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Appraising Drought Tolerance in Barley Genotypes for Advancing Sustainable Food Security Using PCA Analysis

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ABSTRACT

Barley is a globally important crop due to its nutritional value and socioeconomic significance, serving as a primary source of food and feed in diverse environments. This study assessed 50 barley cultivars under contrasting environmental conditions, normal (non-stressed) and drought (stressed), using a randomized complete block design (RCBD) with three replications. Analysis of variance (ANOVA) revealed significant differences among the genotypes for all examined traits under both conditions, highlighting substantial genetic variation. Genotypes G12, G8, G23, G20, and G16 demonstrated superior performance across both environments, while G35, G37, G47, G48, and G42 were identified as drought susceptible. Correlation analysis under non-stressed conditions indicated a significant positive relationship between grain yield per plant and other studied traits. Principal component analysis (PCA) identified four significant components under both conditions, accounting for a cumulative variance of 78.7% (normal) and 74.5% (drought) in PC1. Subsequent components explained 14.6%, 12.2%, and 10.1% of variance under normal conditions, while drought conditions resulted in 16.7%, 11.6%, and 11.1% in PC2, PC3, and PC4, respectively. These findings offer critical insights for breeding programs aimed at developing drought-resilient barley cultivars. The identified genotypes with superior traits can serve as foundational material for enhancing barley productivity under water-limited conditions. This study contributes to the broader efforts of ensuring sustainable food security through genetic improvement and targeted cultivation strategies.

Keywords: drought, grains, flavonoids, association, barley.

INTRODUCTION

Barley (*Hordeum vulgare* L.) is a globally significant cereal crop with diverse applications in food, feed, and industry. As one of the earliest domesticated grains, it has played a fundamental role in human civilization for over 10,000 years (Kebede et al., 2019; Victoria et al., 2023). Barley is widely cultivated due to its adaptability to a range of agro-climatic conditions, including arid and semi-arid regions where other cereals struggle to thrive. Its short growing season, efficient nutrient utilization, and tolerance to abiotic stresses make it a vital crop for ensuring agricultural sustainability. Additionally, barley is rich in bioactive compounds such as β-glucans, phenolics, and antioxidants, which contribute to its nutritional and health benefits (Jouyban et al., 2015; Ghavidel et al., 2024). The crop's versatility, coupled with its genetic diversity, provides opportunities for breeding improved cultivars tailored to specific environmental challenges. Given its economic and ecological significance, barley continues to be a key

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component of global food and feed systems, supporting both rural livelihoods and industrial applications (Khan et al., 2021; Slawin et al., 2024).

Drought is one of the major environmental factors that seriously challenge barley production and gains momentum with the increase in frequency and severity due to climate change. In areas where water availability is erratic, diversity in drought tolerance will determine the sustainability of yields in barley genotypes. Physiological responses of barley to water stress could be very critical to its growth, development, and yield (Kadege et al., 2024; Saeed et al., 2025). Such responses are necessary for developing genotypes that can give high and stable yield under normal conditions as well as under limiting conditions of water. The occurrence and severity of drought are predicted to increase in coming years as a result of the current climate change which will have significant impact on the patterns of precipitation and temperature (Abdelghany et al., 2024). Most significant abiotic stress factor which is causing agricultural yield reductions is drought, hence high-yielding crops are important even in ecologically stressed situations. The situation is not new as the demand is increasing annually due to increase in the population pressure, similar situation was also faced by the world which was mitigated by genetically modified high grain yielding barley crop (Abdelrady et al., 2024).

Tolerance for the drought is intricate with environmental interactions. The evaluation of response in drought environment by plant, its mode and time of response is directly related to the extremity of the cell dehydration during the stress period and the significance of its interaction with both abiotic and biotic stress factors (Alsamadany et al., 2024; Teoh, 2024). The breeding for the drought resistant varieties is a complicated process as many other environmental factors are also involved and compete with the crop plants altogether. The factors like extreme temperature, light intensity, shortage of water and deficiency of nutrients generally effects the normal growing condition but cannot be manageable through conventional farm procedures. Some soil may exhibit certain properties which can also affect the balance of different environmental factors which can be composition and structure (Ashraf et al., 2022). The duration and impact of the water scarcity can determine the loss of yield and flavonoids by decreasing the life cycle and time needed for proper grain filling (Boudiar et al., 2020; Afzal et al., 2024). The rate of transpiration is significantly decreased when plants face water shortage, due to closure of stomata the heat is trapped and leaves temperature is increased, it leads to the disruption of the physiological processes happening in the plant (Elakhdar et al., 2023).

