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GENETIC VARIABILITY OF YIELD AND SOME AGRONOMICAL TRAITS OF PROMISING WHEAT GENOTYPES BY R PROJECT "METAN PACKAGE"

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Plant breeders have to employ strategies and techniques to produce new improved wheat cultivars to increase productivity to meet the needs of the growing population. Therefore, they have to develop a new cultivar for adaptation to a new environment and new management practices. One of the most important criteria plant breeders should focus on is the exploitation of genotype × environment interaction (GEI). Thus, this study aimed to assess the variability of 24 wheat genotypes growing in different seasons by using the R software "Metan Package". Moreover, the study estimates the stability parameters and finally highlights the winning genotypes across seasons. Field experiments were conducted across three consecutive seasons specifically 2019/2020, 2020/2021 and 2021/2022 and at different locations. The assessment was done on traits such as plant height [cm], flag leaf area [cm^2], chlorophyll index [SPAD], spike number [spike/m^2], fertility ratio [%], grain number [grain/spike], grain weight [g], and yield [kg/ha]. Results indicated different performances of wheat genotypes in certain environments as well as across the three environments included in this study. Winner genotypes such as G-20, G-10, G-30, G-4, and IRAQ were selected according to their stability and high grain yield potential. It can be concluded that the use of the Multi-Environment Trail Analysis-METAN package is powerful for detecting promising wheat genotypes with high and stable yields across different environments and under various climate change conditions. Furthermore, it can be recommended that wheat performance needs to be assessed across very wide geographical locations.

Key words: wheat, genotype, METAN, R Package, AMMI

In the last 50 years, the productivity of wheat in Iraq has notably increased to 2.66 t/ha in 2021 but still far below world productivity [3.5 t/ha] (FAOSTAT, 2023). This increase in wheat yield does not meet the requirements of the growing population which is expected to be around 10 billion by 2050 (Al-Ashkar *et al.* 2022). To boost the productivity of the growing population, plant breeders need to employ various strategies and techniques to improve wheat cultivars, and then evaluate and select culti-

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vars based on specific criteria e.g., yield potentials, resistance to biotic and abiotic stresses and quality traits. Recently, plant breeders have developed new cultivars that can adapt to changing environmental conditions and new management techniques. One of the most important criteria plant breeders should focus on is the exploitation of genotype × environment interaction (GEI) (Olivoto & Lúcio 2020), which eventually attain more stable cultivars across various environments. Experiments are routinely carried out to compare different cultivars across different environments (years and locations) for various agronomical traits resulting ultimately in genotype × environmental data. These data provide essential information about the most stable cultivars throughout those environments (Yan & Tinker 2011). Yan and Tinker (2011) indicated that the data collected from such trials are fully exploited due to its limitation to one trait (mainly yield), in addition to the fact that the behaviour of other traits is still uncovered. Moreover, the analysis is limited to the main effect (genotypes), while the interaction with the environments was treated as a noise or confusing factor. Recently, many efforts have been devoted to developing indices for genotype stability and then selecting a more stable one against GEI. Plant breeders model GEI is the most appropriate way to develop what so-called stability analysis which includes ANOVA based method, regression method, and a non-parametric method, Additive Main effect and Multiplicative Interaction (AMMI) and GGE (Genotype by Genotype-Vs-Environments interaction) (Yan & Kang 2002). Then researchers used the aforementioned statistical methods and produced notable advances in multi-environmental trials (MET). R software packages have been developed by the R core team (2019) which provide freely available collections of functions and are designed or are suitable for MET data analysis. Of these functions are the stability package which contains a collection of functions for the stability analysis. The AMMI-stability package calculates the stability parameters based on AMMI, GGE and GGE BiPlots packages that are used for the GGE model. Although the aforementioned R packages are very useful for specific data, they do not sufficiently offer options to complete MET data analysis in terms of stability. Thus, researchers worked hard to create a package that grants an easy workflow and incorporates the most used stability statistics as well as updating the stability methods (Olivoto *et al.* 2019a; 2019b). Olivoto *et al.* (2019a; 2019b) and Olivoto and Lucio (2020) have developed the METAN (Multi-Environment Trail Analysis) package, which is an open-source R package that is designed to provide an efficient and reproducible workflow for MET data analysis. There are five components of the METAN package. It comprises checking, manipulating and summarizing typical MET data, including the analysis of variance within the environment, calculating parametric and non-parametric stability analysis, calculating biometrical models in plant breeding trials (MET data) and finally quickly creating typical plots for two-way data while considering any combination of quantitative and qualitative traits.

