Multiple Stresses of Wheat in the Detection of Traits and Genotypes of High-Performance and Stability for a Complex Interplay of Environment and Genotypes

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Abstract: The effect of traits and the interaction of genotype × environment (GE) is one of the major challenges in detecting traits and genotypes with outstanding performance and stability through various stresses and years. The objective of this study was to identify the genetic influence traits of wheat, and genotypes with outstanding performance and stability under different environmental stress. The trials were carried out in two consecutive seasons with three treatments (optimal irrigation, limited irrigation, and heat stress), totaling six test environments at two different locations. After observing the importance of GE interaction, and the statistical significance for all studied traits, multivariate analysis was applied using stepwise regression (SR) for detecting influenced traits, and AMMI, AMMI’s stability values (ASV), yield stability index (YSI), superiority and GGE biplot methods to identify the genotype’s phenotypic stability. SR analysis showed that nine out of 22 traits have contributed significantly to grain yield (GY), which varied according to the environment. Equations of the models (GY) regression coefficient values reflected the importance seven of them have on a significant positive correlation on GY. The study confirmed the importance of AMMI and GGE biplots in decoding the GEI based on GY data. AMMI1 biplots showed that the three environments E1, E4, and E6 were the stronger interacting environments than E2, E3, and E5, in which the interaction was weak. YSI, superiority analysis, and superiority multi-trait analysis scores were largely compatible. YSI scores described the six genotypes viz, G5 (DHL26), G12 (DHL29), G10 (DHL01), G18 (Sakha-93), G2 (DHL02) and, G6 (Gemmeiza-9), these were marked by high stability and productivity. The GGE biplot analysis showed genotypes (G15 (Misr1) and G4 (DHL07)) recorded the highest grain yield in E3 and E4, whereas genotype G18 (Sakha-93) was in E6. It also showed G19 (Pavone-76) was the best genotype due to being situated in the center of the concentric circles and due to its high-yield. The methods considered were compatible with the detection of promising wheat genotypes with high mean performance and outstanding phenotypic stability across various stresses and years.

Keywords: multiple stress; multi-trait stability; GGE biplots; AMMI

1. Introduction

The world’s total wheat production was estimated at 772 million tons in 2020, second only to maize. Agricultural productivity is lowered by the degradation, desertification, salinization and contamination of land, and by the increasing shortages and contamination of water resources in the region. Multiple stresses such as high-temperature stress and reduced water availability are serious risks to the Arab region [1,2]. Thereby, threatening the sustainability of grain crop production, which caused devastating economic and sociological impacts [3]. The steady rise in population and loss of agricultural lands to sustainable urbanization with a rapidly, negatively, changing environment, is causing serious threats to
the safe production of wheat [4]. A productivity drop is expected in the coming decades for the biggest crops and impending climate change predicts a disaster for food security. The world’s population is expected to grow to 9.6 billion by 2050, requirements for major cereals such as wheat, rice and maize could become a total of 3.3 billion tons a year. So, levels need to be continually increasing by 2–3% each year to meet the needs of the continuing increase in humanity. The mean temperature is expected to rise by 0.3 °C every 10 years [5,6]. The wheat plant can adjust to temperate climates, so its growth and fertility can be adversely affected by both stresses of high temperature and soil water deficits.

Heat intensity and water deficits significantly influence physiological characteristics, which are directly reflected in flowering, pollination, and grain filling. A decrease in the wheat yield of 15–35% in Africa and Asia and 25–35% in the Middle East has been shown when the temperature went up 3–4 °C from the normal levels during the grain-filling period [2,7,8]. Water deficit stress reduces growth traits (plant height and leaf area) and yield traits (grain weight and grain number) [2,9]. The response of a plant to water deficit constraints and high temperatures is always evaluated independently of each other, but in nature they are inseparable [9–11], altering metabolism and gene expression in different ways from that caused by each stress operating independently [12]. Thus, the best understanding of their combined influence will grow in importance if wheat breeding programs can keep up with developments in climate change [9].

Wheat breeding programs focus on increasing wheat productivity by developing new genotypes that are high-yielding and tolerant to multiple stresses [2]. Therefore, it is important to understand the environmental aspects that affect plant growth. Dehydration stress imposed by drought and temperature severity is the most prevalent abiotic stress that limits plant growth and productivity [9]. Exposure to long periods of high temperatures may lead to dehydration. Also, high temperatures may stimulate osmotic pressure if the water evaporates from the soil, leading to high salt concentrations. This affects wheat on a physiological and molecular level and consequently affects the crop and its components [13]. Abiotic stress also affects the quality and yield of wheat varieties used for the production of both bread and pasta flour.

Evaluation of the genetic parameters for agronomic, physiological and biochemical characteristics is important to determine the best genotypes that can be used in breeding programs for selecting promising lines/varieties of wheat tolerant to multiple abiotic stresses [9,10]. In general, the final target for breeding programs is to improve productivity, quantity, and quality under stress. With this aim, methods for detecting multiple stress tolerance of a large number of genotypes need to be inexpensive, quick, and easily measurable [14–16]. In addition to being marked by genetic stability to multiple stresses, heat and drought tolerance are polygenic traits [2,16]. Large datasets from screening tests require the correct, reliable statistical analyses in order to formulate conclusions concerning tolerant and sensitive genotypes. Multivariate analysis, which uses a set of phenotypic traits with high-powered computer modeling, is a useful tool for identifying sources of genetic variation and discriminating their stress tolerance using multiple accurate selection criteria through combining all characteristics [16,17]. Therefore, screening tests are required for statistical analysis with the capacity to analyze genotypes’ stable performance under multiple stresses. Therefore, multivariate analysis techniques (e.g., multicollinearity, multiple regression, principal component analysis, path analysis, MANOVA, discriminant analysis, AMMI model and GGE biplots) could serve as a useful instrument to identify sources of variation in the tolerance of multiple stresses using multiple selection criteria, that are precise and reliable [15–18].

Genotypes should be stable across environments until widely accepted by farmers [2,18,19]. It is therefore important to develop and broaden the efforts made to get climate-resilient genotypes and rigorously evaluate them at different sites and during different seasons [18,20]. This can be achieved by the efficient pooling of suitable parents with high genetic diversity. Expression of the yield trait and its component are influenced by genotype (G), environment (E), and interactions (GEI), which are affected by a multitude
of factors during the growing season, such as water availability and quality, temperature, and the length of the light period. Therefore, several attempts of GEI are being undertaken through genetic studies in the crop-breeding programs using multiplicative trials [21–24]. GEI in multiplicative trials can be analyzed by the additive main effects and multiplicative interaction (AMMI) model [21] to identify the genotypes that are more appropriate for each environment by collecting and analyzing the phenotypic data of an observed trait and a considerable adaptability to the desired area using analysis of variance (ANOVA). The AMMI model combines ANOVA and PCA in a single analysis [25].

The AMMI model and GGE biplots have been widely used in multi-site trials analysis because they offer more accurate estimates and simpler explanations of the GEI with appealing graphical tools [18]. Researchers have been using the GT (genotype × trait) biplot technique in plant breeding for a long time. However, this method fails to give accurate results for breeders to know which cultivar to recommend, select, or eliminate [26]. At present, the GYT (genotype × yield × trait) biplot technique was developed to overcome the shortcomings of the GT biplot model and enable plant breeders to select more efficient genotypes according to their superiority and genetic stability across evaluations of the yield trait and its components [27]. We applied here the multi-trait stability index (MTSI) aimed at strengthening simultaneous selection of high-performance and stable genotypes in METs depending on both a fixed-effect and a mixed-effect model [17]. It has the advantage of a unique selection process that would enable better stability and mean performance by looking into multi-traits based on positive or negative selection differentials required for a particular trait [18].