Under normal water conditions, barley plants tend to exhibit peak growth characterized by a well-developed root system, good foliage, and high rates of photosynthesis. All these in turn contribute to increased grain filling and yield. However, poor water conditions impair physiological events. The rate of water supply affects stomatal conductance. The lower water supply reduces transpiration and hence photosynthesis. Such a water deficit can involve a cascading stress response associated with osmotic adjustment and the production of protective metabolites, enabling these plants to continue cellular functions in conditions of drought stress (Kadege et al., 2024; Saeed et al., 2025). Drought tolerance has often been recorded in those genotypes having deep root systems, helping them absorb moisture from the lower layers of soil. Such genetic adaptations become very important in arid regions where the surface soil moisture may be dissipated rather fast. The morphological traits can include leaf rolling and a reduced leaf area, aiding in reducing water loss through transpiration, hence increasing the capability of plants to survive under prolonged dry conditions. The genetic basis of these traits is complex and multigenic; thus, the selection of genotypes bearing favorable attributes for water-limited environments becomes very crucial in breeding programs. The attributes that influence the grain yield of the barley cultivars are number of panicles, grain weight and biological yield (Baloch et al., 2024; Fatemi et al., 2023).

Considering the limitations posed by climate change and water scarcity, it will be important to improve biomass production and economic yield. Considerable evidence is available that evaluation for drought tolerance needs to be conducted in both normal and stressed environments. Growth chambers and field trials under controlled environment facilitate testing comprehensive performance of genotypes against different levels of water application (Ferioun et al., 2023; Ghazy et al., 2024). Applications such as phenotyping allow precise capture of the physiological and morphological responses of barley to water stress and thereby enable the identification of superior genotypes under less-than-optimum conditions. Beyond yield itself, the impacts of developing drought-tolerant barley varieties stretch into stability in food production systems, ensuring farmers can continue to produce food in the case of bad weather. This kind of stability is vitally important in areas that depend on barley as a primary form of nutrition; crop failures can have wide-ranging results in terms of food insecurity and general economic stability (Irshad et al., 2024; Hebbache et al., 2024).

Drought tolerance assessment in barley genotypes is important for attaining sustainable food security and successful breeding programs. The insight obtained into the physiological and morphological responses of barley under normal and less watered conditions can hence enable the formulation of innovative solutions to answer some of the most current challenges to agricultural productivity in the changing climate. While it is a fact that this drought resilience focus will act as an influencer in improving crop yield, it also consolidates stability and sustainability in food production worldwide (Ijaz et al., 2023). The major aim for the current study is to improve and develop barley cultivars under the drought stress and to increase the yield potential of the barley. The 50 studied genotypes were selected to evaluate with Pearson's correlation and PCA (principal component analysis) under the stressed and non-stressed conditions.

MATERIAL AND METHODS

The present study was taking place in the arid region of the Punjab, specifically at the field of the Department of Plant Breeding and Genetics, The Islamia University of Bahawalpur, Pakistan. Randomized Complete Block design (RCBD) was applied to 50 barley genotypes and were evaluated in three replications under non-stressed (normal) irrigated and stressed (less water) drought environmental condition during the cropping year 2022-2023. Two seeds were sown and later thinning was done to evaluate a single plant. The row-to-row distance was 12 inches. The normal field was irrigated 5 times until the maturity while the drought stresses plot was watered only once at the flowering stage (Anthesis) and no rainfall was reported during growing season. Rate at which the fertilizer was applied was 150:100:50 kilograms N:P:K per hectare which was enough to achieve maximum crop potential. The attributes which were recorded were Plant Height (PH), Flag Leaf Area (FLA), Tillers per Plant (TP), Peduncle Length (PL), Days to Heading (DH), Days to Maturity (DM), Spike Length (SL), Spikelet per Spike (SS), Number of Grains per Spike (NGS), 1000-Grain Weight (TGW), Grain Yield per Plant (GYP), Biological Yield per Plant (BYP) Harvest Index (HI). Analysis of variance and Pearson's correlation was calculated from the collected data using the software statistic 8.1. The correlation cluster map was developed using R-studio and Principal component analysis using XLstat.

RESULTS AND DISCUSSION

The ANOVA (Analysis of Variance) presented in Table 1 indicated a significant difference between treatments and genotypes. The table also represented the significant interaction among the studied genotypes and the treatment, highlighting the influence of environmental conditions on barley performance. The strong genotype-by-treatment interaction suggests that certain genotypes may adapt better under normal and water-deficit conditions. Plant height measurements showed that under normal conditions, the genotypes G23, G20, G12, G8, and G40 had the highest average height of 101.48 cm, whereas G37, G47, G35, G48, and G42 exhibited the lowest, with an average height of 89.48 cm. Under drought conditions, the best-performing genotypes maintained an average height of 90.55 cm, while the poorest-performing genotypes dropped to 78.55 cm (Table 2).

For flag leaf area (FLA), G23, G20, G12, G8, and G40 had the highest average values of 34.48 cm² under normal conditions, while G47, G42, G35, G48, and G37 had the lowest at 22.48 cm². Under drought stress, the highest-performing genotypes retained a mean FLA of 28.43 cm², while the poorest-performing genotypes declined to 16.43 cm² (Table 2). In terms of tiller number per plant, the best-performing genotypes under normal conditions were G23, G20, G12, G8, and G38, averaging 11.07 tillers per plant, whereas the lowest-performing genotypes had an average of 5.07. Under drought stress, G12 retained the highest tiller count of 10.48, while G27 had the lowest at 4.48 (Table 2). Peduncle length assessments showed that under normal conditions, G23, G20, G12, G8, and G40 had the longest lengths (25.44 cm), while G37, G47, G35, G48, and G42 had the shortest (13.44 cm). Under drought stress, G23 and G20 maintained the longest peduncles (20.91 cm), while G37 recorded the shortest at 8.91 cm (Table 2).

