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Screening of Wheat Genotypes for Water Stress Tolerance Using Soil–Water Relationships and Multivariate Statistical Approaches

Mohamed H. Sheta [1], **Mostafa M. A. Hasham** [2], **Kholoud Z. Ghanem** [3], **Hala M. Bayomy** [4], **Abdel-Nasser A. El-Sheshtawy** [5,*], **Rasha S. El-Serafy** [6,*] and **Eman Naif** [7]

[1] Soils and Water Department, Faculty of Agriculture, Al-Azhar University, Cairo 11884, Egypt; mohamedsheta.205@azhar.edu.eg
[2] Agronomy Department, Faculty of Agriculture, Al-Azhar University, Cairo 11884, Egypt; mostafahasham@azhar.edu.eg
[3] Department of Biological Science, College of Science and Humanities, Shaqra University, Riyadh 11961, Saudi Arabia; kghanem@su.edu.sa
[4] Food Science and Nutrition Department, Faculty of Science, University of Tabuk, Tabuk 71491, Saudi Arabia; hm.mohamed@ut.edu.sa
[5] Environment and Bio-Agriculture Department, Faculty of Agriculture, Al-Azhar University, Cairo 11884, Egypt
[6] Horticulture Department, Faculty of Agriculture, Tanta University, Tanta 31527, Egypt
[7] Department of Crop Science, Faculty of Agriculture, Damanhour University, Damanhour 22514, Egypt; eman.naif@agr.dmu.edu.eg
* Correspondence: abdel_nasser2007@azhar.edu.eg (A.-N.A.E.-S.); rasha.elserafi@agr.tanta.edu.eg (R.S.E.-S.)

Abstract: Drought stress constricts crop production around the world. Employing high-yielding cultivars with drought tolerance might be the ideal professional approach to coping with its detrimental outcomes. As a result, the current study was performed to investigate the sensitivity and tolerance of nine wheat genotypes to drought stress. In a randomized block design experiment, nine wheat genotypes were subjected to four water treatments: 100%, 85%, 70%, and 55% of the available water (AW). Four water regimes in two growing seasons were counted as eight environmental zones. The leaf's water relations and photosynthetic pigment were estimated, as well as growth and yield parameters. Univariate and multivariate statistical approaches, including the new method of multi-trait genotype–ideotype distance (MGIDI), were used for evaluation. The analysis of variance revealed that genotype, environment, and their interactions had a highly significant effect on all traits. The same trend was shown by the additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield across the environments. The AMMI biplot study indicated that the G8 genotype is the most stable in terms of water stress. The G7 genotype can withstand droughts up to 55% of the available water, while the G8 and G3 genotypes can withstand droughts up to 70% of the available water. Based on all examined traits, this index was used to identify the stable genotypes G7, G8, and G3, which can therefore be suggested for cultivation during drought conditions. Furthermore, we found a positive correlation between the MGIDI, ANOVA, and tolerance index results, indicating that the same desirable genotypes of G7 and G8 were identified by these procedures as being highly tolerant and stable across a range of soil moisture conditions. Based on MGIDI analysis, we can recommend that the G7 genotype exhibits higher grain yield and yield-related traits with the best drought-tolerant indices.

Keywords: drought tolerance; abiotic stress; drought indices; wheat genotypes; AMMI; MGIDI; available water

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1. Introduction

Wheat (*Triticum aestivum* L.) is the key staple food crop and is considered a strategic commodity all over the world because of its importance in the daily human diet. World wheat production, the primary source of carbohydrates and proteins after maize and rice, could be rated in third place [1]. In addition, grains provide trace amounts of fats, dietary fibers, minerals, B-group vitamins, and other nutrients for human consumption [2,3]. Wheat occupies almost 33% of the entire winter crop area, requires 9% of the water resources, and contributes 17% to the value of all agricultural production in Egypt [4].

Arid and semiarid regions' ability to grow economically is increasingly hampered by water scarcity [5], which has caused global limitations on agricultural yield and plant growth. So, water stress is defined as one of the most important environmental concerns that growers must deal with [6,7]. Also, in developing countries, water shortages result in massive losses of grain annually, and global climate change will probably cause additional losses as well [8,9]. Drought tolerance is the capacity of plants to survive and produce a desired crop in the presence of water scarcity [10].

Enhancing drought tolerance necessitates first understanding plant diversity and drought adaptability [11], and then designing the best selection plan for plant survival and output in water-stressed environments [12]. A successful breeding program aimed at drought tolerance must include an evaluation of genotypic variability under various moisture stress conditions [13,14].

Drought indices based on mathematical correlations between stressful and non-stressful situations have been used in numerous studies to choose stable genotypes based on how well they perform under stress and favorable conditions [15]. These metrics include the yield stability index (YSI) [16], the tolerance index (TOL) and the mean productivity (MP) [17], the geometric mean productivity (GMP), and the drought susceptibility index (DSI) [18]. Each of these indices evaluates the correlation between genotypes' drought resistance, tolerance, and susceptibility from a different perspective [18]. Several selection indices were evaluated by Sofi et al. [19].

A suitable indicator for identifying cultivars characterized by drought tolerance is tightly linked to both non-stressed and stressed grain production [20]. The stress tolerance index (STI), mean harmonic productivity (HMP), and GMP indices can be employed to discover genotypes that produce more both under stressful and non-stressful circumstances [18]. The wheat selection for drought tolerance is based on higher MP, GMP, and STI in stressed and non-stressed conditions [21]. Additionally, Talebi et al. [22] demonstrated statistically significant and positive correlations between grain yield under drought conditions and MP, GMP, and STI, revealing that these indices are more useful in locating high-yielding genotypes under various environmental circumstances.

In wheat, genotypes with high MP, GM, and STI are regarded as tolerable [23]. Landraces with high harmonic mean (HM) values are seen as desirable [24]. Drought resistance index (DI) is a widely used term to describe genotypes that provide good yields under both stressful and non-stressful circumstances [25]. For genotype selection, the STI index has more benefits for stressed and non-stressed crops [26]. Wheat was selected for drought tolerance under both conditions with high MP, GMP, and STI [27,28]. Due to the difficulty of merging numerous desirable features into a single genotype, selecting superior genotypes is sometimes very challenging for economically significant agronomic traits that exhibit quantitative inheritance [29].

As evidenced by a significantly larger environmental effect, a multi-environment experiment (MET) is necessary to find stable, high-yielding genotypes that tend to be more adaptive and compatible for use in certain agro-climatic conditions [30]. Many statistical methods have been used in multi-environment trials (METs), which are usually divided into two groups: univariate and multivariate [31]. A univariate statistical approach titled analysis of variance (ANOVA) can be used to display the significant difference between the levels of the main effects of the factors for each trait. However, ANOVA has substantially less power in interaction tests compared to main effect tests [32]. Understanding the interaction of genotypes with the environment has a key role in genotype cultivation in different environments. It also helps breeders identify genotypes that show broad stability in different environments [33,34]. Genotype × environment interaction (GEI) during yield trials is commonly analyzed using an additive main effect and a multiplicative interaction (AMMI) model [35].

When multiple traits are evaluated at once, correlated traits are unavoidably present. These traits can lead to multicollinearity issues [36], which can produce biased regression coefficients and incorrect conclusions [37]. The multicollinearity problem in multi-trait indexes can be well explained by combining multivariate methodologies [38–40]. In this regard, several statistical techniques were created to determine and measure the impacts of environments and genotypes, enabling the use of these instruments for interpreting biological phenomena [41]. Selecting the optimal genotypes is sometimes impeded by the main problem of expressing the economic value of features and converting them into practical economic weightings [42]. Olivoto and Nardino [36] established the multi-trait genotype–ideotype distance index (MGIDI), which is based on genotype–ideotype distance and factorial analysis, to overcome this constraint. The primary goal of this index is to select superior genotypes when multiple traits have been evaluated. Furthermore, MGIDI shows promise in providing breeding efforts with more effective techniques and genotype selection [43].

Leaf pigments are a helpful index for assessing plant status at a given developmental stage under a specific environmental condition [44,45]. Additionally, carotenoids, a nonenzymatic antioxidant, have a significant role under water stress conditions in avoiding photo-oxidative damage to the second photosystem, thus enabling plants to endure drought [46]. According to Gururani et al. [47] and Khalilzadeh et al. [48], water stress significantly decreases the amount of photosynthetic pigment, which may be due to pigment photo-oxidation and chlorophyll degradation. Drought conditions negatively affect the morphological and physiological traits of wheat cultivars [49,50]. The role and improvement of drought-tolerant wheat genotypes under molecular techniques have garnered significant attention. These endeavors aim to mitigate the adverse effects of drought stress on wheat production [51,52]. According to Randhawa et al. [53], molecular markers supply eminent sources of polymorphism, which assists breeders in choosing economical traits and thus improving crop production.