Most up-to-date analyses aiming to detect stress tolerances in wheat have focused on individual responses to agents such as high-temperature stress and reduced water availability, although they combine and interact in natural situations [9,28,29]. The present objectives were (1) to determine the individual and combined effects for stresses of high-temperature and water shortage on a range of yield traits influencing wheat, (2) to follow the stability of genotypes and determine the relative contributions of the genotype, environment, and their interaction on influencing yield-related traits of wheat genotypes using the AMMI model and GGE biplots, (3) determine a high-yielding and stable wheat genotype across the sites and a suitable genotype for each site. Achieving these goals could be of great importance in supporting plant breeders and cultivators in choosing the appropriate wheat genotypes for each site.

2. Materials and Methods

2.1. Genotypes and Experimental Design

A total of 20 wheat genotypes (6 varieties and 14 lines, Tables S1 and S2) were evaluated in three treatments (optimal irrigation, limited irrigation and heat stress) for two consecutive seasons. The genotypes were obtained, six varieties from the Agricultural Research Center, Egypt, and 14 DHL from the Agronomy Department, Faculty of Agriculture, Al-Azhar University, Nasr City, Cairo, Egypt [30]. Three treatments in two growing seasons were considered as six environments, the experimental design was randomized complete block [31] in three replicates per environment for 20 genotypes used. Sowing dates were as follows: 15th November (E1, optimal irrigation and E2, limited irrigation) and 20th December (E3, heat stress) in the first growing season (S1, 2018/19), and 17th November (E4, optimal irrigation and E5, limited irrigation) and 25th December (E6, heat stress) in the second growing season (S2, 2019/20). Hand sowing was done in five rows of 3.0 m length per plot and 0.17 m in-row spacing, at the King Saud University Agricultural Research Station (24°42’ N, 44°46’ E, 400 m asl). The seedling rate was 360 kernels m$^{-2}$, and the fertilizing rates used were 0.8 kg m$^{-2}$ P$_2$O$_5$ when preparing land for agriculture and 1.2 kg m$^{-2}$ N with irrigation and applied in three doses. The weather condition data (the amount of precipitation (mm), temperature data as maximum, minimum, and average ($^\circ$C), and relative humidity (RH; %)) are presented in Table 1. The type of texture of soil was sandy loam (56.65% sand, 28.46% silt and 14.89% clay). Two irrigation systems were used
after two weeks of sowing. Full irrigation was used in two environmental regimes (optimal irrigation and heat stress) to 100% field capacity upon reaching a cumulative evaporation of 50 mm, limited irrigation was watered to 33% of field capacity upon reaching a cumulative evaporation of 150 mm. The three environment systems in the two seasons were designated as the main plots, while the subplots were designated to the genotypes used.

Table 1. Monthly agro-climatological data at the experimental location during the growing seasons.

| Months   | Precipitation (mm) | Temperature (°C) | Relative Humidity (%) |
|----------|-------------------|------------------|-----------------------|
|          | S1       | S2       | Maximum | Minimum | Average | S1 | S2       |          |          |
| November | 0.31     | 0.27     | 35.37   | 34.82   | 5.05    | 5.84 | 20.21   | 20.33   | 41.69    | 41.21    |
| December | 0.02     | 0.10     | 27.40   | 27.46   | 4.01    | 4.95 | 15.71   | 16.21   | 45.31    | 44.36    |
| January  | 0.10     | 0.05     | 29.34   | 28.65   | 1.23    | 2.01 | 15.29   | 15.33   | 40.19    | 40.68    |
| February | 0.00     | 0.00     | 33.79   | 32.43   | 1.21    | 2.08 | 17.50   | 17.26   | 28.44    | 29.26    |
| March    | 0.00     | 0.00     | 35.80   | 36.19   | 6.98    | 7.01 | 21.39   | 21.60   | 25.69    | 26.02    |
| April    | 0.98     | 1.02     | 39.91   | 38.63   | 14.13   | 15.11 | 27.02   | 26.87   | 31.50    | 30.24    |
| May      | 0.01     | 0.00     | 42.91   | 41.77   | 19.21   | 19.94 | 31.06   | 30.86   | 17.69    | 17.05    |

S1, Season 2019/2020; S2, Season 2020/2021.

2.2. Measurements and Data Collection

2.2.1. Morpho-Physiological Parameters

The data of fourteen morpho-physiological traits were measured and broken down as follows: three parameters of leaf water status at the flowering stage on the flag leaf (canopy temperature (CT), leaf water content (LWC), and relative water content (RWC)) as described by Al-Ashkar et al. [32]. Four parameters of photosynthesis were measured in the grain-filling stage on the upper third of the flag leaves (net photosynthesis (Pn) rate, transpiration rate (E), stomatal conductance (Gs) and intracellular CO2 concentration (Ci)) using a Li-6400 gas exchange system (Li-Cor, Inc., Lincoln, NE, USA), starting at 10:00 a.m. until 12 noon as described by Al-Ashkar et al. [16]. Four parameters of growth at the mid-anthesis stage were measured (green leaves number (GLN), flag leaf area (FLA), and green leaves area (GLA)) as five plants from the middle rows of each pilot module were selected randomly and area (LI 3100; LI-COR Inc., Lincoln, NE, USA) used to calculate surface FLA and GLA. LAI was calculated by the formula = (leaves area/ground cover) of plant. Three parameters of antioxidants were assessed (peroxidase (POD; U g⁻¹ FW mL⁻¹), polyphenol oxidase (PPO; U g⁻¹ FW mL⁻¹) and catalase (CAT; U g⁻¹ FW mL⁻¹)) on 0.5 g fresh leaf to assess enzyme activity. For extraction the leaf was ground in liquid nitrogen, and placed in an ice bath in 50 mM potassium phosphate buffer (pH 7.8), including 1% (w/v) polyvinylpolypyrrolidone, and then centrifuged at 14,000 rpm for 10 min at 4 °C for enzyme extractions. The supernatant was used as extract for assays of CAT, POD and PPO, as described by Aebi [33], Chance and Maehly [34], and Duckworth and Coleman [35], respectively.

2.2.2. Agronomic and Yield Trait Parameters

The data of ten agronomic traits-seven of them were estimates before harvest (days to heading (DH, days), days to maturity (DM, days), grain filling duration (GFD, days), plant height (PH, cm plant⁻¹), spike length (SL, cm), number of spikes (NS, m⁻²), number of spikelets (NSS, spike⁻¹) and the other three (number of kernels (NKS, spike⁻¹), thousand kernel weight (TKW, g) and grain yield (GY, ton ha⁻¹)) after harvest. The ten traits were measured according to the recommendations explained by Al-Ashkar et al. [16].

2.3. Statistical Analysis

2.3.1. Analysis of Variance

The normality of the ANOVA residuals were checked by running a Shapiro–Wilks test [36] for the data of the six environments which established that the data were normally distributed. Bartlett’s test [37] showed homogeneity of data across the two seasons of the same environment type, but it resulted in heterogeneity for the data of the six environments.
Hence, the data of 24 traits under six test environments (a combination of season, location, and abiotic stress) were analyzed by assuming genotypes were fixed and environments and replications were random factors by the general linear mixed model (GLMM) analysis of variance as follows [18].

\[ Y_{ijk} = \mu + G_i + E_j + R_{k(j)} + GE_{ij} + \alpha_{ijk} \]

where \( Y_{ijk} \) is the phenotypic value of the genotype for the studied trait, \( \mu \) is the overall mean, \( G_i \) is the effect of \( i \)th genotype \((i = 1, 2, \ldots, 20)\), \( E_j \) is the effect of \( j \)th environment \((j = 1, 2, \ldots, 6)\), \( R_{k(j)} \) is the effect of \( k \)th replication \((k = 1, 2, 3)\), \( GE_{ij} \) is interaction effect of \( i \)th genotype with \( j \)th environment, and \( \alpha_{ijk} \) is the residual error and was assumed to be normally and independently distributed.