Days to heading (DH) varied across genotypes. Under normal conditions, G37 exhibited the earliest heading (65.51 days), while G33 was the latest (57.67 days). Under drought, G48 and G42 had the earliest heading at 58.3 days (Table 2). Similarly, maturity time under normal conditions was shortest for G48 (107.99 days) and longest for G33 (99.99 days). Under drought, G48 maintained an average maturity time of 98.01 days, while G33 reduced to 90.01 days (Table 2). For spike length, G23, G20, and G16 had the longest spikes (18.12 cm) under normal conditions, while G37 had the shortest (6.12 cm). Under drought, G20 retained a spike length of 14.83 cm, while G47 had the shortest at 2.83 cm (Table 2). Spikelet per spike (SPS) measurements showed G23 and G20 with the highest counts (25.13), while G35 had the lowest (15.13). Under drought stress, G16 dropped to 18.94 spikelets, and G35 declined to 8.94 (Table 2).

Grain number per spike (NGPS) showed that G16 had the highest count (64.87) under normal conditions, while under drought, the highest was 46.54 for G23. In contrast, G35 exhibited the lowest NGPS under both conditions (Table 2). Thousand-grain weight (TGW) was highest for G23 under normal conditions (58.29 g), while under drought, G20 decreased to 42.34 g. Grain yield per plant (GYP) showed G12 as the highest performer under normal conditions (31.4 g), whereas G20 declined to 17.78 g under drought stress (Table 2). For biological yield, G20 had the highest under normal conditions (66.42 g), while G35 had the lowest (60.42 g). Under drought, G35 and G37 exhibited significant reductions, approximately 49 g (Table 2). The harvest index (HI) was highest for G50 under normal conditions (48.75%), whereas G7 had the lowest (39.07%). Under drought, the lowest HI was recorded for G6 at 32.26% (Table 2).

Correlation analysis

Pearson’s correlation analysis revealed significant associations among various studied attributes under both normal and drought-stressed conditions. The flag leaf area (FLA) and plant height (PH) displayed a highly significant positive correlation with traits such as tillers per plant (TP), peduncle length (PL), biological yield per plant (BYP), spike length (SL), spikelets per spike (SPS), number of grains per spike (NGS), thousand-grain weight (1000-GW), and grain yield per plant (GYP) (Figures 1 and 2). Similarly, tillers per plant showed a strong, statistically significant positive association with PL, BYP, SL, SPS, NGS, 1000-GW, and GYP under both conditions. Peduncle length correlated positively and significantly with BYP, SL, SPS, and NGS in both environments, while its association with 1000-GW was highly significant only under normal conditions.

Biological yield per plant exhibited a highly significant positive correlation with SL, SPS, NGS, and GYP under both conditions. A significant association was observed between BYP and 1000-GW under drought stress, whereas under normal conditions, this association was highly significant. Days to maturity and days to heading correlated positively and significantly with each other but had a highly significant negative correlation with traits such as SL, SPS, NGS, and 1000-GW. Spike length exhibited a highly significant positive correlation with SPS, NGS, 1000-GW, and GYP under both conditions, while the harvest index (HI) showed a significant association with spike length under normal conditions but not under drought stress.

Spikelets per spike showed a highly significant positive association with NGS, 1000-GW, and GYP under both conditions, and also exhibited a positive correlation with SL. NGS showed a highly significant positive association with 1000-GW and GYP. Under normal conditions, 1000-GW had a highly significant positive association with HI but a negative correlation with GYP. Under drought conditions, 1000-GW correlated significantly and positively with GYP, while HI had a non-significant positive association with 1000-GW. GYP showed a non-significant but positive correlation with HI under normal conditions, while a highly significant positive correlation was observed under drought stress (0.69**). Traits such as FLA, TP, PH, PL, SL, BYP, SPS, NGS, and 1000-GW showed a negative correlation with HI under normal conditions, while under drought stress, HI had a positive but non-significant association with these traits.

Principal Component Analysis (PCA)

Principal Component Analysis (PCA) was employed to explain the variability and interrelationships among barley attributes under normal and drought environments. The analysis was conducted on 50 barley genotypes, identifying significant variations in only four attributes under both conditions, as shown in Table 3. Under normal conditions, PC1 explained 78.7% of the variance, followed by PC2 (14.6%), PC3 (12.2%), and PC4 (10.1%). In drought conditions, PC1 accounted for 74.5%, PC2 for 16.7%, PC3 for 11.6%, and PC4 for 11.1%, as depicted in Table 3. PCA has been widely used in breeding programs for selecting parental genotypes (Khodadadi et al. 2011).

Under normal conditions, PC1 was highly correlated with plant height (0.32), peduncle length (0.32), and spike length (0.32), while it negatively correlated with days to heading (-0.24), days to maturity (-0.24), and harvest index (-0.12). PC2 showed strong positive correlations with the number of grains per spike (0.31) and spikelets per spike (0.21), but it negatively correlated with plant height (-0.12), flag leaf area (-0.06), peduncle length (-0.25), tillers per plant (-0.38), and biological yield per plant (-0.33), as outlined in Table 4.