The assessment of agronomic, physiological and biochemical traits is very important to select the superior genotypes that can be used in plant breeding programs for the new promising wheat genotypes that are stable in various environments. Thus, it is highly important to exert more efforts to develop climate-resilient genotypes and test them in various environments and different growing seasons (Yan *et al.* 2007; Gauch *et al.* 2008; Al-Ashkar *et al.* 2022). This can be achieved by using modern statistical analysis tools. Yield potentials can be affected by genotypes (G), environments (E), and interactions (GEI) and multiple environment trials are crucial for the plant breeders who work hard to boost food security by increasing the productivity of wheat. The analysis of such trials Requires effective tools to manipulate, visualize and model data obtained from those trials. R software, specifically the METAN package provides a group of functions that can achieve data manipulation, summarization and visualization (Olivoto & Lúcio 2020). Metan package is a rich environment that consists of many tools that facilitate the comprehensive MET data analysis. In this context, this paper aimed to assess the variability of wheat genotypes growing in different seasons by using the R software "Metan Package" as well as estimate the stability parameters and finally highlight the winner genotype across seasons.

MATERIAL AND METHODS

The Field experiments were conducted across three consecutive seasons specifically 2019/2020, 2020/2021 and 2021/2022 in three different locations (Table 1). The average of the monthly temperature [°C], relative humidity [%] and precipitation [mm/day] of the three seasons of 2019/2020, 2020/2021, and 2021/2022 were summarised in Figure 1. The physical and chemical properties of the soil for each season and each location are presented in Table 2. Each experiment included in total of 24 genotypes which were evaluated according to their agronomic performance. 21 genotypes were introduced to Iraq by the Agriculture Research Directorate/Ministry of Science and Technology. They are supposed to be suitable for arid and semi-arid areas beside the other local cultivars (IRAQ, Al Mahmodia and Al Diyar).

Field practices were done consequently starting with ploughing, smoothing and then leveling. The field was divided into three blocks which were divided into 24 experimental units according to the experimental design (Randomized Complete Block Design-RCBD). The area of each experimental unit was 3 × 3 m^2 where each unit consisted of 12 lines and the distance between each two lines was 25 cm. The depth of each hole was 5 cm, and the number of seeds was 10 g/line. The experimental field had been fertilised with Diammonium phosphate (DAP) at a level of 5 g per line [66.67 kg/ha] at the time of planting. While urea [N 46%] was used as the source of nitrogen fertiliser that was added as 30 g of nitrogen [33.34 kg/ha] for each experimental unit. Nitrogen was added at the elongation stage of the plant (Z40-Z54) (Zadoks *et al.* 1974). Planting was done manually on the 4th of December 2019, 20th of November 2020 and 26th of November 2021 for the three seasons respectively. Agricultural practices were performed such as hoeing and weeding as needed.

The following morphological traits were measured for each trial:

1- Plant height (PH) [cm]: It was measured from the base of the plant up-to the last node of the stem, by taking an average of ten randomly plants from one of the middle lines and for each experimental unit.
2- Flag leaf area (FLA) [cm^2]: It was calculated as an average of ten flag leaf randomly taken per experimental unit according to the equation:

$$\text{Flag leaf area } [cm^2] = L \times W \times 0.95$$

Where: L – The length of the flag leaf; W – maximum width of the flag leaf.

3- Chlorophyll index (Chl) [SPAD]:
4- Number of spikes [Spike/m] (SPN): it was calculated for the group of plants for the same harvested area, then converted to square meters.
5- Fertility ratio (FR) [%]: it was estimated according to the following equation:

$$\text{Fertility Ratio } [\%] = \frac{\textit{Grain numbers per spike}}{\textit{Spikletes number per spike}}$$

(Scott & Langer 1977)

6- Grain number [grain/spike] (GN): Number of grains per spike: It was calculated from the average of grains in 10 spikes randomly taken from the harvested spikes for each experimental unit.
7- 1,000 grain weight (GW) [g]: A sample of 1,000 grain was randomly taken from grain yield samples of each experimental unit and then

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The description of study locations and seasons

Location	Season	Geographical coordinates	Description
Hit 2020	2019/2020	Latitude 33°39 N and Longitude 42°47 E	Hit city/Qenan region- Anbar
ResSt1 2021	2020/2021	Latitude 33°39 N and Longitude 44°33 E	Research Station 1 of Agriculture College/ University of Anbar- Al Hamdhiyah
ResSt2 2022	2021/2022	Latitude 33°45 N and Longitude 43°32 E	Research Station 2 of Agriculture College/ University of Anbar- Al Boaitha