Hence, this study was performed to assess and employ ANOVA, correlation analysis, AMMI, and MGIDI in evaluating nine wheat genotypes and to identify the best drought-tolerant genotype under drought stress (100%, 85%, 70%, and 55% of the available water) in two cropping seasons based on drought tolerance indices and multiple traits.

2. Materials and Methods

2.1. Plant Materials

Nine wheat genotypes of Gemmeiza-9 (G1), Gemmeiza-10 (G2), Gemmeiza-11 (G3), Gemmeiza-12 (G4), Giza-168 (G5), Giza-171 (G6), Sakha-95 (G7), Shandweel-1(G8), and Sids-14 (G9) were provided from the Wheat Research Department, Field Crops Research Institute, Agricultural Research Center (ARC), Agricultural Ministry and Land Reclamation, Giza, Egypt. The genotype pedigrees are presented in Table S1.

2.2. Experimental Site and Growth Conditions

At the Experimental Farm of the Agronomy Department, Faculty of Agriculture, Al-Azhar University, Cairo, Egypt (30°03′16.4″ N 31°19′12.3″ E, 92 m above sea level), two pot experiments were performed from November to May of 2020/2021 and 2021/2022. The climate conditions of the experimental area for the two seasons were obtained from the Central Laboratory for Agricultural Climate (CLAC), the Ministry of Agriculture's Research Center, and tabulated in Table 1. On 25 November 2020 and 27 November 2021, ten seeds of each wheat genotype were sown separately in plastic pots (35 × 40 cm) containing 10 kg of soil collected from the surface layer (0–20 cm) of the experimental farm. The seedlings were thinned to five plants per pot three weeks later. To prevent natural precipitation, the experimental pots were put under a rain shelter. In each season, three soil samples were collected for physicochemical property determination using the standardized methods of

Page et al. [54] and Klute [55], and their results are presented in Table 2. All agricultural practices and NPK fertilizer applications for different wheat cultivars were carried out in accordance with the recommendations of the Egyptian Ministry of Agriculture and Land Reclamation. The amount of rainfall in the first season was 132.87 mm and 58.14 mm in the second.

Table 1. Temperature (°C), wind speed (m s^{-1}), relative humidity (%), average precipitation (mm day^{-1}), and surface pressure (kPa) of experimental site during 2020/2021 and 2021/2022 growing winter seasons.

Month	**Temperature (°C)**		**Wind Speed (m s^{-1})**		**Relative Humidity (%)**	**Average Precipitation (mm day^{-1})**	**Surface Pressure (kPa)**
	Max	**Min**	**Max**	**Min**			
2020/2021							
November	24.64	13.66	5.15	1.87	63.38	0.36	100.10
December	22.57	10.47	5.08	1.97	60.63	0.02	100.14
January	21.52	8.33	5.82	2.34	59.04	0.07	100.26
February	21.78	8.29	5.26	2.05	61.52	0.72	100.26
March	23.27	9.20	6.11	2.09	62.38	3.36	100.06
April	29.43	11.71	6.54	2.63	50.20	0.13	99.98
May	36.84	17.90	6.72	2.40	36.64	0.00	99.64
2021/2022							
November	27.71	15.14	4.81	1.96	61.68	0.67	100.02
December	19.37	8.96	5.84	2.17	68.45	0.34	100.19
January	16.76	5.40	5.51	2.14	67.08	1.08	100.30
February	19.48	6.57	5.67	2.20	66.60	0.39	100.22
March	21.82	7.46	6.87	2.36	54.20	0.06	100.21
April	32.22	14.14	6.82	2.73	38.93	0.02	99.61
May	33.80	16.94	7.21	2.63	39.17	0.04	99.74

Table 2. Some physical and chemical properties of the experiment soil at sowing in both 2020/2021 and 2021/2022 growing winter seasons.

Property	**2020/2021**	**2021/2022**	**Property**	**2020/2021**	**2021/2022**
Particle size distribution:			Available water (AW, %)	9.51	9.43
Coarse sand (%)	5.20	5.47	Bulk density (Mg m^{-3})	1.51	1.53
Fine sand (%)	76.56	76.54	Total porosity (%)	43.02	42.26
Silt (%)	4.81	5.31	pH (1:2.5 soil water suspension)	8.21	8.11
Clay (%)	13.43	12.68	EC_e (soil paste extract, dS m^{-1})	1.65	1.69
Textural class	Sandy loam	Sandy loam	Organic carbon (g kg^{-1})	3.23	3.26
Field capacity (θ_{FC} , %)	15.05	14.89	Organic matter (g kg^{-1})	5.56	5.61
Permanent wilting point (θ_{PWP} , %)	5.54	5.46	$CaCO_3$ content (g kg^{-1})	16.55	17.00
Soluble cations:			Soluble anions:		
Ca^{2+} (mmolc L^{-1})	8.24	8.59	$CO_3{}^{2-}$ (mmolc L^{-1})	0.00	0.00
Mg^{2+} (mmolc L^{-1})	5.23	5.39	$HCO_3{}^{-}$ (mmolc L^{-1})	8.56	9.33
Na^{+} (mmolc L^{-1})	1.72	1.69	Cl^{-} (mmolc L^{-1})	6.23	6.45
K^{+} (mmolc L^{-1})	1.26	1.27	$SO_4{}^{2-}$ (mmolc L^{-1})	1.66	1.16

Table 2. *Cont.*

Property	2020/2021	2021/2022	Property	2020/2021	2021/2022
Available macro- and micro-nutrients:					
N (mg kg^{-1})	29.36	31.67	Mn (mg kg^{-1})	1.91	1.86
P (mg kg^{-1})	6.44	6.74	Zn (mg kg^{-1})	0.88	0.91
K (mg kg^{-1})	122.65	125.23	Cu (mg kg^{-1})	1.11	1.15
Fe (mg kg^{-1})	2.78	2.69			

2.3. Experimental Design and Treatment Details

After 21 days from sowing, nine wheat genotypes were subjected to four water treatments: 100% (control), 85%, 70%, and 55% of the available water (AW). Four water regimes in two growing seasons were counted as eight environments. The experiment was performed in a randomized block design [56] and replicated three times per environment for nine genotypes; each replicate has 10 pots. The eight environments were as follows: E1: 100% AW × first season, E2: 85% AW × first season, E3: 70% AW × first season, E4: 55% AW × first season, E5: 100% AW × second season, E6: 85% AW × second season, E7: 70% AW × second season, and E8: 55% AW × second season.

The soil moisture content at field capacity (θ_{FC}) and permanent wilting point (θ_{PWP}) were determined with the pressure plate apparatus at suction pressures of −0.33 and −15.00 bar, respectively, as described by Klute [55], and the values obtained were 15.05 and 5.54% in the 1st season and 14.89 and 5.46% in the 2nd season, respectively. The available water (AW) was computed by subtracting θ_{PWP} from θ_{FC} . Pots were maintained by daily weighing to determine water loss and supplementing the required water quantity to maintain a constant level at each of their four levels (100, 85, 70, and 55% of AW).

2.4. Measurements

2.4.1. Water Relations

Relative turgidity (RT), relative water content (RWC), and water deficit (WD) traits of wheat genotype leaves at the flowering stage (anthesis) were estimated according to Weatherley [57], Barrs [58], and Grzesiak et al. [27] procedures, respectively.

2.4.2. Photosynthetic Pigment Estimation

Photosynthetic pigments (mg g^{-1} fresh weight) of chlorophyll a (Chl a), chlorophyll b (Chl b), total chlorophyll (T Chl), and carotenoids (CARs) were estimated spectrophotometrically at the flowering stage (anthesis) from each genotype using a methanol solvent following the Dere et al. [59] method.

2.4.3. Growth and Yield Parameters

At the harvest stage (3rd and 5th of May 2020/2021 and 2021/22022, respectively), ten plants were harvested from each replicate, one plant from each pot, and the plant in the center of the pot was selected for guarding by the rest of the plants to measure the studied traits. An average of ten plants in each replicate was used to apply statistical methods, and their plant height (PH) in cm, spike length (SL) in cm, number of grains spike^{-1} (NGS^{-1}), grain yield (GY) in g plant^{-1}, straw yield (SY) in g plant^{-1}, and biological yield (BY) in g plant^{-1} were assessed. Harvest index (%) and crop index were calculated using the following equation:

$$\text{Harvest index } (\%) = \frac{\text{Grain yield } \left(\text{g plant}^{-1}\right)}{\text{Biological yield } \left(\text{g plant}^{-1}\right)} \times 100$$

$$\text{Crop index }(\%) = \frac{\text{Grain yield }\left(\text{g plant}^{-1}\right)}{\text{Straw yield }\left(\text{g plant}^{-1}\right)} \times 100$$

2.4.4. Drought Tolerance Indices

Drought tolerance indices were calculated by dividing the percentage of grain yield in each water regime by 100% AW in each season separately. Thus, we obtained six cases (C) of the values of the drought tolerance indices, which were as follows:

C1: E2 /E1, C2: E3 /E1, C3: E4 /E1, C4: E6 /E5, C5: E7 /E5, and C6: E8 /E5. Drought tolerance indices were estimated as presented in Table 3.