Under drought conditions, PC1 displayed strong associations with plant height (0.32), flag leaf area (0.31), spike length (0.30), and spikelets per spike (0.30) while negatively correlating with days to heading (-0.24) and days to maturity (-0.24). PC2 had positive correlations with spikelets per spike (0.26), thousand grain weight (0.26), and number of grains per spike (0.20) but negatively correlated with spike length (-0.03), flag leaf area (-0.05), days to heading and maturity (-0.41), and peduncle length (-0.15), as shown in Table 4. The projection of attributes onto PC1 and PC2 under non-stressed conditions indicated that plant height, flag leaf area, peduncle length, spike length, biological yield per plant, and tillers per plant were positively associated, whereas days to heading and maturity showed negative correlations with most yield traits (Figure 3). Under drought stress, traits such as thousand grain weight, spikelets per spike, and number of grains per spike exhibited a strong positive association among themselves but negatively correlated with other yield-related traits

(Figure 4). Under normal conditions, genotypes G12, G33, and G45 were distinct from G48, G35, G47, G42, and G37. Similarly, G20, G23, G8, G6, and G10 contrasted with G39, G43, G41, and G29 (Figure 5). In drought conditions, genotypes G23, G12, and G45 were distinct from G48, G42, G47, G37, and G35, while G43 and G39 opposed G20, G8, and G10, highlighting the clear distinction between drought-tolerant and susceptible genotypes (Figure 6).

Table 1. Analysis of variance for studied attributes under normal and drought conditions of 50 barley genotypes

SOV	Replication	Genotypes	Treatment	Genotypes*Treatment	Error	Total
DF	2	49	1	49	198	299
PH	0.01	12.98**	6709.79**	19.5**	0.08	
FLA	0.002	4.409**	864.13**	2.62**	0.004	
TPP	0.00457	0.118**	0.7834**	0.1653**	0.00265	
PL	0.0111	0.355**	96.141**	0.4403**	0.0062	
DTH	0.073	2.43**	875.86**	2.098**	0.022	
DTM	0.00143	5.770**	2122.57**	4.6351**	0.0112	
SL	18.5	69.7**	20003.4**	78.4**	18	
SPS	0.03	7.52**	1012.37**	5.77**	0.01	
NGS	0.81	9.62**	3310.71**	11.95**	0.6	
TGW	0.058	0.425**	240.263**	0.473**	0.091	
GYP	0.0028	0.343**	94.7532**	0.4332**	0.0035	
BYP	0.02418	73.35**	29024.3**	53.7684**	0.01477	
HI	0.052	0.26**	248.084**	0.218**	0.008	

*SOV (source of variance), DF (degree of freedom), ** (highly significant), Plant Height (PH), Flag Leaf Area (FLA), Tillers per Plant (TP), Peduncle Length (PL), Days to Heading (DH), Days to Maturity (DM), Spike Length (SL), Spikelet per Spike (SS), Number of Grains per Spike (NGS), 1000-Grain Weight (TGW), Grain Yield per Plant (GYP), Biological Yield per Plant (BYP) Harvest Index (HI).*

Table 2. Best and Worst performer genotypes under normal and drought conditions in 50 barley genotypes using 13 yield and yield related traits