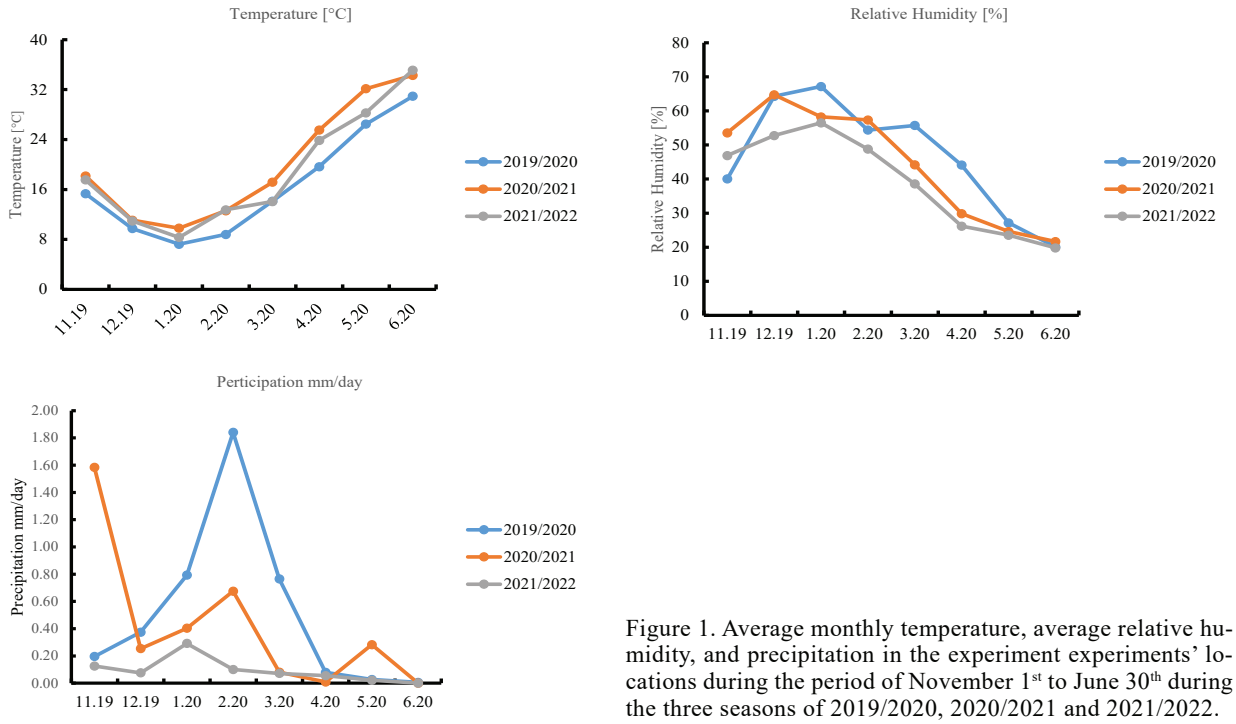


Figure 1. Average monthly temperature, average relative humidity, and precipitation in the experiment experiments' locations during the period of November 1st to June 30th during the three seasons of 2019/2020, 2020/2021 and 2021/2022.

T a b l e 2

Soil physical and chemical characteristics of the land of experiments in the three locations

Characteristics*	Unit	Hit (2019/2020)	Al Hamdhiyah (2020/2021)	Al Boaitha (2021/2022)
pH	–	8.40	7.14	7.70
Electrical conductivity (EC) (1:1)	[ds/m]	0.30	1.62	2.40
Soil organic matter	[g/kg]	1.27	5.40	0.69
Bulk density	[g/cm^3]	1.63	1.30	1.57
Cation exchange capacity (CEC)	[Cmolc/kg soil]	22.13	23.80	20.1
Ca	[Milliequivalent/L]	7.45	6.23	7.50
Mg		5.65	3.89	5.00
Na		7.30	5.60	8.70
K		2.34	1.39	2.10
SO_4		11.36	7.52	12.80
HCO_3		2.06	1.69	2.00
Cl		7.88	6.70	10.00
Available N	[mg/kg soil]	15.00	12.20	56.00
Available P		7.90	10.30	12.50
Available K		225.00	130.40	286.00
Soil separates	Sand [%]	22.00	68.40	42.40
	Silt [%]	38.00	11.20	44.00
	Clay [%]	40.00	20.40	13.60
Soil texture		Clay loam	Sand-clay loamy	Loamy soil

*Soil analysis was conducted in a central lab of the College of Agriculture-University of Anbar.

weights were measured by sensitive electronic balance.