2.3.2. Stepwise Multiple Linear Regression Analysis (SMLRA)

Data of 22 independent traits from six test environments were subordinated to the SMLRA that was used to determine the most important independent traits that contribute to the most variability in the investigated variable (GY). The twelve predictive relationships were analyzed for the single data per environment, across environments, across years, and across all pooled data.

2.3.3. GEI Analysis

AMMI Analysis

GY data from six test environments were subordinated to the AMMI method that combined analysis of variance (ANOVA) and principal component analysis (PCA) into an integrated approach [18]. The main additive effects of treatments (genotypes and six test environments) were fitted to traditional ANOVA, followed by PCA which explained the non-additive section (GEI, genotype \times \) environment interaction). AMMI analysis was used to identify stable genotypes within each environment [38]. AMMI biplots were established by the main effect of means against the first principal component axis (PCA1) and between PCA1 vs. PCA2. The genotypes were categorized based on AMMI’s stability values (ASV), yield stability index (YSI) and superiority.

ASV was computed using the formula:

\[ \text{ASV} = \sqrt{\left(\frac{\text{PCA}_1 \text{ SS}}{\text{PCA}_2 \text{ SS}} + \text{PCA}_1 \text{ Score}^2\right) + \text{PCA}_2 \text{ Score}^2} \]

(As described by Purchase et al. [39]), where SS is sum of squares, PCA1 is interaction of PCA first axis, PCA2 is interaction of PCA second axis. PCA1 score is the genotype scores of first axis and PCA2 score is of the second axis in AMMI’s model. The larger the PCA score (as absolute value), the greater adapted a genotype is to a specific environment. Lower ASV values point to a genotype more stable in various environments. YSI was computed using the formula:

\[ \text{YSI} = rY + r\text{ASV} \]

(As described by Singamsetti et al. [18]), where \( rY \) is the rank of genotype-based on mean yield and \( r\text{ASV} \) is the rank of genotype-based on AMMI’s stability values.

Superiority scores based on GY trait and/or multi-trait analysis (MTA) were calculated after the data was converted to standard values for each genotype to evaluate the extent to the overall performance different from the mean using the formula:

\[ Z = \frac{(x - \mu)}{\sigma} \]

where \( Z \) is the standard value, \( x \) is the mean grain yield and/or multi-trait of each genotype, \( \mu \) is the overall mean for all the genotypes (for grain yield and/or multi-trait), and \( \sigma \) is the standard deviation (for grain yield and/or multi-trait).
GGE Biplot

GY data from six environments were subordinated to the establishment of GGE biplot using the PCA1 and PCA2 according to the model [18,40,41]. GGE (Genotype Main Effect plus Genotype-Environment Interaction) biplots were establishment based on site regression analysis [18,42]. GGE biplot tools were used to identify highly adaptable wheat genotypes with maximum mean productivity by ‘Mean vs. Stability’ [43]. The average-environment coordinate (AEC) visualization of GGE biplot revealed the maximum mean yielders and stable genotypes and the ‘which-won-where’ pattern, exhibited of the biplot for genotype by environment data set.

2.4. Statistical Software

Combined ANOVA and all the genetic variability parameters for season, location, and abiotic stress were calculated in SAS v9.4 software package (Beijing, China). Univariate plots and SMLRA were carried out in XLSTAT package (vers. 2019.1 Addinssoft, New York, NY, USA) GEI and GGE biplots were carried out in RStudio, R version 4.1.1 (Boston, MA, USA) by using ‘metan’ [44] R packages.

3. Results

3.1. ANOVA and Mean Performances of 20 Genotypes

Combined ANOVA for the six environments considered showed the existence of highly significant differences for the 24 studied traits. Mean sum of squares showed significant variation for the 24 studied traits to sources of three variations (environments, genotypes and GEI) in Table 2. The analysis described the percent variation contributed whole variability (G + E+ GEI), the contribution of environments is higher for CT (75.29) followed by DM (66.84), DFD (56.50), NSP (54.84) and Ci (53.34). Whereas genotype contributed about 78.05% for FLA followed by Pn (77.27%), DH (67.03%), POD (66.07%), CAT (61.99%), NG (57.64%), GLA (52.82%), and GY (51.79%). Contribution of GEI is maximal for PPO (35.04%) followed by POD (33.91%), NL (31.53%) and LWC (31.38%) of the whole variation. GY showed 51.79% variation contributed by genotype whereas 28.05% and 20.04% were contributed by environment and GEI from whole variation, respectively. GY was reported in the range of 3.760 (E6) to 5.426 (E4) t/ha with a mean of 4.539 t/ha. Mean values of all traits studied in two environments (E1 and E3) were greater than the four other environments (E2, E3, E4, and E6), except the CT and Pn traits as shown in the Figure 1. The same applied to maximum values, which were recorded in the E1 and E4 environment, except for the CT, Pn and POD traits, which recorded maximum values under environments of limited irrigation (E2 and E4) and/or heat stress (E3 and E6) as shown in the Figure 2.

3.2. Identification of Traits Associated with Grain Yield

The data obtained from the 22 traits measured were used to identify the traits associated with grain yield under six different environments. The relationships were analyzed using the single data per environment, across environments and across all pooled data for genotypes used in the current study. The stepwise regression analysis was applied to identify the traits which have contributed significantly to grain yield. The results show that nine out of 22 traits have contributed significantly to grain yield, which varied according to the agricultural environment. The FLA had shown a strong correlation in nine cases ($R^2$ ranging from 0.306 in the case of all pooled data to 0.585 in the case of single data per environment, E5), as listed in the partial coefficient of determination (Table 3). The POD had shown a strong correlation in seven cases ($R^2$ ranging from 0.106 in the case of all pooled data to 0.607 in the case of single data per environment, E6). Also, the TKW had shown a significant correlation in seven cases ($R^2$ ranging from 0.018 in the case of pooled data across S1 (E1, E2 and E3) to 0.584 in the case of single data per environment, E4). Both GLA and PH had shown a significant correlation in four cases, and both GFD and Pn had shown a significant correlation in three cases. The four traits POD, FLA, GLA and TKW
were the maximum rates of contribution to grain yield, as listed in the partial coefficient of determination. The $R^2$ cumulative demonstrated a larger contribution in the case of single data per environment (E6, $R^2$ was 0.920) compared to case pooled data across S1 ($R^2$ was 0.818). Equations of the models (GY, Table 4) used to predicate the GY value. Regression coefficient values reflect the importance of the most direct impact of the selected trait on GY. The results showed that seven (DH, GFD, PH, Pn, FLA, GLA, TKW) out of nine traits have a significant positive correlation with GY, while the remaining two traits (POD and LWC), revealed a strong negative correlation with GY, which vary their performance from one agricultural environment to another.