2.4.5. Analysis of Variance

To verify the analysis of variance assumptions, data normality was checked using the Shapiro–Wilk test [60]. The homogeneity of variances was checked by Bartlett's test [61]. The general linear mixed model of analysis of variance was applied to 10 traits, which were studied according to the next model:

$$Y_{ijk} = \mu + G_i + E_j + R_{k(j)} + GE_{ij} + \varepsilon_{ijk}$$

where Y_{ijk} is the observation obtained with ith genotype in the jth environment and kth block, μ is the overall mean, G_i is the genotype effect, E_j is the environment effect, $R_k\ (_j)$ is the impact of three replications within the environment, GE_{ij} is the interaction effect of genotype and environment, and ε is the random error associated with Y_{ijk}, with a mean of 0 and a variance of σ^2 [38]. An analysis of variance for drought tolerance indices was performed for each case individually. XLSTAT (2019, Addinsoft, New York, NY, USA) statistical package. Tukey's multiple range test was carried out to evaluate mean comparisons.

Table 3. Drought tolerance indices, formula equations, and references.

No.	Drought Tolerance Indices	Formula Equations	References
1	Tolerance index (TOL)	$\mathrm{TOL} = \mathrm{Yp} - \mathrm{Ys}$	[17]
2	Mean productivity (MP)	$\mathrm{MP} = (\mathrm{Yp} + \mathrm{Ys})/2$	[17]
3	Geometrical mean productivity (GMP)	$\mathrm{GMP} = \sqrt{(\mathrm{Yp} \times \mathrm{Ys})}$	[18]
4	Harmonic mean (HM)	$\mathrm{HM} = [2 \times (\mathrm{Yp} \times \mathrm{Ys})]/(\mathrm{Yp} + \mathrm{Ys})$	[62]
5	Golden Mean (GM)	$\mathrm{GM} = (\mathrm{Yp} + \mathrm{Ys})/(\mathrm{Yp} - \mathrm{Ys})$	[63]
6	Yield stability index (YSI)	$\mathrm{YSI} = \mathrm{Ys}/\mathrm{Yp}$	[16]
7	Sensitivity drought index (SDI)	$\mathrm{SDI} = (\mathrm{Yp} - \mathrm{Ys})/\mathrm{Yp}$	[64]
8	Drought susceptibility index (DSI)	$\mathrm{DSI} = \left(1 - \frac{\mathrm{Ys}}{\mathrm{Yp}}\right)/(\bar{\mathrm{Y}}\mathrm{s}/\bar{\mathrm{Y}}\mathrm{p})$	[65]
9	Stress tolerance index (STI)	$\mathrm{STI} = \frac{\mathrm{Yp} \times \mathrm{Ys}}{\bar{\mathrm{Y}}\mathrm{p}^2}$	[18]
10	Drought resistance index (DI)	$\mathrm{DI} = \frac{\mathrm{Ys} \times \frac{\mathrm{Ys}}{\mathrm{Yp}}}{\bar{\mathrm{Ys}}}$	[25]

In these formulas, Yp, Ys, $\bar{\mathrm{Y}}$p, and $\bar{\mathrm{Y}}$s are the final yield of each genotype under non-stress conditions, the yield of each genotype under stress conditions, the average yield of all genotypes under non-stress conditions, and the average of all genotypes under stress conditions, respectively.

2.4.6. Additive Main Effects and Multiplicative Interaction (AMMI)

The AMMI analysis was assessed to consider G, E, and GEI effects on grain yield traits via the following linear model according to Zobel et al. [66]:

$$Y_{ij} = \mu + G_i + E_j + \sum \lambda_{n}\_\alpha_{in}\gamma_{jn} + \theta_{ij}$$

where: Y_{ij} is mean yield of ith genotype in the jth environment, μ is overall mean, Gi is the ith genotypic effect, E_j = jth location effect, λ_n is the eigenvalue of the principal component axis n, $\alpha_{in}\gamma_{jn}$ is the ith genotype, jth environment principal component analysis (PCA) scores for the PCA axis θ_{ij} is the residual, and n is the number of PCA axes retained in the model.

2.4.7. Multi-Trait Genotype–Ideotype Distance Index (MGIDI)

The MGIDI was assessed to determine the optimal genotype in each environment [36]. All the analyzed attributes must be thoughtfully planned for use in this indicator. The ten studied traits were used for each of the eight environments. The phenotyping procedure was based on a two-way table rescaling of best linear unbiased prediction (BLUP) for genotypes and traits [38]. After applying the factor analysis to cluster correlated traits into factors, the factorial scores for each genotype were estimated after the varimax rotation criterion [67]. The $\mathrm{MGIDI_i}$ index was computed by the formula:

$$\mathrm{MGIDI}_i = \sum_{\mathrm{j=1}}^{\mathrm{f}} \left[\left(\mathrm{y_{ij}} - \mathrm{y_j} \right)^2 \right]^{0.5}$$

where MGIDIi is the multi-trait genotype–ideotype distance index for the ith genotype, $\mathrm{y_{ij}}$ is the score of the ith genotype in the jth factor (i = 1, 2, . . ., g; j = 1, 2, . . ., f), g and f are the numbers of genotypes and factors, respectively, and $\mathrm{y_j}$ is the jth score of the ideotype. Data manipulation and index computation were performed in R software system version 4.0.3 using the package metan 1.12.0 [68].

3. Results

3.1. Analysis of Variance

The result of Bartlett's test of homogeneity among eight environments indicated that all traits were homogenous ($p > 0.05$); therefore, a joint analysis was processed (Table S2). On the other hand, the Shapiro test revealed that 60% of the traits were normally distributed ($p > 0.05$), with four traits not being normally distributed. However, this observation was not considered due to the large sample size (n = 216).

It is clearly shown in Table 4 that the mean squares of the joint analysis for the main effects of the E, G, and E × G displayed highly significant differences ($p < 0.01$) for all studied traits. Regarding the coefficients of variation for the traits, the values of the coefficients show that every trait had a low coefficient of variation, demonstrating the accuracy with which the treatments were carried out, and the measurements were recorded during the experiment.

The results presented in Table S3 indicate the mean values of the studied traits in the eight environments. Water levels had an adverse effect on all traits under study, as the values of the studied traits gradually decreased, reaching the lowest values in the environments with the lowest water level (55% AW). The highest values of water status, photosynthetic pigments, and plant growth were obtained by E1. Yield traits showed the highest values at E1, as recorded by the highest SL, with greater NGS giving the highest GY (4.58 g/plant), followed by E5, which ranked second in this respect. On the other hand, E8 exhibited the lowest values in GY, 51.5% lower than E1. Results in Table S4 show the mean values of the studied traits of the nine genotypes under study. The maximum yield traits of SL, NGS, GY, and BY were produced by G7, which gave 11.1 cm, 56.5, 3.98 g, and 13.3 g, in contrast to G1 and G2, which produced the lowest GY with non-significance among them.

Table 4. Mean squares of the combined analysis for the main effects of irrigation, wheat genotypes, and the interaction for studied traits.

Traits	Mean Square					C.V%
	Environments (E)	**Rep. within Environment R(E)**	**Genotypes (G)**	**E × G**	**Error**	
df	**7**	**16**	**8**	**56**	**128**	
RT	960.91 **	6.71	137.79 **	7.05 **	1.85	1.80
RWC	775.69 **	12.39	394.91 **	130.02 **	13.19	5.46
WD	960.91 **	6.71	137.79 **	7.05 **	1.85	5.51
T Chl	0.422 **	0.002	0.398 **	0.008 **	0.001	3.13
CARs	0.1123 **	0.0006	0.0671 **	0.0016 **	0.0005	4.99
PH	3140.80 **	2.74	302.53 **	31.90 **	2.58	1.85
SL	40.578 **	0.542	6.436 **	0.554 **	0.250	4.67
NGS	1032.07 **	2.89	212.80 **	10.22 **	5.36	4.41
GY	20.698 **	0.059	3.573 **	0.069 **	0.023	4.53
BY	163.120 **	0.282	22.823 **	0.598 **	0.173	3.55

df: degree of freedom; **: statistically significant differences at $p \leq 0.05$ and $p \leq 0.01$, respectively; ns: non-significant differences; RT: relative turgidity; RWC: relative water content; WD: water deficit; T Chl: total chlorophyll; CARs: carotenoids; PH: plant height; SL: spike length; NGS: number of grains per spike; GY: grain yield; BY: biological yield.

3.2. AMMI Analysis for Grain Yield

AMMI analysis demonstrated that grain yield presents a strong significant ($p < 0.001$) influence by E, G, and E × G (Table 5). E made a higher contribution (79.93%) towards the sum squares for grain yield, followed by G (15.77%) and E × G (2.12%). Also, E × G was significantly explained by the first IPC. IPC1 contributed 80.6% towards the total E × G, while 11.5, 6.35, and 1.18% were shown by the second, third, and fourth IPCs, respectively.