8- Yield (YLD) [t/ha]: After the manual threshing of the harvested plants for one of the midline lines of 1.5 m length from each experimental unit, and after isolating the straw from the grains and cleaning them well, the grains were weighed in addition to the grains used in estimating the weight of 1,000 grains for the same treatment, and then converting the weight from [g/m^2] to [t/ha].

Statistical analysis

Collected data from studied traits were tabulated and then subjected to the R software v4.3.0; metan package v1.18.0 to get the descriptive statistics, ANOVA, AMMI models and GGE BiPlots (Olivoto & Lúcio 2020).

RESULTS AND DISCUSSION

ANOVA analysis and mean performance of 24 genotypes

Data collected from 8 measured traits for 24 genotypes of wheat were subjected to pooled ANOVA analysis using R packages (metan, function: anova_joint (data, env, gen, rep, resp, block=NULL, verbose=TURE) (Table 3). The mean sum of squares indicated significant effects of either genotypes, environment, or their interaction on the eight traits included in this study except for grain weight [g] which did not vary because of environment and its interaction with genotypes. The results indicated a big impact of the environment as well as for the genotypes on the performance of wheat genotypes. As for the interaction between replication and environment, it affected the flag leaf area ($P<0.05$), spikes number per square meter ($P<0.01$) and grain yield ($P<0.01$). It was clear that there was an interaction between genotypes and the environment and this is very important for plant farmers, breeders and agronomists (Swarup *et al.* 2021; Alfalahi *et al.* 2022). This enables selection of the most suitable, stable and adapted wheat genotypes for certain environments (Bhandari *et al.* 2024). In addition to that, it helps optimise the best crop management practices and consequently improves and sustains the acceptable productivity of wheat (Wang *et al.* 2023). Results of this study indicated different performances of the 24 wheat genotypes, and this makes them a good tool for conventional plant breeding programs although they were planted in close regions (Table 1) but in different seasons (2019/2020, 2020/2021, and 2021/2022 respectively).

As per performances for each trait across the environments, Table 4 shows that wheat genotypes

Table 3

Analysis of variance for 24 wheat genotypes for the eight traits included in the study over three environments

Parameters	Genotypes (G)	Environments (E)	Genotypes: Environments (GE)	Environments: Replications	Residuals
Degree of Freedom	23	2	46	6	138
PH	145.40^{+++}	3,396.10^{+++}	82.00^{+++}	43.60	37.10
FLA	68.60^{++}	8,145.10^{+++}	92.60^{+++}	88.90^{+}	35.00
Chl.	16.42^{++}	1,895.25^{+++}	11.45^{+}	12.72	7.19
SPN	7,536.00^{+}	90,983.00^{+++}	7,125.00^{++}	14,897.00^{++}	3,885.00
FR	0.2406^{+++}	3.7768^{+++}	0.1172^{++}	0.11	0.06
GN	104.57^{+++}	122.547^{+}	56.7^{+++}	33.38	27.63
GW	55.242^{+++}	13.46	14.22	13.36	12.40
YLD	3.99^{++}	760.91^{+++}	3.85^{++}	5.86^{++}	1.96

Significance codes: $^{+}$, $^{++}$, and $^{+++}$ indicate significance at $P<0.05$, 0.01, and 0.001 respectively.
Traits codes: PH – plant height; FLA – flag leaf area; Chl. – chlorophyll content; SPN – spikes number per square meter; FR – fertility ratio; GN – grain number per spike; GW – grain weight; YLD – yield.

varied and a group of genotypes were superior for each trait and this confirmed that those genotypes are suitable for growing in arid and semi-arid areas (Al-Temimi & Abed 2016; Abdul-Hassan & Al-Issawi 2021; Mansoor *et al.* 2021). Genotypes such as G-3, G-5, G-6, G-7, G-9, G-11, and G-19 were superior in plant height (PH) compared to the rest of the genotypes included in this study of which G-19 [96.38 cm] was the tallest, while Al Diyar genotypes [78.88 cm] indicated the shortest plants. Four genotypes were superior in flag leaf area namely G-9, G-11, IRAQ, and Al Mahmodia as they showed 38.15, 35.71, 41.21 and 36.60 cm^2 for the aforementioned genotypes respectively in comparison with G-7 which showed the lowest flag leaf area [29.31 cm^2]. The chlorophyll index [SPAD] was prominent in 19 out of 24 genotypes included in this study. More specifically, G-30 gave the highest chlorophyll content [49.87 SPAD], while G-5 gave the lowest content of this trait [43.69 SPAD]. Many