Traits	Best performer genotypes		Worst performer genotypes	
	Normal	Drought	Normal	Drought
PH	G23 (101.48), G20 (101.48), G12 (101.48), G8 (100.48), G40 (98.48)	G23 (90.55), G12 (90.55), G8 (90.55), G20 (89.55), G40 (87.55)	G37 (89.48), G47 (89.98), G35 (90.48), G48 (90.48), G42 (91.48),	G37 (78.55), G42 (79.05), G35 (79.55), G48 (79.55), G47 (80.55)
FLA	G23 (34.48), G20 (34.48), G12 (34.48), G8 (33.48), G40 (31.48)	G20 (28.43), G12 (28.43), G8 (28.43), G23 (27.43), G40 (25.43)	G47 (22.48), G42 (22.98), G35 (23.48), G48 (23.48), G37 (24.48)	G37 (16.43), G42 (16.93), G35 (17.43), G48 (17.43), G47 (18.43)
TPP	G23 (11.07), G20 (11.07), G12 (11.07), G8 (11.07), G38 (11.07)	G12 (10.48), G8 (10.48), G20 (10.48), G23 (10.48), G38 (10.48)	G27 (5.07), G29 (5.07), G39 (5.07), G2 (6.07), G3 (6.07)	G27 (4.48), G29 (4.48), G39 (4.48), G2 (5.48), G3 (5.48)
PL	G23 (25.44), G20 (25.44), G12 (25.44), G8 (24.44), G40 (22.44)	G23 (20.91), G20 (20.91), G12 (20.91), G8 (19.91), G40 (17.91)	G37 (13.44), G47 (13.94), G35 (14.44), G48 (14.44), G42 (15.44)	G37 (8.91), G47 (9.41), G35 (9.91), G48 (9.91), G42 (10.91)
DH	G37 (65.51), G48 (64.67), G42 (64.51), G35 (63.84), G47 (63.67)	G48 (58.3), G42 (58.3), G35 (58.3), G47 (57.3), G37 (57.3)	G33 (57.67), G32 (58.34), G31 (58.51), G45 (58.51), G19 (58.67)	G33 (50.3), G1 (51.3), G19 (51.3), G31 (51.3), G32 (51.3)
DM	G48 (107.99), G47 (107.99), G37 (107.99), G42 (106.99), G35 (106.99)	G47 (98.01), G42 (98.01), G37 (98.01), G48 (97.01), G35 (97.01)	G33 (99.99), G1 (100.99), G19 (100.99), G31 (100.99), G32 (100.99)	G33 (90.01), G1 (91.01), G19 (91.01), G31 (91.01), G32 (91.01)
SL	G23 (18.12), G20 (18.12), G16 (18.12), G8 (17.12), G40 (15.12)	G20 (14.83), G12 (14.83), G8 (14.83), G23 (13.83), G40 (11.83)	G37 (6.12), G42 (6.62), G35 (7.12), G48 (7.12), G47 (8.12)	G47 (2.83), G42 (3.33), G35 (3.83), G48 (3.83), G37 (4.83)
SPS	G23 (25.13), G20 (25.13), G12 (25.13), G16 (23.13), G8 (23.13)	G16 (18.94), G12 (18.94), G8 (18.94), G23 (16.94), G20 (16.94)	G35 (15.13), G42 (15.13), G47 (15.13), G48 (15.13), G37 (17.13)	G35 (8.94), G42 (8.94), G47 (8.94), G48 (8.94), G37 (10.94)

Traits	Best performer genotypes		Worst performer genotypes	
	Normal	Drought		Normal
NGPS	G16 (64.87), G12 (64.87), G8 (64.87), G23 (59.72), G20 (59.72)	G23 (46.54), G12 (46.54), G8 (46.54), G20 (41.59), G16 (41.59)	G35 (39.12), G42 (39.12), G47 (39.12), G48 (39.12), G37 (44.27)	G35 (21.78), G37 (21.78), G42 (21.78), G48 (21.78), G47 (26.74)
TGW	G23 (58.29), G12 (58.29), G8 (58.29), G20 (53.14), G16 (53.14)	G20 (42.34), G12 (42.34), G8 (42.34), G23 (37.39), G16 (37.39)	G35 (32.53), G42 (32.53), G47 (32.53), G48 (32.53), G37 (37.68)	G35 (17.58), G37 (17.58), G42 (17.58), G48 (17.58), G47 (22.53)
GYP	G12 (31.4), G8 (31.4), G23 (30.91), G20 (30.91), G16 (30.42)	G20 (17.78), G8 (17.51), G16 (17.51), G12 (17.51), G6 (17.46)	G35 (24.67), G37 (24.78), G47 (24.8), G48 (24.8), G42 (25.07)	G37 (14.76), G42 (14.76), G35 (14.76), G48 (14.76), G27 (14.98)
BYP	G20 (66.42), G16 (66.42), G8 (66.42), G12 (66.42), G23 (66.42)	G20 (55.12), G16 (55.12), G12 (55.12), G8 (55.12), G38 (55.12)	G35 (60.42), G37 (60.42), G42 (60.42), G47 (61.42), G48 (61.42)	G35 (49.12), G37 (49.12), G42 (49.12), G47 (50.12), G48 (50.12)
HI	G50 (48.75), G46 (48.75), G49 (48.74), G45 (48.74), G44 (48.74)	G6 (32.26), G8 (32.25), G5 (32.25), G7 (32.22), G4 (32.22)	G7 (39.07), G9 (39.07), G11 (39.07), G10 (39.07), G23 (39.07)	G35 (29.44), G42 (29.44), G43 (29.44), G47 (29.44), G44 (29.45)

The significant variation in ANOVA results underscores the importance of genotype selection for stress tolerance. The strong genotype-by-treatment interaction suggests differential adaptability among genotypes, with some demonstrating greater stability under drought stress (Mwadzingeni et al., 2016; Kadege et al., 2024). Plant height stability under drought stress indicates that taller genotypes may have a competitive advantage in light capture and photosynthesis, contributing to better overall yield. This reinforces the importance of selecting genotypes with consistent height for drought tolerance breeding (Kadege et al., 2024; Saeed et al., 2025). Flag leaf area (FLA) is crucial for photosynthesis, and its decline under drought stress highlights the susceptibility of certain genotypes. The better adaptability of genotypes with higher FLA suggests that this trait should be prioritized in breeding programs for drought resilience (Khan et al., 2021; Slawin et al., 2024). The ability to maintain tiller production under drought stress is critical for yield stability. Genotypes with higher tiller counts under stress exhibited better adaptability, confirming that tiller retention is an essential trait for drought tolerance (Mariey et al., 2022; Manju et al., 2023). Longer peduncles are beneficial for structural integrity and grain filling, particularly under drought conditions. The observed reduction in peduncle length among drought-sensitive genotypes suggests that this trait plays a role in maintaining yield stability under stress (Hejazi and Panahi, 2025).