Table 5. AMMI analysis of variance for grain yield with explained variation in seed yield of tepary bean accessions evaluated in four environments.

Source	df	SS	MS	F-Value	*p*-Value	TSS (%)	E × G (%)
E	7	144.88	20.698	352.4	0.000	79.93	
Rep. (E)	16	0.939	0.058	2.51	0.002	0.52	
G	8	28.583	3.573	152.4	0.000	15.77	
E × G	56	3.840	0.068	2.93	0.000	2.12	
Residuals	128	3.00	0.023			1.66	
Total	215	181.24					
IPC1	14	3.095	0.221	9.43	0.000		80.60
IPC2	12	0.441	0.036	1.57	0.108		11.50
IPC3	10	0.244	0.024	1.04	0.414		6.35
IPC4	8	0.045	0.006	0.24	0.982		1.18
IPC5	6	0.011	0.002	0.08	0.998		0.36
IPC6	4	0.003	0.001	0.03	0.998		0.01
IPC7	2	0.002	0.001	0.03	0.970		0.00

E: environment; G: genotype; df: degrees of freedom; SS: sum of squares; MS: mean sum of squares; TSS: total sum of squares; IPC: interaction principal component.

AMMI1 stability indicates an association between G and E. The biplot's origin represents the overall mean of GY (Figure 1A). G7 presented the highest grain productivity (3.98 g plant^{-1}), followed by G6 (3.81 g plant^{-1}), G5 (3.64 g plant^{-1}), and G8 (3.58 g plant^{-1}). While G1, G2, G3, G4, and G9 have lower-than-average production on average, these genotypes should not be recommended. The graph's *x*-axis presents the average grain yield of genotypes, while the graph's *y*-axis presents the IPC1 of the E × G interaction.

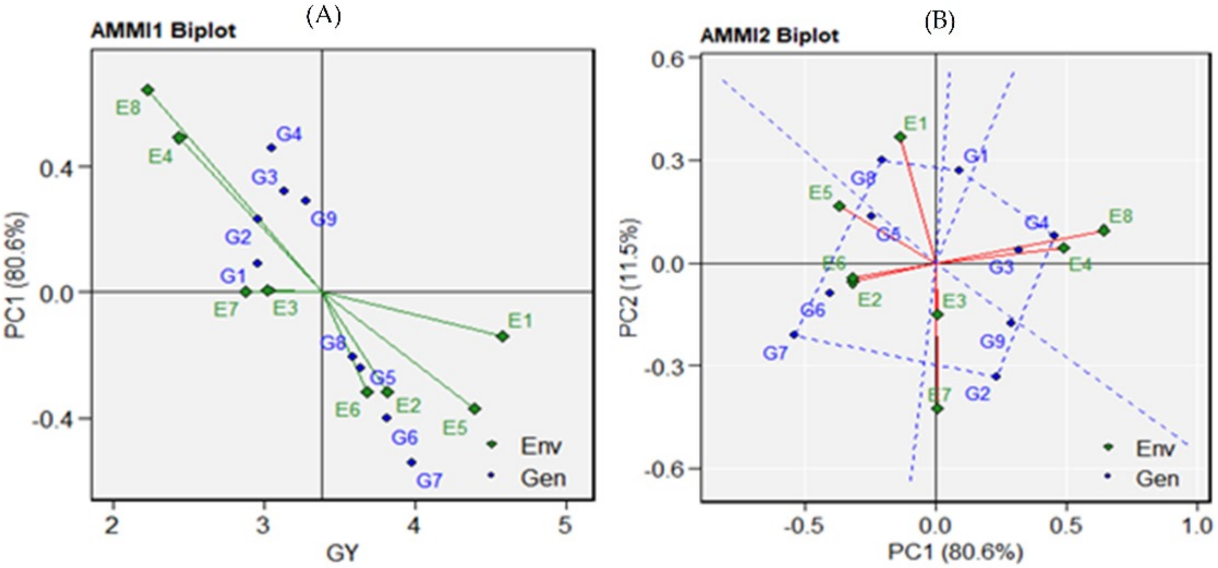

Figure 1. (**A**) AMMI1 biplot presenting mean grain yield versus PC1; (**B**) AMMI2 biplot showing PC1 and PC2 scores of nine wheat genotypes tested in eight environments. G: wheat genotypes, E: environments.

A few environments were particularly noteworthy because they contributed little to the interaction: (E3 and E7; 70% AW) contributed moderately to the interaction; (E2 and E6: 85% AW) had shorter vectors with weaker contact forces and were closer to the origin; (E1 and E5: 100% AW) and (E4 and E8: 55% AW) were far from the origin with longer vectors, which exhibited a high E × G (Figure 1). The only environments where averages were higher than the overall averages (3.38 g plant^{-1}) were E1, E2, E5, and E6, suggesting that these were the best conditions for obtaining a high mean. Based on the IPC1 value, E3 and E7 (70% AW) are estimated to be the major players in the stability of genotype performance. On the other hand, G1 and G8 secure an IPC1 value close to zero, indicating low environmental influence on these genotypes (Figure 1A).

Individual data points represent different genotypes, and the arrangement of these points indicates both the average yield and the interaction effect of each genotype. In contrast to genotypes that appear further apart, which typically have divergent mean yields and/or interaction effects, genotypes that appear close to one another in the graph typically have comparable mean yields and interaction effects. Basically, genotypes that are grouped together behave similarly in various contexts. In contrast to genotypes with higher absolute IPC values, the combination of good yields and low IPC absolute values aids in the selection of genotypes that yield stable grain yields. Thus, the G8 genotype in this study is thought to be the most stable in terms of wheat yield (Figure 1A).

The AMMI2 biplot depicts the interaction between nine genotypes and eight environmental conditions (Figure 1B). The IPC1 and IPC2 represented 92.10% of the E×G, where IPC1 and IPC2 contributed 80.60% and 11.50% of the total variation, respectively. AMMI2 can help assess the best genotype growth in specific environments. Lower IPC1 and IPC2 values, the most stable G, and E secure a closer position to the origin and show a lower G × E. In the present study, wheat genotypes G5 and G3 are the most stable in terms of yield (Figure 1B) because of their positions near the origin. In terms of the environments, E2, E3, E6, and E7 exhibited the most stable environments for the genotypes used in GY due to their positions near the origin.

The most reactive genotypes (G4, G1, G8, G7, and G2) are displayed as minimum or maximum GY with specific adaptations to the agricultural environment and are connected by dotted lines at the apex of the polygon view form. The degree of interaction with the environment is determined by a vertical projection from the genotype to the environmental vector. These five genotypes of G4, G1, G8, G7, and G2, with varying GY and unstable average performance in various agricultural environments, were displayed in the plot (Figure 1B).

The which-one-where structure of the biplot analysis for GY of nine wheat genotypes distributed over all five sectors or sections is shown in Figure 1B, whereas the yield of the eight tested environments is distributed over four sectors. E4 and E8 with wheat genotypes G3 and G4 make up sector 2 in terms of yield; E3 and E7 with G2 and G9; E2, E5, and E6 with G5, G6, and G7; and E1 with G8 make up sector 5 (Figure 1B). Although less stable and with poorer performance across environments in different sectors, the genotypes are more appropriate and confer a high level of performance and stability in the environment within the same sector.

3.3. Correlation Analysis for Drought Indices

The correlation coefficients between drought tolerance indices were performed using pooled data for nine wheat genotypes in six cases (Figure 2). Crop yield under normal irrigation (Yp) showed a positive correlation with MP, GMP, HM, STI, and DI. Crop yield under stress (Ys) was found to be positively correlated with MP, GMP, HM, GM, YSI, STI, and DI. Ys, on the other hand, had negative correlation coefficients with TOL, SDI, and DSI. The highly positive indices correlated with Yp and Ys were MP, GMP, HM, and STI.