Table 2. Analysis of variance along with their contribution towards total variation for 20 genotypes of wheat for all the traits studied in six test environments.

| S.O.V | Environment (E) | Genotypes (G) | GEI | Error |
|-------|----------------|---------------|-----|-------|
| df    | 5              | 19            | 95  | 238   |
| Traits| Mean Squares   | % (G + E + GEI) Mean Squares | % (G + E + GEI) Mean Squares | % (G + E + GEI) Mean Squares |
| CT    | 94,606 ***     | 75.291        | 3.441 ***  | 10.406 | 0.939 ***  | 14.201 | 0.078   |
| LWC   | 519,504 ***    | 42.010        | 84.017 *** | 25.818 | 20.426 *** | 31.383 | 8.156   |
| RWC   | 1030.553 ***   | 39.732        | 225.212 ***| 32.994 | 35.812 *** | 26.233 | 15.893  |
| Pn    | 24.459 ***     | 12.139        | 40.972 *** | 77.274 | 1.109 ***  | 10.462 | 0.689   |
| Gs    | 0.037 ***      | 39.001        | 0.009 ***  | 35.554 | 0.001 ***  | 25.307 | 0.000   |
| Ci    | 54,819.43 ***  | 53.337        | 8120.35 ***| 30.023 | 793.908 ***| 14.676 | 230.166 |
| E     | 8.444 ***      | 47.235        | 1.333 ***  | 28.326 | 0.229 ***  | 24.386 | 0.031   |
| POD   | 0.000 ***      | 0.016         | 0.009 ***  | 66.068 | 0.001 ***  | 33.912 | 0.000   |
| PPO   | 0.001 ***      | 16.329        | 0.001 ***  | 48.615 | 0.000 ***  | 35.403 | 0.000   |
| CAT   | 0.000 ***      | 8.547         | 0.001 ***  | 63.625 | 0.000 ***  | 27.819 | 0.000   |
| GLN   | 3.093 ***      | 20.737        | 1.855 ***  | 47.235 | 0.248 ***  | 31.529 | 0.064   |
| FLA   | 199.631 ***    | 12.531        | 327.214 ***| 78.048 | 7.824 ***  | 9.331  | 1.169   |
| GLA   | 8783.515 ***   | 30.323        | 4026.602 ***| 52.824 | 253.939 ***| 16.657 | 29.207  |
| LAI   | 87.866 ***     | 56.499        | 9.802 ***  | 23.949 | 1.599 ***  | 19.536 | 0.030   |
| DH    | 357.610 ***    | 30.122        | 206.951 ***| 67.028 | 1.662 *    | 2.705  | 1.204   |
| MD    | 2412.849 ***   | 72.206        | 184.713 ***| 21.005 | 11.877 *** | 6.753  | 1.613   |
| GFD   | 976.502 ***    | 8.444         | 61.481 *** | 15.992 | 13.144 *** | 17.095 | 2.200   |
| PH    | 1064.972 ***   | 12.531        | 48.130.84 ***| 21.392 | 10.648.73 ***| 23.665 | 737.254 |
| SL    | 46.666 ***     | 37.542        | 11.201 *** | 34.241 | 1.835 ***  | 28.054 | 0.210   |
| NSS   | 100.678 ***    | 33.624        | 32.430 *** | 41.157 | 3.871 ***  | 24.565 | 0.405   |
| NGS   | 635.356 ***    | 23.742        | 405.946 ***| 57.643 | 26.121 *** | 18.546 | 3.933   |
| TKW   | 1627.585 ***   | 44.743        | 473.567 ***| 49.470 | 10.918 *** | 5.702  | 3.339   |
| GY    | 28.119 ***     | 28.053        | 13.660 *** | 51.786 | 1.057 ***  | 20.036 | 0.062   |

* and *** indicate significance at $p < 0.05$ and 0.001, respectively, canopy temperature (CT), leaf water content (LWC), relative water content (RWC), net photosynthesis (Pn) rate, stomatal conductance (Gs), intracellular CO2 concentration (Ci), transpiration rate (E), peroxidase (POD), polyphenol oxidase (PPO), catalase (CAT), green leaf number (GLN), flag leaf area (FLA), and green leaf area (GLA), leaf area index (LAI), days to heading (DH), days to maturity (DM), grain filling duration (GFD), plant height (PH), spike length (SL), number of spikes (NS), number of spikelets (NSS), number of kernels (NKS), thousand-kernel weight (TKW), and grain yield (GY).

![Figure 1](Cont.)
Figure 1. Boxplots illustrating the descriptive statistics of 12 measured traits in six environments of 20 genotypes wheat. The plus signs are treatment means, and the horizontal lines dividing the box represent the first quartile (25th percentile), medians and 3rd quartile (75th percentile). The lower and higher whiskers reflect the minimum and maximum values, respectively. The letters denote significant variation between the six environments at 0.01% levels of probability. Units of traits are as follows: canopy temperature (CT), Leaf water content (LWC), relative water content (RWC), net photosynthesis (Pn) rate, stomatal conductance (Gs), intracellular CO2 concentration (Ci), transpiration rate (E), peroxidase (POD), polyphenol oxidase (PPO), catalase (CAT), green leaf number (GLN), flag leaf area (FLA).
Figure 2. Boxplots illustrating the descriptive statistics of 12 measured traits in six environments of 20 genotypes wheat. The plus signs are treatment means, and the horizontal lines dividing the box represent the first quartile (25th percentile), medians and third quartile (75th percentile). The lower and higher whiskers reflect the minimum and maximum values, respectively. The letters denote significant variation between the six environments at 0.01% levels of probability. Units of traits are as follows: and green leaf area (GLA), leaf area index (LAI), days to heading (DH), days to maturity (DM), grain filling duration (GFD), plant height (PH), spike length (SL), number of spikes (NS), number of spikelets (NSS), number of kernels (NKS), thousand-kernel weight (TKW), and grain yield (GY).
Table 3. Stepwise regression analysis for grain yield (dependent variable) with 22 traits (independent variables) for the single data per environment, across environments, and across all pooled data.

| Environments | No. of Variables | Variables | Variable IN/OUT | $R^2$ | $R^2$ Com. | Pr > F  |
|--------------|------------------|-----------|-----------------|-------|------------|---------|
| E1           | 1                | TKW       | TKW             | 0.584 | 0.584      | <0.0001 |
|              | 2                | GLA/TKW   | GLA             | 0.265 | 0.850      | <0.0001 |
| E2           | 1                | FLA       | FLA             | 0.466 | 0.466      | <0.0001 |
|              | 2                | FLA/POD   | POD             | 0.433 | 0.899      | <0.0001 |
| E3           | 1                | FLA       | FLA             | 0.506 | 0.506      | <0.0001 |
|              | 2                | PH/FLA    | PH              | 0.199 | 0.705      | <0.0001 |
|              | 3                | PH/FLA/TKW| TKW             | 0.149 | 0.853      | <0.0001 |
|              | 4                | PH/FLA/TKW/Pn| Pn        | 0.034 | 0.888      |         |
| E4           | 1                | GLA       | GLA             | 0.540 | 0.540      | <0.0001 |
|              | 2                | GLA/TKW   | TKW             | 0.301 | 0.841      | <0.0001 |
| E5           | 1                | FLA       | FLA             | 0.585 | 0.585      | <0.0001 |
|              | 2                | FLA/POD   | POD             | 0.279 | 0.863      | <0.0001 |
| E6           | 1                | POD       | POD             | 0.607 | 0.607      | <0.0001 |
|              | 2                | FLA/POD   | POD             | 0.313 | 0.920      | <0.0001 |
| pooled data (E3 and E6) | 1        | FLA       | FLA             | 0.462 | 0.462      | 0.001   |
|              | 2                | FLA/Pn    | Pn              | 0.272 | 0.734      | <0.0001 |
|              | 3                | FLA/Pn/POD| POD             | 0.225 | 0.859      | <0.0001 |
|              | 4                | PH/FLA/Pn/POD| PH        | 0.014 | 0.873      | <0.0001 |
| pooled data (E2 and E5) | 1        | FLA       | FLA             | 0.515 | 0.515      | <0.0001 |
|              | 2                | FLA/POD   | POD             | 0.369 | 0.884      | <0.0001 |
| pooled data (E1 and E4) | 1        | GLA       | GLA             | 0.506 | 0.506      | <0.0001 |
|              | 2                | GLA/TKW   | TKW             | 0.338 | 0.844      | <0.0001 |
| pooled data (S1) | 1        | FLA       | FLA             | 0.427 | 0.427      | 0.000   |
|              | 2                | GFD/FLA   | GFD             | 0.144 | 0.571      | <0.0001 |
|              | 3                | GFD/FLA/GLA| GLA          | 0.111 | 0.682      | <0.0001 |
|              | 4                | GFD/FLA/GLA/LWC| LWC     | 0.110 | 0.792      | 0.005   |
|              | 5                | GFD/FLA/GLA/LWC/TKW| TKW   | 0.018 | 0.810      | 0.002   |
|              | 6                | DH/GFD/FLA/GLA/LWC/TKW/DH| DH   | 0.008 | 0.818      | 0.000   |
| pooled data (S2) | 1        | FLA       | FLA             | 0.309 | 0.309      | <0.0001 |
|              | 2                | GFD/FLA/POD| POD          | 0.228 | 0.537      | <0.0001 |
|              | 3                | GFD/FLA/POD/GFD| GFD    | 0.143 | 0.680      | <0.0001 |
|              | 4                | GFD/PH/FLA/POD| PH     | 0.116 | 0.796      | 0.002   |
|              | 5                | GFD/PH/FLA/POD/Pn/TKW| Pn  | 0.039 | 0.835      | <0.0001 |
|              | 6                | GFD/PH/FLA/TKW/Pn/POD/TKW| TKW | 0.029 | 0.864      | <0.0001 |
| All pooled data (S1 and S2) | 1        | FLA       | FLA             | 0.306 | 0.306      | <0.0001 |
|              | 2                | GFD/FLA   | GFD             | 0.201 | 0.507      | <0.0001 |
|              | 3                | GFD/PH/FLA| PH              | 0.121 | 0.628      | 0.019   |
|              | 4                | GFD/PH/FLA/POD| POD        | 0.106 | 0.734      | <0.0001 |
|              | 5                | GFD/PH/FLA/TKW/POD| TKW    | 0.035 | 0.769      | 0.002   |
|              | 6                | DH/GFD/PH/FLA/TKW/POD/DH| DH  | 0.029 | 0.798      | <0.0001 |
|              | 7                | DH/GFD/PH/FLA/TKW/POD/LWC| LWC | 0.023 | 0.821      | <0.0001 |