The early heading trait is advantageous for avoiding terminal drought stress, making it a valuable characteristic for drought-prone environments. The observed variation in heading and maturity times suggests that breeding efforts should focus on genotypes that combine early maturity with high yield potential (Hejazi and Panahi, 2025; Saidi et al., 2024). Spike length and spikelet retention under drought conditions are critical for maintaining grain production. The reduction in spikelet count under stress reinforces the need to select genotypes capable of maintaining high SPS under drought conditions (Slawin et al., 2024). The decline in NGPS and TGW under drought conditions underscores the negative impact of water stress on grain production. Selecting genotypes that maintain high NGPS and TGW is crucial for enhancing drought resilience in barley (Thabet et al., 2022; Song et al., 2024). Yield components such as GYP, biological yield, and HI are vital for overall productivity. The observed reductions in these traits under drought conditions highlight the susceptibility of certain genotypes, emphasizing the need for targeted breeding strategies to improve yield stability (Thabet et al., 2022; Visioni et al., 2023; Song et al., 2024). In this study, genotypes G12, G8, G23, G20, and G16 demonstrated superior drought tolerance across multiple traits, making them suitable candidates for breeding programs. In contrast, G35, G37, G47, G48, and G42 were highly susceptible to drought, indicating their limited suitability for water-deficit environments. These findings provide valuable insights for developing resilient barley varieties to mitigate climate change impacts (Mwadzingeni et al., 2016; Kadege et al., 2024).

Correlation Analysis

The correlation analysis provides insights into the relationships among yield-contributing traits in barley genotypes under different environmental conditions. The significant positive correlations between FLA and key yield attributes confirm its role in improving plant performance, especially under drought stress. Previous studies have reported similar findings, indicating that increased FLA enhances photosynthesis and contributes to better yield outcomes (Visioni et al., 2023; Hebbache et al., 2024). The observed reduction in PH due to drought stress aligns with existing literature, which attributes this decline to reduced water availability affecting nutrient uptake and photosynthetic efficiency (Hasanuzzaman et al., 2019; Hebbache et al., 2024).

Tillers per plant emerged as a crucial trait, positively associated with multiple yield attributes under both conditions. The reduction in tiller count under drought conditions suggests that water stress negatively affects tiller retention, ultimately impacting yield (Afzal et al., 2024; Slawin et al., 2024). However, maintaining tillering capacity under stress conditions could be a beneficial strategy for sustaining yield performance. Peduncle length also demonstrated a positive correlation with key yield components, reinforcing its role in supporting grain development, particularly under normal conditions (Baloch et al., 2024).

Biological yield per plant exhibited a strong association with SL, SPS, NGS, and GYP, highlighting its fundamental role in determining yield potential. The differential association of BYP with 1000-GW under drought and normal conditions suggests that grain-filling dynamics vary with water availability. The negative correlation between days to maturity and heading with other yield traits suggests a potential trade-off between earliness and yield-related attributes, which may be useful in breeding programs targeting optimal phenological adaptation (Kumar et al., 2022; Ghazy et al., 2024). The positive correlation of spike length with yield attributes emphasizes its significance in determining productivity. Previous studies have similarly reported strong associations between SL and GYP, particularly under water-deficit conditions (Nasri et al., 2014). The observed relationships suggest that selection for longer spikes could enhance grain yield in barley breeding programs. Likewise, the significant associations of SPS, NGS, and 1000-GW with yield components confirm their importance in improving productivity (Irshad et al., 2024; Saidi et al., 2024).

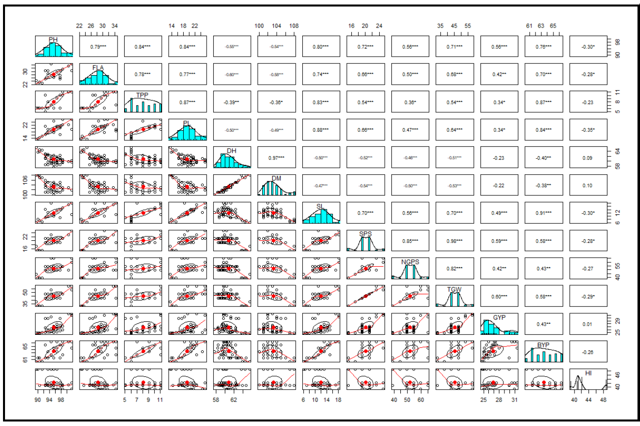
Overall, the findings highlight critical trait associations that can be exploited in barley breeding programs for climate resilience. The positive correlations of SL, SPS, and NGS with GYP underscore their predictive value in yield improvement strategies. The negative trade-offs observed with days to heading and maturity indicate potential breeding targets for optimizing phenology and yield performance. These results advocate for an integrated breeding approach that considers interrelated traits to enhance barley adaptation and productivity in diverse environmental conditions (Mwadzingeni et al., 2016; Kadege et al., 2024)