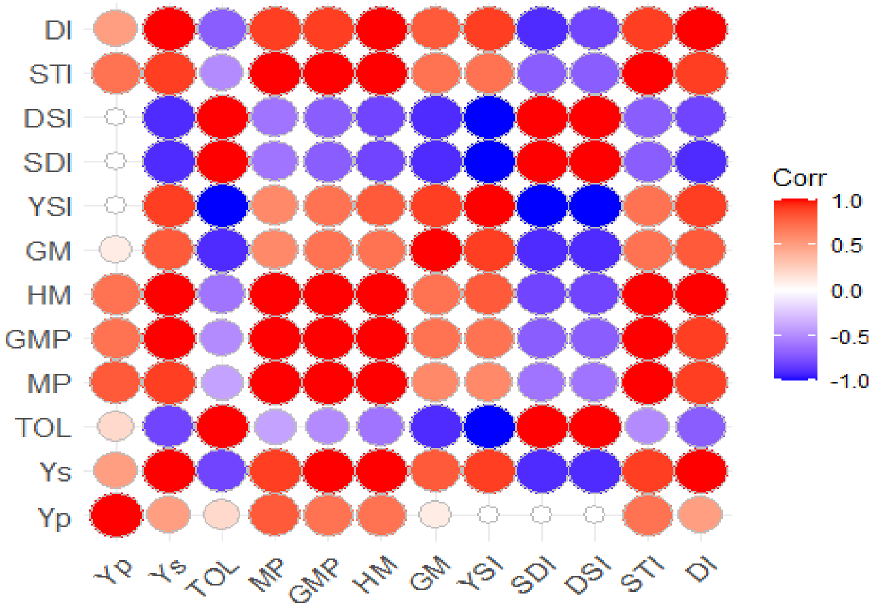

Figure 2. Correlation heat map for drought indices. Yp: grain yield in non-stress condition; Ys: grain yield in stress condition; TOL: tolerance index; MP: mean productivity; GMP: geometrical mean productivity; HM: harmonic mean; GM: golden mean; YSI: yield stability index; SDI: sensitivity drought index; DSI: drought susceptibility index; STI: stress tolerance index; DI: drought resistance index.

GMP was chosen as a representative of the arithmetic, geometric, and harmonic means of productivity because the four selected drought indicators have positive relationships with one another. Its value falls between the arithmetic and harmonic means. Additionally, the STI was selected since it had the lowest variance inflation factor after the multicollinearity of the four indicators was tested. Consequently, GMP and STI will be used in each case to compare the genotypes.

3.4. Analysis of Variance for Genotypes under Six Cases Using GMP and STI Values

The analysis of variance for GMP and STI indices for each case indicates that there is a significant difference between G for each case using GMP and STI (Table 6). By comparing the means of the genotypes using Tukey's multiple range test, it was found that G7 had the largest value in GMP and STI, but there is not a significant difference between G7 and G6 for all cases using GMP values except C5. Regarding STI values, there is not a significant difference between G7 and G6 for all cases except C2 and C5. The genotypes can also be arranged in descending order according to the highest index values, as follows: G7, G6, G5, G8, and G9.

Table 6. GMP and STI means and genotype ranks for six cases.

Index	Genotype	C1	C2	C3	C4	C5	C6
GMP	G1	3.79 c (7)	3.32 cd (8)	3.00 c (8)	3.57 c (7)	3.00e (9)	2.70 d (9)
	G2	3.66 c (9)	3.23 d (9)	2.91 c (9)	3.53 c (8)	3.10 e (8)	2.72 d (8)
	G3	3.87 c (6)	3.45 cd (6)	3.18 c (6)	3.67 c (6)	3.20 e (6)	2.96 cd (6)
	G4	3.76 c (8)	3.39 cd (7)	3.16 c (7)	3.52 c (9)	3.17 e (7)	2.93 cd (7)
	G5	4.51 b (3)	4.00 b (3)	3.56 ab (3)	4.38 b (3)	3.85 bc (3)	3.36 ab (3)
	G6	4.70 ab (2)	4.15 ab (2)	3.68 a (2)	4.61 ab (2)	4.05 b (2)	3.43 a (2)
	G7	4.90 a (1)	4.40 a (1)	3.79 a (1)	4.76 a (1)	4.30 a (1)	3.55 a (1)
	G8	4.45 b (4)	3.95 b (4)	3.52 ab (4)	4.33 b (4)	3.76 c (4)	3.35 ab (4)
	G9	3.96 c (5)	3.62 c (5)	3.27 bc (5)	3.80 c (5)	3.52 d (5)	3.12 bc (5)
STI	G1	0.68 c (7)	0.52 cd (8)	0.43 c (8)	0.66 c (7)	0.47 e (9)	0.37 d (9)
	G2	0.64 c (9)	0.50 d (9)	0.40 c (9)	0.65 c (8)	0.50 e (8)	0.38 d (8)
	G3	0.71 c (6)	0.57 cd (6)	0.48 c (6)	0.70 c (6)	0.53 e (6)	0.45 cd (6)
	G4	0.67 c (8)	0.55 cd (7)	0.47 c (7)	0.64 c (9)	0.52 e (7)	0.44 cd (7)
	G5	0.97 b (3)	0.76 b (3)	0.60 ab (3)	1.00 b (3)	0.77 bc (3)	0.59 ab (3)
	G6	1.05 ab (2)	0.82 b (2)	0.65 a (2)	1.10 ab (2)	0.85 b (2)	0.61 a (2)
	G7	1.14 a (1)	0.92 a (1)	0.68 a (1)	1.18 a (1)	0.96 a (1)	0.65 a (1)
	G8	0.94 b (4)	0.75 b (4)	0.59 ab (4)	0.97 b (4)	0.73 c (4)	0.58 ab (4)
	G9	0.75 c (5)	0.62 c (5)	0.51 bc (5)	0.75 c (5)	0.64 d (5)	0.51 bc (5)

C1: E2/E1, C2: E3/E1, C3: E4/E1, C4: E6/E5, C5: E7/E5, and C6: E8/E5. Means with the same letter in the same column for each index are not significant for $\alpha = 0.05$ according to Tukey's test.

3.5. Genotype Selection Is Based on Multiple Traits Using MGIDI

3.5.1. Phenotypic Correlation among Traits

To identify a suitable genotype, a multi-trait approach was employed that considered all the investigated traits. On the other hand, assessing numerous traits at once probably results in the presence of correlated traits, which may lead to issues with multicollinearity. Pooled data for nine wheat genotypes under different water levels was used to create a correlation heatmap of the studied traits (Figure 3). A significant positive correlation was detected between GY with all studied traits except WD, which had a negative correlation with all studied traits. GY exhibited a high correlation with BY (r = 0.99), PH (r = 0.89), RT (r = 0.88), SL (r = 0.67), and NGS (r = 0.81) at $p < 0.001$. At the same time, PH had a high positive correlation with yield-related traits. On the other hand, the correlation between T Chl with GY and BY was weak and significant at $p < 0.05$. A greater SL was expected to result in a substantial improvement in the grain yield. Furthermore, the NGS demonstrated a robust and statistically significant positive correlation with SL and GY at a significant level of $p < 0.001$. Additionally, 66.6% of traits (RT, CARs, SL, PH, NGS, and BY) showed a strong, positive, and significant correlation with GY, 22.3% of traits (RWC and T Chl) showed a moderate, positive, and significant correlation with GY, and 11.1% of the traits (WD) showed a strong, negative, and significant correlation with GY. Therefore, the GY trait has a positive and significant correlation with 88.9% of the studied traits. Because we cannot determine the individual effect of each trait on other traits, since we are primarily interested in stress studies on grain yield and find that grain yield is related to all traits, it is necessary to separate the studied traits into independent groups.

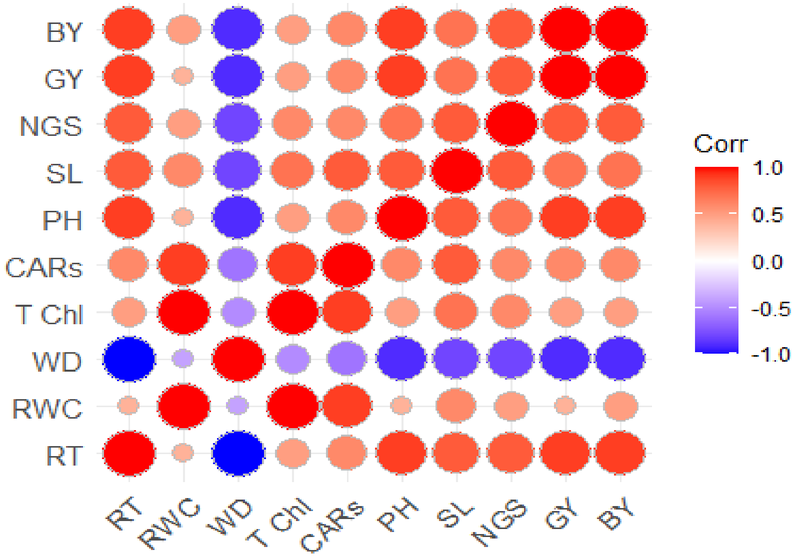

Figure 3. Correlation heatmap for studied traits. GY: grain yield; RT: relative turgidity; RWC: relative water content; WD: water deficit; T Chl: total chlorophyll; CARs: carotenoids; PH: plant height; SL: spike length; NGS: number of grains per spike; BY: biological yield.