Leaf water content (LWC), net photosynthesis (Pn) rate, peroxidase (POD), flag leaf area (FLA), and green leaf area (GLA), days to heading (DH), grain filling duration (GFD), plant height (PH) and thousand-kernel weight (TKW), coefficient partial determination ($R^2$ Par.), cumulative coefficient determination ($R^2$ Com.).


Table 4. Selection of the most influential traits for predicted grain yield (GY) based on stepwise multiple linear regression analysis.

| Environments | Equation |
|--------------|----------|
| E1           | GY = −2.636 + 0.034 × GLA + 0.102 × TKW |
| E2           | GY = −1.586 + 0.035 × GLA + 0.085 × TKW |
| E3           | GY = 1.504 + 0.1394 × FLA + 12.3144 × POD |
| E4           | GY = 1.575 + 0.140 × FLA + 12.244 × POD |
| E5           | GY = −1.420 + 0.380 × PH + 0.131 × FLA − 0.040 × TKW + 0.1891 × Pn |
| E6           | GY = 0.810 + 0.124 × FLA + 49.752 × POD |
| pooled data (E3 and E6) | GY = −2.275 + 0.034 × GLA + 0.094 × TKW |
| pooled data (E2 and E5) | GY = 1.490 + 0.143 × FLA + 12.094 × POD |
| pooled data (E1 and E4) | GY = −1.698 + 0.017 × PH + 0.128 × FLA + 0.234 × Pn − 18.686 × POD |
| pooled data (S1) | GY = −3.110 + 0.036 × DH + 0.080 × GFD + 0.150 × FLA + 0.006 × GLA − 0.031 × LWC + 0.028 × TKW |
| pooled data (S2) | GY = −2.431 + 0.024 × GFD + 0.015 × PH + 0.146 × FLA + 0.022 × TKW + 0.074 × Pn + 9.121 × POD |
| All pooled data (S1 and S2) | GY = −3.265 + 0.034 × DH + 0.031 × GFD + 0.009 × PH + 0.145 × FLA − 0.013 × LWC + 0.028 × TKW + 6.115 × POD |

Leaf water content (LWC), net photosynthesis (Pn) rate, peroxidase (POD), flag leaf area (FLA), and green leaf area (GLA), days to heading (DH), grain filling duration (GFD), plant height (PH) and thousand-kernel weight (TKW).

3.3. GEI Analysis

The AMMI analysis of variance for grain yield (t/ha) of 20 wheat genotypes was evaluated in six environments (Table 5). The analysis demonstrated that wheat was significantly (p < 0.001) strongly influenced by environments (E), genotypes (G) and GEI. Genotypes alone contributed about 50.30% of the total variation due to treatments (G + E + GEI), and the remainder from total variation was 27.25% and 19.46%, which was contributed by environment effects and GEI, respectively. Analysis revealed significant differences between genotypes across the six agricultural environments. Mean performance variation significance of all the traits, including grain yields, and classification of genotypes across environments indicate that the GEI was a crossover type (Figure 3). The implementation of the AMMI model for the splitting of GEI stated that the first four interaction principal component axes (IPCA) of AMMI were highly significant (p < 0.001) using an approximate F-statistic [45]. The results showed that the first two (IPCA1 and IPCA2) explained multiple factors about 48.71% and 40.64% of GEI total variation, respectively. Whereas the third and fourth (IPCA3 and IPCA4) explained about 6.28% and 4.28% of GEI total variation, respectively (Table 5).

Table 5. AMMI analysis of variance for grain yield among 20 genotypes across six test environments.

| Source                  | df  | SS     | MS   | F-Value | Total Variation Explained (%) |
|-------------------------|-----|--------|------|---------|------------------------------|
| Total                   | 359 | 515.90 | 1.437|         | 97.034                       |
| Treatments              | 119 | 500.60 | 4.206| 67.18 ***| 50.300                       |
| Genotypes               | 19  | 259.50 | 13.660|218.17 ***| 27.253                       |
| Environments            | 5   | 140.60 | 28.119|310.94 ***| 19.461                       |
| Block                   | 12  | 1.10   | 0.090| 1.44 ns | 0.213                        |
| Interactions            | 95  | 100.40 | 1.057| 16.88 ***| 0.010                        |
| IPCA [1]                | 23  | 48.70  | 2.117| 33.8 *** | 0.010                        |
| IPCA [2]                | 21  | 41.00  | 1.952| 31.18 ***| 0.010                        |
| IPCA [3]                | 19  | 6.30   | 0.334| 5.33 *** | 0.010                        |
| IPCA [4]                | 17  | 4.30   | 0.235| 4.07 *** | 0.010                        |
| Residuals               | 15  | 0.10   | 0.004| 0.07 ns | 0.010                        |
| Error                   | 228 | 14.30  | 0.063|         | 0.010                        |

df—Degrees of freedom, SS—Sum of squares, MSS—Mean sum of squares, *** Significant at 0.001, ns—no significant.
Figure 3. AMMI1 Biplot (mean grain yield vs. IPC1) for grain yield (t/ha) of 20 wheat genotypes and six environments. The genotype (G) code was indicated according to Table 6.

