lowest performances in both conditions. Pearson's Correlation exhibited that all the studied indices had significant association with each other in both environments except relative water content, chlorophyll content and grain yield per plant in normal condition which showed non-significant relation with spikelets per spike. Principal component analysis revealed that on two PCs were significant out of eight. In normal condition, the cumulative variation showed by these PCs were 78.0% and in water deficit condition, the cumulative variation was 77.2% showed by significant PCs. Cluster heat map displayed different values by a color coding scheme. The gradient in this heat map was yellow-to-red, with increasing intensity (from yellow to dark red) signifying an increase in the magnitude of the characteristic. 100% accuracy of neural network makes it a reliable tool for screening of germplasm. Future wheat breeding programs will benefit from the best performing genotypes under drought stress and selection based on researched characteristics will be effective for creating high-yielding, drought-tolerant cultivars for sustained food security.

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Novelty Statement

Current investigation provides a novel technique to identify the drought tolerant genotypes of bread wheat with precision through integrating AI tools and morphophysiological traits.

Author's Contribution

Ali Saeed Alkhalifa: Writing manuscript draft and perform statistical analysis
Mueen Alam Khan: Designed the experiment and supervision
Sajjad Hussain Qureshi: Perform AI based work and execution of field study
Adel A. Rezk: Reviewed the final draft

Generative AI and AI-assisted technology statement
The authors declare that no generative AI and AI assisted technology was used in the creation of this manuscript.

Conflicts of interest
All co-authors declare no conflicts of interest.

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