3.5.2. Multi-Trait Genotype–Ideotype Distance Index (MGIDI)

Considering every measured trait, the MGIDI index was employed to choose the ideal wheat genotype. Factor analysis is computed, the distance between each genotype and the ideotype is ascertained, and the trait is scaled using BLUP for genotype mean performance. Understanding the results of multi-environment trials requires analyzing the elements that contribute to the traits during genotype selection. REML/BLUP and the mixed-effects model were used to estimate the variance components. The likelihood ratio test results showed that, for all traits examined, the effect of genotype was highly significant ($p <$ 0.01), except for RT and WD in E6, PH in E1, SL in E2, E3, and E8, and NGS in E1 and E2 (Table S5).

The factor analysis in each environment was found through additional trait analysis using REML/BLUP, and these components collectively account for most of the variation in the traits.

In terms of E1, there were four factors (FA) with eigenvalues > 1, which explained 90.9% of the variance (Table S6). Additionally, with an average of 0.91, the communality values for the traits varied from 0.65 for the PH trait to 0.99 for GY and BY. The traits in E1 were grouped into the following four factors: FA1, which included RT, RWC, and WD; FA2, which included TChl and CARs; FA3, which included GY and BY; and FA4, which included PH, SL, and NGS.

Regarding E2, four factors with eigenvalues >1 were kept and contributed to 91.7% of the variation in traits. Furthermore, the communality values for the traits ranged from 0.75 for the NGS trait to 0.98 for the CARs trait, with an average of 0.92. The traits for E2 were grouped into four factors: in FA1, SL, GY, and BY; in FA2, TChl and CARs; in FA3, RT, WD, and NGS; and in FA4, RWC and PH (Table S6).

In terms of E3, three factors with eigenvalues >1 were kept and contributed to 81.5% of the variation in traits. Furthermore, the communality values for the traits ranged from 0.40 for the NGS trait to 0.96 for the TChl and CARs traits, with an average of 0.92. The traits for E4 were grouped into four factors: in FA1, SL, GY, and BY; in FA2, TChl and CARs; in FA3, RT, WD, and NGS; and in FA4, RWC and PH (Table S6).

E5 showed that four factors with eigenvalues > 1 were kept and contributed to 90% of the variation in traits. Also, the communality values for the traits ranged from 0.58 for the NGS trait to 0.98 for CARs and the GY trait, with an average of 0.90. The traits for E5 were grouped into four factors: in FA1, RT, RWC, WD, and NGS; in FA2, GY and BY; in FA3, PH and SL; and in FA4, TChl and CARs (Table S6).

E6 showed that three factors with eigenvalues > 1 were kept and contributed to 81.8% of the variation in traits. Furthermore, the communality values for the traits ranged from 0.66 for the NGS trait to 0.94 for the GY trait, with an average of 0.82. The traits for E6 were grouped into three factors: in FA1, RWC, SL, GY, and BY; in FA2, PH and NGS; in FA3, RT, WD, TChl, and CARs (Table S6).

E7 showed that four factors with eigenvalues > 1 were kept and contributed to 89.4% of the variation in traits. Furthermore, the communality values for the traits ranged from 0.45 for the NGS trait to 0.99 for the GY and BY traits, with an average of 0.90. The traits for E7 were grouped into four factors: in FA1, GY, and BY; in FA2, PH and NGS; in FA3, RT, RWC, WD, and SL; in FA4, TChl and CARs (Table S6).

Regarding E8, three factors with eigenvalues > 1 were kept and contributed to 88.6% of the variation in traits. Furthermore, the communality values for the traits ranged from 0.71 for the NGS trait to 0.99 for the RWC trait, with an average of 0.88. The traits for E8 were grouped into three factors: in FA1, RT, WD, TChl, and PH; in FA2, SL and NGS; in FA3, GY and BY (Table S6).

Considering the MGIDI index, G7 was the best genotype at E1 and E5 (100% AW) (Figure 4). While the best genotype differed at the level of 85% AW from E2 to E6, as G3 was at E2, and G8 was at E5 (Figure 5). In terms of 70% AW, the best genotype also differed from E3 to E7, as G8 was the best at E3, and G7 was at E7 (Figure 6). Moreover, the G7 genotype also showed superiority over the other genotypes in the most severe cases of water stress (55% AW) in E4 and E8 (Figure 7).

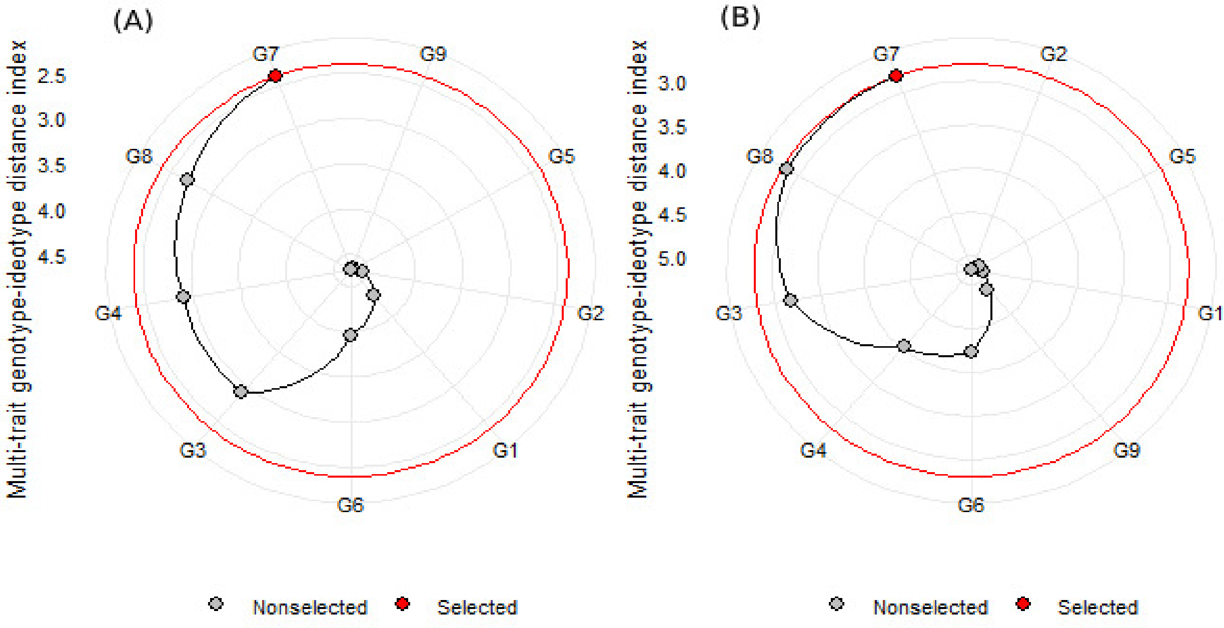

Figure 4. Ranking of genotypes based on the multi-trait genotype–ideotype distance index (MGIDI) for E1 (**A**) and E5 (**B**).

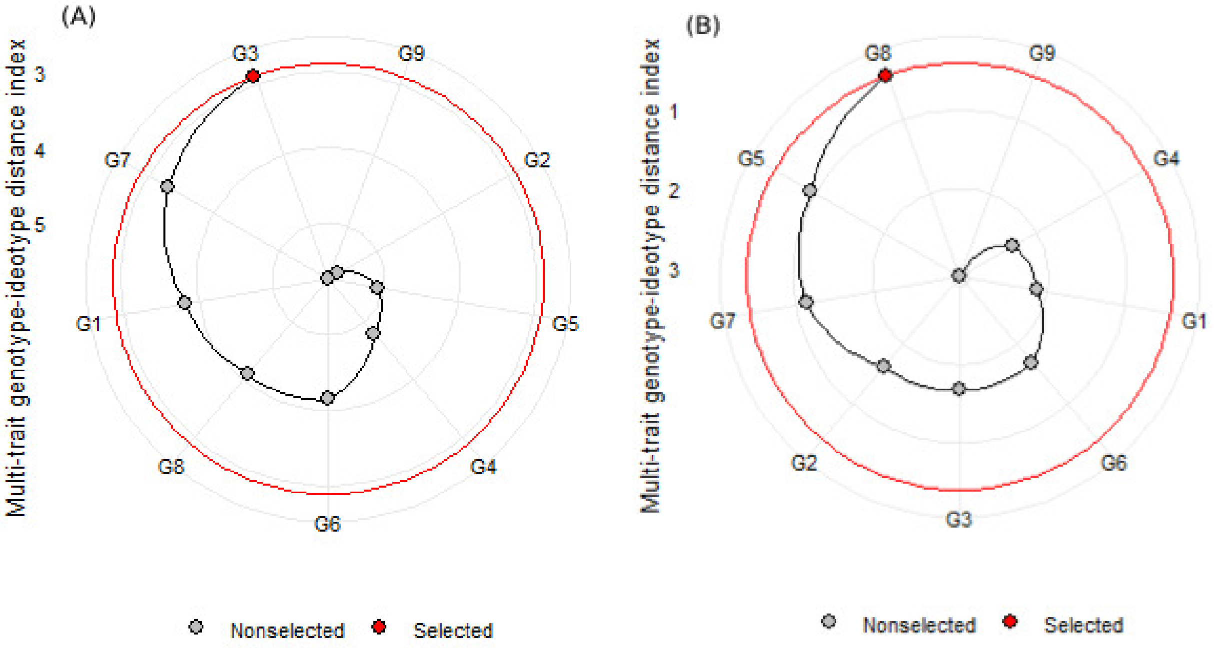

Figure 5. Ranking of genotypes based on the multi-trait genotype–ideotype distance index (MGIDI) for E2 (**A**) and E6 (**B**).