3.4. AMMI Biplot

Yield potential of the 20 wheat genotypes used, stability levels and agricultural environments were visually represented by AMMI biplots. AMMI stability shows the relationship between wheat genotypes under adverse abiotic stress environments in grain yield vs. IPC1 scores i.e., AMMI1 (Figure 3). The environments E1, E4 and E6 are far from the origin with longer vectors, which indicate the interaction force, but the environments E2, E3 and E5 are close to the center with shorter vectors which indicates a weak interaction. Genotype viz., G17 (DHL23) followed by G10 (DHL01), G15 (Misr1), G18 (Sakha-93) and G8 (KSU106) showed higher grain yield than overall mean yield. Genotypes such as G2 (DHL02), G15 (Misr1), G19 (Pavone-76), G6 (Gemmeiza-9) and G20 (DHL08) are placed nearer to origin; Those that can be widely adopted or insensitive to the environments with a productive capacity near to the overall mean yield. The AMMI2 biplot, constructed between the first two (IPCA1 and IPCA2) explained 89.43% of GEI, which IPCA1 and IPCA2 contributed 48.70% and 40.64% of the total variation, respectively (Figure 4). In the polygon view form, dotted lines connected with the apex six genotypes that are shown maximum or minimum for GY with concrete adaptation to the agricultural environment. A vertical projection from the genotype to the environmental vector detected the volume of interaction with the specific environment. The plot showed that six genotypes (G4 (DHL07), G17 (DHL23), G20 (DHL08), G9 (Gemmeiza-12), G19 (Pavone-76), G15 (Misr1)) are with higher or lower GY and have unstable average performance across the agricultural environments.
Table 6. Mean grain yield (t/ha), AMMI stability values (ASV), superiority, and ranking orders of the 20 wheat genotypes tested across six environments.

| Genotypes      | Gm  | Score (A) | IPCAg [1] | Score [1] | IPCAg [2] | Score [2] | ASV  | Score (B) | YSI (A + B) | Superiority |
|----------------|-----|-----------|-----------|-----------|-----------|-----------|------|-----------|-------------|-------------|
| DHL12 (G1)     | 3.232 | 20 | 0.275 | 10 | 0.014 | 3 | 11.583 | 3 | 23 | 2.273 | 20 | 0.771 | 12 |
| DHL02 (G2)     | 4.660 | 10 | −0.036 | 3 | 0.407 | 13 | 13.658 | 5 | 15 | 0.908 | 9 | 0.706 | 10 |
| DHL25 (G3)     | 4.005 | 15 | 0.283 | 11 | 0.330 | 10 | 15.765 | 8 | 23 | 1.460 | 15 | 0.983 | 19 |
| DHL07 (G4)     | 5.997 | 2 | −0.683 | 17 | 0.798 | 19 | 26.302 | 19 | 21 | 0.040 | 1 | 0.362 | 1 |
| DHL26 (G5)     | 4.869 | 6 | 0.015 | 1 | −0.395 | 11 | 11.215 | 2 | 8 | 0.819 | 5 | 0.637 | 5 |
| Gemmeiza-9 (G6)| 4.459 | 11 | −0.233 | 9 | −0.233 | 7 | 12.861 | 4 | 15 | 1.076 | 11 | 0.543 | 2 |
| DHL11 (G7)     | 3.922 | 16 | 0.513 | 15 | −0.274 | 8 | 18.057 | 14 | 30 | 1.621 | 17 | 0.638 | 6 |
| KSU106 (G8)    | 4.841 | 7 | 0.403 | 14 | −0.306 | 9 | 17.654 | 11 | 18 | 0.879 | 8 | 0.657 | 9 |
| Gemmeiza-12 (G9)| 4.885 | 5 | 0.020 | 2 | −0.644 | 18 | 18.280 | 15 | 20 | 0.849 | 7 | 1.007 | 20 |
| DHL01 (G10)    | 5.087 | 4 | 0.620 | 16 | 0.006 | 2 | 17.304 | 10 | 14 | 0.728 | 4 | 0.945 | 18 |
| DHL14 (G11)    | 3.870 | 17 | 0.348 | 13 | 0.408 | 14 | 19.932 | 17 | 34 | 1.592 | 16 | 0.804 | 14 |
| DHL29 (G12)    | 4.318 | 12 | −0.133 | 8 | −0.176 | 5 | 10.460 | 1 | 13 | 1.183 | 12 | 0.543 | 3 |
| DHL15 (G13)    | 4.213 | 14 | −0.345 | 12 | 0.223 | 6 | 14.489 | 7 | 21 | 1.245 | 14 | 0.548 | 4 |
| DHL06 (G14)    | 3.684 | 18 | −0.081 | 5 | 0.446 | 15 | 16.226 | 9 | 27 | 1.734 | 18 | 0.877 | 16 |
| Misir1 (G15)   | 4.83 | 8 | −1.073 | 20 | 0.004 | 1 | 21.211 | 18 | 26 | 0.832 | 6 | 0.901 | 17 |
| DHL05 (G16)    | 4.23 | 13 | −0.046 | 4 | 0.489 | 17 | 17.774 | 12 | 25 | 1.227 | 13 | 0.808 | 15 |
| DHL23 (G17)    | 3.37 | 19 | 0.090 | 6 | 0.405 | 12 | 13.988 | 6 | 25 | 2.082 | 19 | 0.789 | 13 |
| Sakha-93 (G18) | 6.04 | 1 | 0.092 | 7 | −0.452 | 16 | 17.973 | 13 | 14 | 0.252 | 2 | 0.641 | 7 |
| Pavone-76 (G19)| 5.49 | 3 | −0.758 | 19 | −0.964 | 20 | 28.417 | 20 | 23 | 0.541 | 3 | 0.653 | 8 |
| DHL08 (G20)    | 4.79 | 9 | 0.728 | 18 | −0.087 | 4 | 19.600 | 16 | 25 | 0.940 | 10 | 0.713 | 11 |
Figure 4. AMMI2 Biplot (IPC1 vs. IPC2) for grain yield (t/ha) of 20 wheat genotypes evaluated across six environments. The genotype (G) code is indicated according to Table 6.

The yield stability index (YSI) was calculated, which combines statistics of AMMI’s stability values (IPCA1 and IPCA2) and mean GY to identify and categorize the genotypes (Table 6). Lower YSI scores describe the genotypes which have high stability and productivity. According to YSI, genotypes viz, G5 (DHL26, YSI = 8), G12 (DHL29, YSI = 13), G10 (DHL01) and G18 (Sakha-93) (YSI = 14), G2 (DHL02) and G6 (Gemmeiza-9) (YSI = 15) were selected as top genotypes with high stability and productivity (Table 6). Also revealed were the genotypes viz, G7 (DHL11, YSI = 30) and G11 (DHL14, YSI = 34) with low stability and productivity. Superiority analysis scores for GY were very much compatible with YSI scores (this was at 7 out 20 genotypes), and two of them were identical (G10 (DHL01) and G14 (DHL06)). Superiority multi-trait analysis scores (SMTAS) for the combined nine traits showed eight genotypes only were compatible with superiority scores for GY.

3.5. GGE Biplots

The polygon view of the 20 genotypes and the six environments in the GGE biplot is shown in Figure 5. The first two (IPCA1 and IPCA2) scores were significant and explained 74.85% and 12.30%, respectively, of GEI total variation (together they explained 87.15%). The polygon view of the GGE biplot displayed the “which-won-where” pattern (Figure 5). The corners of the polygon were the genotype markers situated far away from the biplot origin in different directions, which made all genotypes within the resulting polygon. The GGE biplot was divided into eight sectors, and two environments; one was a mega-environment (it’s been able to cover five environments (E1, E2, E3, E4 and E5) and the another was a small environment (E6). The biplot showed eight vertex genotypes (G1 (DHL12), G4 (DHL07), G7 (DHL11), G14 (DHL06), G15 (Misr1), G17 (DHL23), G18 (Sakha-93) and G20 (DHL08)). The plot showed that genotypes (G15 (Misr1) and G4 (DHL07)) recorded the highest grain yield in E3 and E4 whereas genotype G18 (Sakha-93) was in E6. No environment fell within the sector with (G1 (DHL12), G7 (DHL11), G14 (DHL06), G17 (DHL23) and G20 (DHL08)), indicating that these genotypes were not the best in any of the mega-environments, or they were the poorest genotypes in some or all of the environments. Genotypes within the polygon were less suited than the vertex
genotypes. Genotypes located near to the origin of the polygon such as, G5 (DHL26), G6 (Gemmeiza-9) and G12 (DHL29) were more adaptable to low-productivity locations as opposed to the genotypes situated at the vertex.