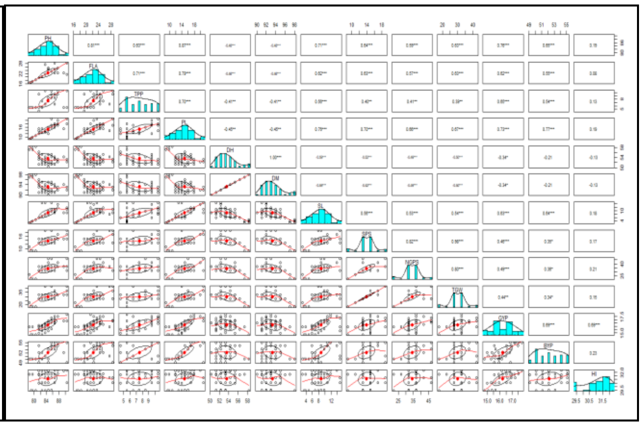
Principal Component Analysis (PCA)

Principal Component Analysis provided insight into the variability and interrelationships among barley attributes under normal and drought conditions. The identification of only four significant traits with eigenvalues greater than one suggests that these are critical for discriminating genotypes, particularly in relation to drought tolerance (Mwadzingeni et al., 2016; Baloch et al., 2024; Kadege et al., 2024). Traits with eigenvalues greater than one were considered significant, while those below this threshold were considered non-significant (Kaiser, 1960; Kumar et al., 2022; Klaus et al., 2024).

The first principal component, explaining the highest variation, was associated with plant height, flag leaf area, and spike length, which positively correlated with yield attributes but negatively with days to heading and maturity. This implies that growth-enhancing traits may delay maturity, which could influence yield advantage under drought stress. Negative associations in the second and subsequent components indicate a trade-off between key yield components such as grain number per spike and biological yield under water stress. The ability of PCA to separate drought-tolerant and susceptible genotypes highlights its value in breeding programs. It allows breeders to select parental lines that maximize yield potential while enhancing drought resistance (Ashraf et al., 2022; Song et al., 2024).

The results emphasize the importance of plant height, flag leaf area, and spike length in selecting drought-resilient genotypes. Additionally, the genetic divergence observed among genotypes under normal and drought conditions suggests that targeted breeding strategies can improve seed yield in barley under water-limited environments. This study reinforces previous findings that breeding programs should focus on integrating these key traits to develop cultivars capable of sustaining productivity under varying environmental conditions, thereby contributing to food security (Leilah and Al-Khateeb, 2005; Ahsan et al., 2024; Kadege et al., 2024).





Plant Height (PH), Flag Leaf Area (FLA), Tillers per Plant (TP), Peduncle Length (PL), Days to Heading (DH), Days to Maturity (DM), Spike Length (SL), Spikelet per Spike (SS), Number of Grains per Spike (NGS), 1000-Grain Weight (TGW), Grain Yield per Plant (GYP), Biological Yield per Plant (BYP) Harvest Index (HI).

Figure 1. Correlation cluster map of 13 yield and yield related traits under normal conditions

Figure 2. Correlation cluster map of 13 yield and yield related traits under drought conditions

Table 3. Eigen analysis of 13 yield and yield related indices under irrigated and stressed conditions

Env.	Eigenvalue		Proportion		Cumulative	
	Normal	Drought	Normal	Drought	Normal	Drought
PC1	7.87	7.45	0.61	0.57	0.61	0.57
PC2	1.46	1.67	0.11	0.13	0.72	0.70
PC3	1.22	1.16	0.09	0.09	0.81	0.79
PC4	1.01	1.11	0.08	0.09	0.89	0.88
PC5	0.49	0.52	0.04	0.04	0.93	0.92
PC6	0.32	0.32	0.03	0.02	0.95	0.94
PC7	0.20	0.25	0.02	0.02	0.97	0.96
PC8	0.18	0.23	0.01	0.02	0.98	0.98
PC9	0.11	0.17	0.01	0.01	0.99	0.99
PC10	0.06	0.08	0.01	0.01	0.99	1.00
PC11	0.05	0.03	0.00	0.00	1.00	1.00
PC12	0.02	0.01	0.00	0.00	1.00	1.00
PC13	0.01	0.00	0.00	0.00	1.00	1.00

Table 4. PCA Variability of 13 yield and yield related traits under normal and less water environmental conditions

Variable	PC1	PC2	PC3	PC4
PH	0.32	-0.12	-0.03	0.08
PH	0.32	-0.12	0.12	-0.07
FLA	0.31	-0.06	-0.14	0.02
FLA	0.31	-0.05	0.24	-0.13
TPP	0.29	-0.38	-0.17	0.12
TPP	0.26	-0.19	0.07	-0.33
PL	0.32	-0.25	-0.15	-0.04
PL	0.34	-0.15	0.18	-0.04
DH	-0.24	-0.44	0.45	-0.01
DH	-0.24	-0.41	0.39	0.29
DM	-0.24	-0.47	0.42	0.03
DM	-0.24	-0.41	0.39	0.29
SL	0.32	-0.21	-0.03	0.06
SL	0.3	-0.03	-0.06	-0.22
SPS	0.31	0.21	0.33	-0.07
SPS	0.3	0.26	0.17	0.38
NGPS	0.26	0.31	0.34	-0.19
NGPS	0.28	0.2	0.1	0.36
TGW	0.31	0.2	0.32	-0.07
TGW	0.29	0.26	0.19	0.39
GYP	0.2	0.07	0.46	0.44
GYP	0.29	-0.39	-0.27	0.11
BYP	0.3	-0.33	-0.08	0.12
BYP	0.25	-0.4	0.11	-0.15
HI	-0.12	0.19	-0.09	0.85
HI	0.11	-0.32	-0.66	0.45