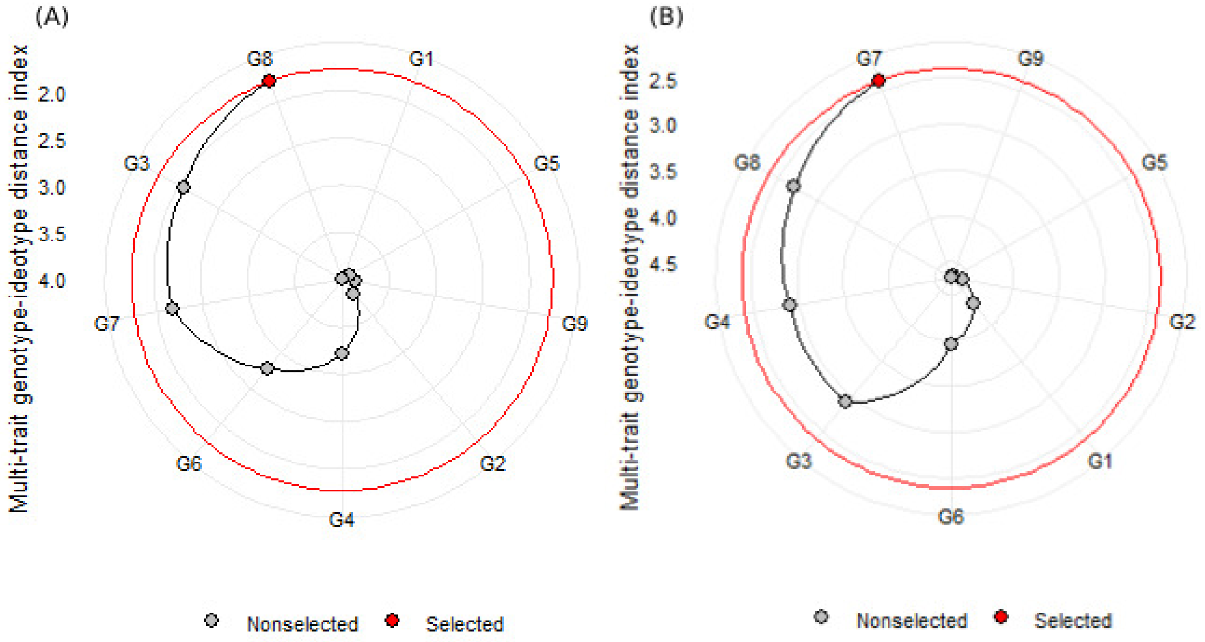

Figure 6. Ranking of genotypes based on the multi-trait genotype–ideotype distance index (MGIDI) for E3 (**A**) and E7 (**B**).

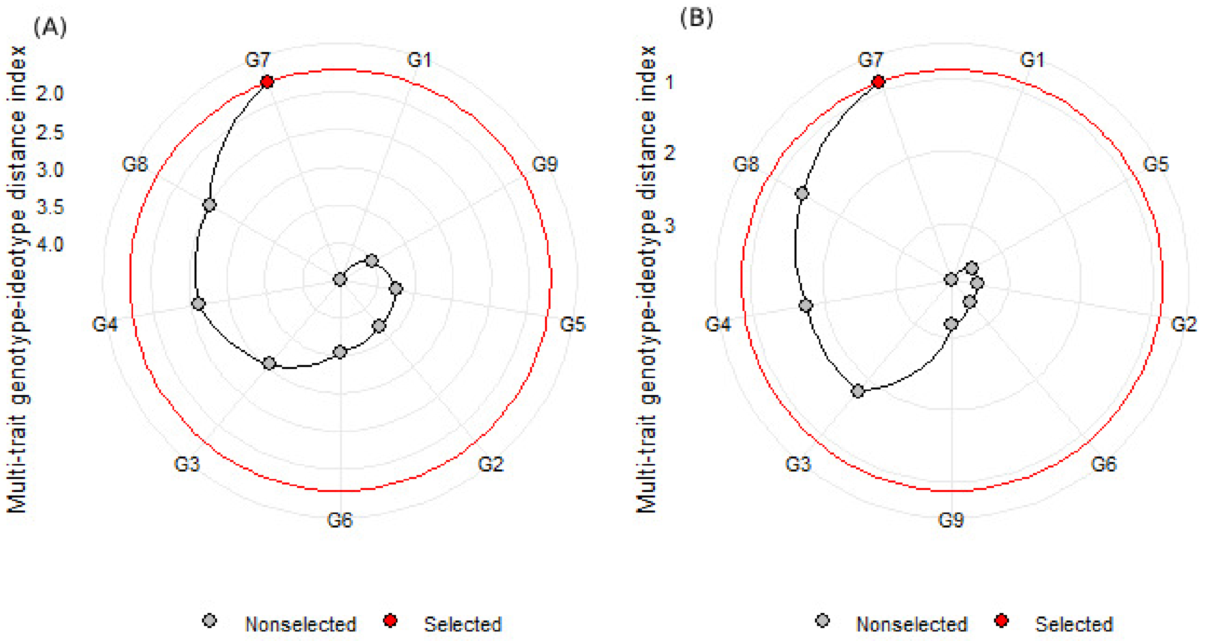

Figure 7. Ranking of genotypes based on the multi-trait genotype–ideotype distance index (MGIDI) for E4 (**A**) and E8 (**B**).

4. Discussion

Plant breeders face a difficult task in developing and identifying genotypes that combine high productivity and stability under a variety of abiotic stressors [69]. Abiotic stressors mainly impact crop productivity and yield due to adverse changes in the surrounding environment [70]. One of the main abiotic factors influencing wheat production and yield globally is drought stress. About 42% of wheat production is impacted by drought stress [71]. Probably the most effective way to reduce the risks associated with abiotic factors is to develop genotypes that are adapted to the widest range of environmental conditions [72]. In the current study, we examined the stability and performance of nine wheat genotypes using ANOVA, AMMI, correlation analysis, and MGIDI in different environments based on ten traits and ten drought tolerance indices.

Our findings revealed that under severe water stress, wheat genotypes showed a significant reduction in RT, RWC, and WD values compared to unstressed plants. Under drought stress, plants have dangerously low water status and transpiration ratios [73]. Drought-tolerant genotypes use water more effectively than sensitive genotypes [74], while sensitive genotypes are unimportant. Wheat utilizes less water when grown under conditions of water shortage than when it is well watered. Better water efficiency is linked to stomatal closure, which decreases transpiration [75], so stomata closure is the primary driver of drought-tolerant genotypes to improve water usage efficiency. The stomata's closure impacts physiological and biochemical activities, including the reduction in leaf water content, chlorophyll quantity, and photosynthesis, while controlling leaf expansion [76]. RWC is regarded as a sign of the water state of a plant, which controls metabolic activity in tissues. Turgor pressure is intimately linked to stomatal closure and cell development; leaf water potential is crucial for plant development and photosynthetic activities [77]. The ability to tolerate mild to severe water stress depends on maintaining the leaf's water potential.

Water stress treatments caused a gradual decrease in the growth, yield, and yield-related traits in all tested genotypes. In this study, all wheat genotypes showed a gradual decrease in plant height with increasing water stress. The reduction in plant height under water stress can be attributed to the decrease in gibberellic acid (GA3), which is necessary for stem elongation and is associated with water deficits [78,79]. Hessini et al. [80] had the same results under drought conditions and stated that the decline in biomass content contributed to a decline in plant height and leaf biomass. Furthermore, the mean values of all characteristics were lower than they would have been in a normal situation due to the drought, and the same patterns were noted for the durum, spring, and winter wheat varieties [81]. Water is essential for all physiological and biochemical processes in plant cells. It is the medium for the stimulation of all cellular functions. It is critical for the plant's ability to divide, expand, and elongate its cells, which increases plant height, biomass, yield, and yield-related traits [9,82].

In this study, yield components of wheat genotypes, including SL, NGS, and GY, decreased with decreasing soil moisture levels (E3, E4, E7, and E8). Such results were obtained by Khakwani et al. [83], who illustrated that six wheat genotypes exposed to different water levels produced a significant decline in yield and yield components. Water scarcity during the development and reproduction stages reduced spike number, floret fertility, and thus grain number [84]. The significant decreases in the number of grains per spike under severe water stress (E3 and E7: 70% AW; E4 and E8: 55% AW) may be due to the water deficit during the booting period. This could be an explanation, as it could affect the flower/spike primordia that form during the stem elongation period [85]. The decrease in the number of grain spikes was caused by the intense competition for assimilates that occurred between plant organs during vegetative development and stem elongation [86].