Figure 5. A “which won where” biplot based on grain yield of 20 wheat genotypes evaluated in six environments. The genotype (G) code is indicated according to Table 6.

Genotypes were categorized based on both mean GY and stability performance of the genotypes used, with a view to identifying high stability and productivity genotypes (Figures 6 and 7). Genotypes that are situated in the center of the united concentric circles are the ideal (highest stability and productivity). The AEC (average environment coordination) abscissa (represented by single-arrowed line) indicated a higher yield across the environments (Figure 6). Thus, genotype G4 (DHL07) had a higher yield across environments followed by G19 (Pavone-76), while G1 (DHL12) and G7 (DHL11) recorded the lowest yields. A line perpendicular to the AEC, AEC ordinate, pointed towards greater variability (lower stability) in the two directions. Thus, genotypes G2 (DHL02), G6 (Gemmeiza-9) and G20 (DHL08) showed more variability i.e., highly unstable, whereas genotypes G19 (Pavone-76), G5 (DHL26) and G3 (DHL25) were more stable.

The GGE biplot identified G19 (Pavone-76) as superior, since they were situated in the center of the concentric circles and had the highest productivity and therefore the most perfect genotype. The GGE biplot established genotypes (G5 (DHL26), G9 (Gemmeiza-12) and G10 (DHL01)) as superior since they were situated close to the center of the concentric circles. Both had high productivity but G4 (DHL07) had the highest productivity and therefore the most perfect genotype after G19 (Pavone-76) genotype. These genotypes were followed by the G8 (KSU106) genotype (Figure 6). Ten genotypes (G1 (DHL12), G3 (DHL25), G6 (Gemmeiza-9), G7 (DHL11), G11 (DHL14), G12 (DHL29), G13 (DHL15), G14 (DHL06), G16 (DHL05) and G17 (DHL23)) were situated far from the vertical axis at the left and far from the center of the concentric circle, therefore they were more degraded genotypes in terms of both stability and productivity.
Figure 6. The “mean vs. stability” view showing 20 wheat genotypes’ mean performance and stability across six test environments. The genotype (G) code is indicated according to Table 6.

Figure 7. The discrimination and representativeness view of the GGE biplot for 20 wheat genotypes evaluated across six test environments. The genotype (G) code is indicated according to Table 6.
4. Discussion

The wheat cereal crop in the agroecosystem completes its life cycle subjected to multiple fluctuations of abiotic stress conditions, i.e., water deficiency and high temperatures within the same growing season. The majority of the wheat mega environment is in the Asian tropical waterfalls, especially in the Arab region, which is a rainfed environment particularly affected by climate change. The GEI complexity requires the use of an appropriate statistical tool to identify adaptable and stable genotypes to disseminate stress-resilient wheat genotypes in a particular environment. The difference was statistically significant among evaluated genotypes across the water deficiency and high-temperature environments and provides the possibility of choosing genotypes suitable and preferred in both stressed and non-stressed environments. Different levels of grain yield reduction under stressed conditions compared to non-stressed depended on the severity of stress to which the wheat genotype had been subjected, especially in the critical times of its life [18,23,46]. A review of many previous studies reported significant differences among wheat genotypes that were assessed under poor stress conditions for grain yield [23,47,48].

Combined analysis of variance across the six environments showed that six traits (MD, GFD, NSP, LAI, CT and Ci) showed >50% variation contributed by six environments (Table 2). The maximum part of the variance was contributed by genotypes (>50%) for nine traits (DH, PH, FLA, GLA, NG, Pn, POD, CAT and GY). The maximum part of the variance contributed by GEI (>30%) for the four traits (NL, LWC, POD and PPO), and selection of these traits across the environments would bring benefits as a result of being affected by the environmental stress type on the trait’s expression, as is evident from mean values and range across the six environments. The box plots indicated that mean values were lower for most traits under abiotic stress conditions compared to optimized growth conditions (Figures 1 and 2), resulting in lower productivity to GY as expected, whereas the high-value CT trait, which acts by cooling leaves because the association is negative between temperature and transpirational cooling of the leaf. Genotypes tolerant for abiotic stress are capable of lower CT, gas exchange and transpiration compared to other genotypes living under the same abiotic stress [16,49]. Some limited exceptions in the box plots of tested traits were probably the result of conflicting expressions because of the type or severity of stress and/or interaction of genotype with it (Figures 1 and 2). In general, adverse environmental conditions and biotic stress conditions (lack of water and high temperatures) work to accelerate wheat crop maturity, and hence survival through tolerance. This has caused a lot of damage to grain yield and reduced productivity depends on the growing stage of the plant, especially critical periods of life, and the duration of the stress period [16,50]. The variation in plant traits as yield components, leaf water status, photosynthetic and morphological measures, reflect integrating many critical processes on the whole plant or through different phases of the life cycle, some reflect radiation use efficiency, plant competition, photosynthesis and evaporation/transpiration rates, and transpiration capacity and the status of crop growth under biotic stress conditions [16,51,52].

In this study, we conducted a SMLR analysis of each environment individually and combined, with a view to searching for all traits that affect GY under all biotic stress conditions (Table 3). We have completed this, after multicollinearity analysis, which excluded the DM trait (VIF > 10). SMLR is a more proactive instrument for understanding explanatory traits and influences on yield [2,16]. Using simple correlation without the need for the interactions between explanatory traits of yield does not achieve successful breeding programs [15,16]. The results show that nine (DH, GFD, PH, Pn, FLA, GLA, TKW, POD and LWC) out of 22 traits have contributed significantly to grain yield, which varied according to the environment of agriculture. R² values ranged from 0.818 (across S1 combined) to 0.920 (E6). Four traits (POD, FLA, TAFLA and TKW) out of nine selected, showed strong contributions, which varied according to the environment of agriculture. The regression coefficients path reflected the importance of the selected traits. The results showed that seven (DH, GFD, PH, Pn, FLA, GLA, TKW) out of nine traits have a positive path, while the POD and LWC traits have a negative path on grain yield (Table 4). Thus, knowing the
most important traits of the yield components that help to achieve higher yield potential under biotic stress conditions would improve the screening. Therefore, the knowledge of the effects of biotic stress conditions on the physiological and metabolic processes of the wheat plant would allow the researchers to breed promising genotypes for biotic stress tolerance. However, complexities of GEI, breeding programs focused on yield as a selection criterion [16,52].