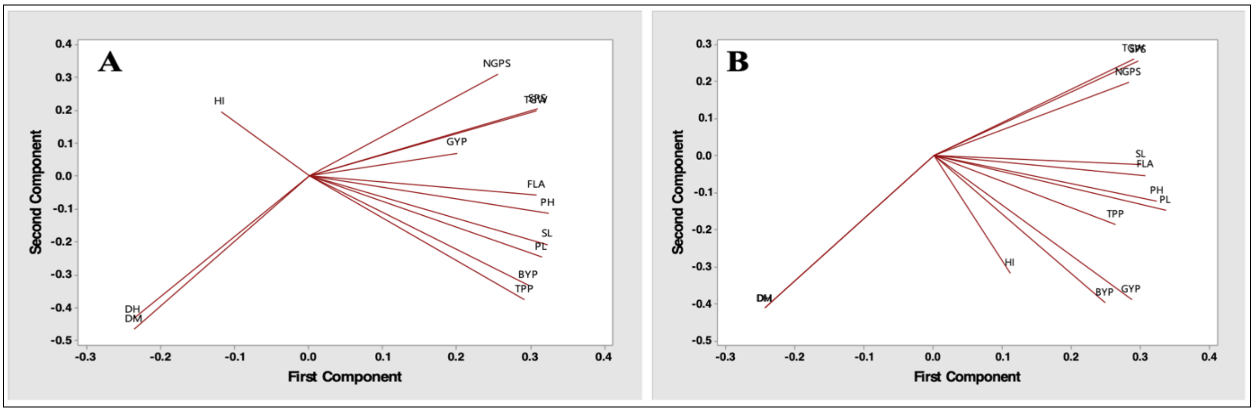


Figure 3. PCA of Loading Plot for13 yield and yield related traits under normal (3A) and drought (3B) conditions

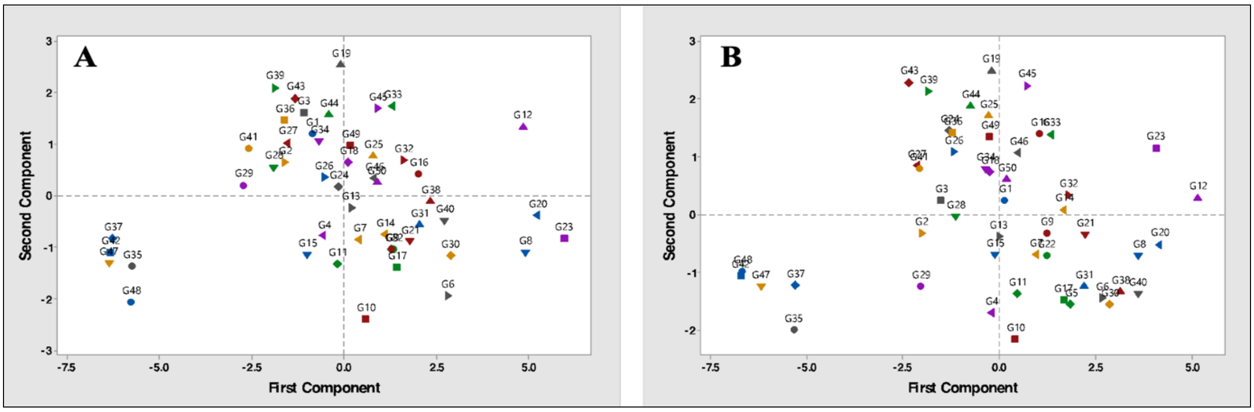


Figure 4. PCA of score plot for 50 barley genotypes under normal (4A) and drought (4B) environments

CONCLUSIONS

This study provides valuable insights into the genetic variability and drought response of 50 barley genotypes, offering critical evidence for advancing sustainable food security. The integration of ANOVA, correlation analysis, and PCA not only revealed significant genotypic variation under normal and drought conditions but also pinpointed drought-resilient genotypes such as G12, G8, G23, G20, and G16. These genotypes demonstrate strong potential for direct cultivation in water-limited regions and can serve as core material in future breeding programs. Beyond identifying promising genotypes, the multivariate approach underscored the complex trait associations that influence drought tolerance, emphasizing the importance of multi-trait selection in crop improvement. The outcomes of this research contribute meaningfully to addressing the global challenge of crop resilience under climate stress. Moving forward, molecular validation of identified genotypes, exploration of gene-environment interactions, and multi-location trials are essential steps to further enhance drought tolerance in barley. This work sets a foundation for the strategic development of climate-resilient barley cultivars.

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