Water scarcity reduced wheat production and productivity by influencing nutrient uptake, net assimilation, photosynthetic rate, and, ultimately, biomass and productivity [87]. Also, Attia et al. [9] stated that water stress decreased grain filling, grain weight, and grain production in the post-anthesis period. Furthermore, water shortage affects the amount of photo-assimilates needed to fill grains, the sink power needed to absorb them, the time it takes for grains to fill, the maturity of the plant, and the rate of photosynthesis, all of which diminish grain output [85]. In our study, unstressed plants produced higher grain, straw, and grain yields than stressed plants. From the previous literature, it can be concluded that under water stress, the grain yield reduction was mostly due to the decrease in the number of grains per spike [9].

According to Kirigwi et al. [88], the optimal genotype is one that can yield a satisfactory amount when cultivated in stressed environments. In our investigation, all wheat genotypes produced a higher amount of grain when provided with increased soil moisture. Nonetheless, the genotyping analysis revealed notable differences in most of the features under investigation among the three water regimes. The nine genotypes varied based on the traits; therefore, G9 was the best genotype for RT, RWC, and WD traits. G4 displayed the highest value in NGS, whereas G3 had the best genotype for leaf pigments. G7 was the genotype with the highest grain yield, as well as improvements in biological and straw yields. G8 was tolerant of water deficit and produced a moderate amount of grain. The discrepancies in grain yield are attributed to the variances in the wheat genotypes' NGS potential. G7 was ranked first, followed by G6, G5, and G8, based on grain yield estimates for all genotypes examined. The same result was observed by Esmail et al. [89].

The parametric test results are unaffected by the significance of the normality test for sample sizes of 200 or above. In very large samples, we may be unable to check for the presumed normality of the data [90]. According to ANOVA analysis, the main and interaction effects were significant for all traits. The results of our study exhibited that the response of the nine wheat genotypes to water stress is dependent on the intensity of water stress. Panda et al. [91] stated that under water deficiency, wheat growth behavior changed based on the genotypes and growth stage. Related species differ significantly regarding the way they respond to drought stress, even within the same variety and genotype [49,50]. Drought adversely affects wheat cultivars' morphological and physiological characteristics [92], resulting in a 50–90% decrease in wheat yields [2]. The coefficient of variation value was 5.46%, indicating that the experiment has a good degree of precision since this value is less than 10 [93].

Correlations showed that GY was positively associated with all traits but negatively with WD. Therefore, it was used to calculate drought tolerance indicators and interpret the interaction between the environment and genotypes. Correlation analysis between drought tolerance indices was an important method to evaluate drought indices [15]. In this study, the MP, GMP, HM, and STI were significantly correlated with GY for normal irrigation and drought stress levels. The MP, GMP, HM, and STI indices were more effective in selecting genotypes with the highest tolerance. The best indicators are those that exhibit a strong relationship with GY in both stressful and non-stressful circumstances [18]. Moreover, a trustworthy criterion for determining the best cultivars and indices to use is correlation analysis between grain yield and drought tolerance indices [94]. Similar results were reported by Anwaar et al. [95], who found that MP and GMP are better suited for screening for drought tolerance in wheat genotypes with high yields under both drought and normal conditions. Additionally, Talebi et al. [22] stated that YP's significant and positive associations with MP, GMP, and STI suggest that these indices are better at selecting genotypes with high yields in a variety of environmental settings. Abdelghany et al. [96] reported that selecting genotypes depending on STI gave genotypes with high drought tolerance. Based on the analysis of variance for the drought indices, we found that G7 is the best wheat genotype, followed by G6, G5, G8, and G9 in all cases. The same result was reported by Abd El-Aty et al. [97], who reported that G7 and G9, with a high tolerance index (STI), would be more tolerant of drought stress.

The presence of multicollinearity in the data is indicated by the linear correlation between the studied traits. Consequently, depending solely on these traits when multicollinearity is present results in suboptimal selection of the desired genetic traits under various environmental conditions [98]. To solve this issue, some traits must be eliminated, sacrificing some data without understanding the significance of the conclusions and explanations it holds [99]. Thus, using GY as the sole variable, AMMI was used to evaluate the nine genotypes in the eight environments.

In our results, the contribution of environments was found to be greater than the combined effect of E × G and genotypes on total variances, which revealed that the test environments were highly variable [30,71]. The effects of AMMI analysis of variance were significant ($p < 0.01$) for Env, G, and E × G. The significant main effects and interactions show that there is a strong relationship between these factors and grain yields under various soil moisture levels and cultivation seasons. These results align with the findings of [100]. The significance of E × G's impact on performance stability under various conditions makes it a valuable diagnostic tool for evaluating superior genotypes [101]. In this investigation, the multiplicative variance of the treatment sum of squares resulting from interactions revealed the presence of seven significant interaction principal components. The first two PCs accounted for 92.1% of the overall variation, with PC1 contributing 80.6% and PC2 contributing 11.5%. The AMMI1 biplot analysis was used to display the variation resulting from the main effect (grain yield) and IPCA scores [102]. Low interaction effects were exhibited in environments and genotypes that had IPCA1 scores close to zero [103] and were deemed stable [104]. Our findings showed that E3, E7, G1, and G8 secured an IPCA1 value close to zero.

The genotypes are more appropriate and confer a high level of performance and stability in the environment within the same sector. Here, the observed variation in genotype and E × G made it easier to choose the best genotypes for the desired characters. Minimizing the potential environmental component effects is critical [30]. Based on their placement close to the origin, AMMI2 revealed wheat genotypes of G5, G3, and other genotypes that are thought to be the most stable in terms of yield to sectors with the best genotype for near environments: G3 for E4 and E8, G2 for E3 and E7, G9 for E2 and E5, G5, G6, and G7 for E6, and G8 for E1. However, in AMMI, the graphical images are used to answer critical queries about E × G evaluation on a visual basis [105]. AMMI2 was thought to be the most useful analytic pattern to explain the genotypic stability of yield [106]. Since only the first component showed significance, calculating the WAAS values was not effective for comparing the constructs because they would be the absolute values of the loading coefficients on the first component.

Assessing the use of multivariate approaches to the selection of appropriate genotypes that have higher yields under various environmental conditions is an objective of plant breeders [98]. Factor analysis is an introduction to MGIDI, whose results varied from reducing the number of traits studied to three or four factors in each of the eight environments with eigenvalues greater than 1 [67]. The criteria dictated that only factors with eigenvalues greater than 1 were considered in factor analysis, with the value of the variance explained by those factors ranging from 81.5% for E3 to 97.3% for E4. The MGIDI index gave an overview of the advantages and disadvantages of different genotypes, which made it simple to determine both their positive and negative aspects [36]. Although less stable and with poorer performance across environments in different sectors, the genotypes are more appropriate and confer a high level of performance and stability in the environment within the same sector.

By applying the previously mentioned statistical techniques, whether they involve one or more variables, and connecting the outcomes from each statistical technique, we were able to identify three wheat genotypes with desirable performance from our screening for drought tolerance: G7 (Sakha 95), G8 (Shandweel 1), and G3 (Gemmeiza-11).

5. Conclusions

The study's findings suggest that the mechanism by which drought stress manifests itself can vary depending on the genetic composition of the wheat cultivar under investigation. Because of their appropriate agronomic, biochemical, and physiological performance, the G7 genotype can withstand drought up to 55% of the available water (AW), while the G8 and G3 genotypes can withstand droughts up to 70 and 85% of the AW. The maximum yield traits of SL, NGS, GY, and BY were produced by G7, which gave 11.1 cm, 56.5, 3.98 g, and 13.3 g. These genotypes can be grown for commercial use under water-stress conditions. We demonstrated that the MGIDI index can be effective in identifying stable and high-yield genotypes in wheat through multi-environment trials to assess genotypes. Based on all examined traits, this index was used to identify the stable genotypes G7, G8, and G3, which can therefore be suggested for cultivation during drought conditions. Furthermore, we demonstrated a positive correlation between the MGIDI, ANOVA, and tolerance index results, indicating that the same desirable genotypes (G7 and G8) were identified by these procedures as being highly tolerant and stable across different soil moisture conditions. We can conclude that the G7 genotype showed superiority over the other genotypes in the most severe cases of water stress.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agronomy14051029/s1, Table S1. Wheat genotype names and their pedigrees; Table S2. Test statistics and *p*-value for Bartlett's test and Shapiro–Wilk test for ten traits; Table S3. Means of eight environments for studied traits; Table S4. Means of nine genotypes for studied traits; Table S5. *p*-values for genotypes effect for REML/BLUP method of the analyzed traits; Table S6. Eigenvalues, explained variance, and factor loadings after varimax rotation and commonalities obtained in the factor analysis for the traits for eight environments.

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