Significant differences between environment, genotype and GEI highlighted that each of the six environments was markedly different from one another. Significant GEI in combination with combined ANOVA and IPCs from AMMI and GGE biplot results, suggests cross-reaction which led to a comprehensive response and classification of the genotypes during the different biotic stress conditions (Table 5). According to biplot results, genotypes such as G1 (DHL12), G4 (DHL07), G15 (Misr1), G16 (DHL05) and, G17 (DHL23) placed farther from the biplot origin revealed robust interaction with some environments in both directions (positive and negative) from IPCA1 scores (Figure 3). These genotypes are extremely environment sensitive, require unique circumstances, and have comparable grain yield, which suggests differences among the genotypes in response to various environmental conditions. Also, genotypes such as G2 (DHL12), G5 (DHL26), G9 (Gemmeiza-12), G12 (DHL29) and G15 (Misr1) placed close to the biplot origin with IPCA1 score nearer to zero, were considered as environmentally insensitive genotypes with mean yield across different biotic stress conditions [18,53]. AMMI1 biplot clearly described that the effect of the environments was more than that of genotypes, where it had long vectors of the three environments (E1, E4 and E6) but most of the genotypes scattered around the origin [23,48]. The obtuse angle of vectors optimal conditions (E1 and E4) with E2 and E5 and E6 points out the negative association between them, whereas the 90-degree angle between E6 with E2 and E5 points out the absence of any association between them. A vertical projection from the genotype to the environmental vector detected the volume of interaction with the specific environment. The plot showed that six genotypes (G4 (DHL07), G17 (DHL23), G20 (DHL08), G9 (Gemmeiza-12), G19 (Pavone-76), G15 (Misr1)) have a higher or lower GY and an unstable average performance across the agricultural environments (Figure 4).

The stability ranking of genotypes based on lower absolute (IPCA1 and IPCA2) scores, and mean GY identifies and categorizes the genotypes (Table 6), as reported by [18,54]. YSI was used to identify desired genotypes under different biotic stresses, and optimal conditions, and they had high productivity and stability. According to YSI, genotypes viz., G5 (DHL26, YSI = 8), G12 (DHL29, YSI = 13), G10 (DHL01) and G18 (Sakha-93) (YSI = 14), G2 (DHL02) and G6 (Gemmeiza-9) (YSI = 15) were selected as top genotypes with high stability and productivity (Table 4). The term superiority is used to refer to the test of non-equality, which would help prove establishing superiority of one genotype over another [55–57]. Superiority analysis scores for GY were very much compatible (this was 7 out 20 genotypes), and two of them were identical (G10 (DHL01) and G14 (DHL06)). Superiority multi-trait analysis scores (SMTAS) for the combined nine traits showed eight out of 20 genotypes were largely compatible with superiority scores for GY. Two genotypes were fully conforming (G4 (DHL07) and G5 (DHL26)), three genotypes [G2 (DHL02), G8 (KSU106) and G20 (DHL08)] deviated by one value (+ or −) and three genotypes (G11(DHL14), G14 (DHL06) and G16 (DHL05)) deviated by two values (+ or −).

The GGE biplots for GY explained the potential benefit of assessing the genotypes under the different abiotic stress conditions. Differences in abiotic stress environments and genetic variation of genotypes together are instrumental in arriving at the genotypes suitable for the abiotic stress and the seasons. So, it is a useful instrument for wheat breeders to identify high-yielding and stable genotypes under different abiotic stresses at once, by considering the genotype and the level of its interaction with environment. The presumably desirable wheat genotypes that had high (IPC1) and low (IPC2) values, can be readily selected through GGE biplot analysis. In the present study, the IPC1 (48.70%) and IPC2 (40.60%) explained multiplicative factors (nearly 89% of total variation) from
GEI in the AMMI analysis, whereas 87.23% was in the GGE biplot analysis, which means that IPC1 (74.85%) was higher than IPC2 (12.30%). A total of 60.0% contribution recorded GEI by IPC1 and IPC2 was reported by [18] in maize hybrids across moisture regimes in India; 96.0% recorded by [23] of wheat yield suitable for selection in different seed priming conditions in Serbia; 73.00% recorded by [58] of performance and stability of commercial wheat cultivars under terminal heat stress in Egypt. While more than 74.00% contribution recorded GGE biplot by [18,58]; 51.0% recorded by [59] of yield stability of maize single cross hybrids developed from tropical inbred lines in Cameroon. High yielding genotypes under the different abiotic stress conditions and non-stress conditions with high stability across the seasons were seen, which shows that some genotypes might be relatively high yield under optimal and abiotic stress (heat and drought) environments.

Thus, a particular rearing procedure could be created to further develop genotypes with stable execution across various abiotic stress conditions or genotypes with explicit variation to a specific climate. There was compatibility with the previous reports to many scholars [17,18,23,59], who explained the general variation of a specific genotype and contrasted it with different genotypes across so many different environments by GGE biplots (Figure 5). The polygon view of the GGE biplot, ‘Which-won-where’ pattern of information is important in the division of the environments into mega-environments for recommending appropriate and stable genotypes for different mega-environments [18,60,61]. The biplot for 20 genotypes was divided into eight sectors, and two environments- one mega-environment (it’s been able to cover five environments (E1, E2, E3, E4, and E5)) and the other was a small environment; different genotypes should be chosen and deployed to similar environments [62]. A mega-environment is defined as a subset of sites that consistently share the best set of genotypes over the years and the growing sites are rather homogenous with different stresses (biotic and abiotic) and cropping systems [63]. In the polygon view, the peak genotype per sector constitutes the more productive genotype in the environment that falls under that concerned sector [41,59,62]. Accordingly, the biplot showed eight peak genotypes (G1 (DHL12), G7 (DHL11), G14 (DHL06), G17 (DHL23), G20 (DHL08)). The mega-environment determined by the GGE biplot covered both optimum (E1 and E4), drought (E2 and E5) and heat (E3). This suggests that years may have not accounted for environmental differences and different genotypic responses [59,62]. While the environment of heat (E6) was completely separated (Figure 5). This is probably due to a similar difference in the amount and distribution of heat as well as abiotic stresses during each season of each year [59], which might have caused the 20 genotypes to have a relatively similar performance from one environment to another. Yan and Tinker [41] pointed out that the ideal genotype must combine both the performance of high yield and high stability across different environments; it must be on ACE on positive direction and with a vector length equal to the longest vector of the genotype as shown by an arrow indicating it. Accordingly, the GGE biplot determined G4 (DHL07) and G19 (Pavone-76) as closest to the promising genotype, and therefore ideal. In the selection process for broad adaptation to abiotic stresses in wheat production, the promising or ideal genotype must-have high performance and high-stability (Figures 6 and 7). So, G4 (DHL07) and G19 (Pavone-76) which were high-performance and high-stability genotypes across abiotic stresses environments should be selected.

5. Conclusions
SR analysis showed that nine out of 22 traits have contributed significantly to GY, which varied according to the environment. Equations of the models (GY) of regression coefficient values reflected the importance seven of them that have a significant positive correlation with GY. This study confirmed the importance of AMMI and GGE biplots in decoding the GEI based on GY data. AMMI1 biplots showed that the three environments E1, E4 and E6 were more forceful interactions than the environments E2, E3, and E5, where the was interaction weak. YSI, superiority analysis, and superiority multi-trait analysis scores were largely compatible. YSI scores described the six genotypes viz, G5 (DHL26),
G12 (DHL29), G10 (DHL01), G18 (Sakha-93), G2 (DHL02) and G6 (Gemmeiza-9), these were marked by high stability and productivity. The GGE biplot analysis showed genotypes (G15 (Misr1) and G4 (DHL07)) recorded the highest grain yield in E3 and E4 whereas genotype G18 (Sakha-93) in E6 and showed G19 (Pavone-76) was the best genotype due to being situated in the center of the concentric circles and its high-yield. Overall, these genotypes can serve as stable and performant resources under abiotic stress conditions. The methods considered were compatible with the detection of promising wheat genotypes with high mean performance and outstanding phenotypic stability across the various stress and years.

**Supplementary Materials:** The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agronomy12102252/s1, Table S1: Names and pedigree of the 20 bread wheat genotypes (6 cultivars and 14 doubled haploid lines (DHLs)) used in this study; Table S2: Details of genotype codes and names of 20 bread wheat genotypes (6 cultivars and 14 doubled haploid lines (DHLs)) used in this study.

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