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Mean of the traits of the 24 wheat genotypes across the studied environments

Genotypes	Plant height [cm]	Flag leaf area [cm^2]	Chl. [SPAD]	Spike No Per m^2	Fertility ratio [%]	Grain No per spike	Grain weight [g]	Yield [t/ha]
G-3	96.64^{a}	29.49^{e}	47.39^{a-e}	416.07^{a-e}	2.71^{abc}	48.72^{a-d}	49.20^{d-g}	7.57^{abc}
G-4	89.98^{b-f}	29.78^{de}	49.81^{ab}	400.83^{a-f}	2.87^{a}	52.69^{a}	50.68^{c-f}	8.08^{ab}
G-5	94.41^{ab}	31.23^{cde}	43.69^{f}	396.74^{b-f}	2.48^{def}	44.23^{d-i}	49.62^{def}	6.47^{c-f}
G-6	94.06^{abc}	33.51^{b-e}	48.05^{a-d}	364.96^{efg}	2.68^{a-e}	50.06^{abc}	48.36^{fg}	6.47^{c-f}
G-7	91.01^{a-e}	29.31^{e}	47.41^{a-e}	457.04^{a}	2.70^{a-d}	48.03^{a-e}	49.34^{d-g}	8.23^{a}
G-9	91.46^{a-e}	38.15^{ab}	47.99^{a-d}	393.04^{b-g}	2.72^{abc}	47.97^{a-e}	49.64^{def}	7.32^{a-d}
G-10	90.69^{b-f}	34.74^{b-e}	48.40^{a-d}	365.33^{efg}	2.89^{a}	51.61^{ab}	52.28^{b-e}	6.66^{cde}
G-11	93.16^{a-d}	35.71^{abc}	47.95^{a-e}	378.15^{c-g}	2.47^{def}	42.49^{ghi}	52.45^{bcd}	6.39^{c-f}
G-18	88.60^{c-f}	34.66^{b-e}	48.79^{a-d}	350.67^{fg}	2.40^{f}	42.78^{ghi}	57.55^{a}	6.01^{ef}
G-19	96.38^{a}	33.53^{b-e}	47.89^{a-e}	411.28^{a-e}	2.86^{a}	47.73^{b-f}	53.80^{bc}	7.42^{a-d}
G-20	90.49^{b-f}	32.67^{b-e}	47.36^{b-e}	386.37^{b-g}	2.90^{a}	46.86^{b-g}	49.73^{def}	6.25^{def}
G-24	85.21^{fg}	33.41^{b-e}	48.40^{a-d}	385.81^{b-g}	2.50^{c-f}	41.74^{hi}	48.27^{fg}	6.19^{def}
G-25	89.61^{b-f}	29.59^{de}	45.48^{ef}	379.11^{c-g}	2.41^{f}	41.456^{i}	51.32^{c-f}	5.30^{f}
G-28	86.85^{efg}	33.80^{b-e}	48.38^{a-d}	394.89^{b-f}	2.53^{b-f}	43.71^{e-i}	46.12^{g}	6.56^{c-f}
G-29	87.64^{efg}	33.67^{b-e}	48.46^{a-d}	383.63^{b-g}	2.72^{abc}	48.77^{a-d}	49.65^{def}	7.22^{a-e}
G-30	87.42^{efg}	30.85^{cde}	49.87^{a}	429.57^{abc}	2.55^{b-f}	47.71^{b-f}	51.12^{c-f}	6.69^{cde}
G-31	87.06^{efg}	30.72^{cde}	49.06^{a-d}	389.18^{b-g}	2.57^{b-f}	46.41^{c-h}	49.52^{def}	6.12^{def}
G-32	88.70^{c-f}	33.91^{b-e}	49.15^{a-d}	427.70^{a-d}	2.47^{ef}	43.70^{e-i}	50.02^{def}	7.44^{a-d}
G-36	87.20^{efg}	34.21^{b-e}	47.24^{cde}	437.63^{ab}	2.45^{ef}	43.33^{e-i}	48.07^{fg}	6.59^{c-f}
G-39	87.88^{d-g}	35.03^{bcd}	47.99^{a-d}	387.93^{b-g}	2.88^{a}	48.79^{a-d}	49.13^{efg}	6.55^{c-f}
G-41	82.87^{gh}	32.21^{cde}	48.41^{a-d}	434.85^{abc}	2.54^{b-f}	42.99^{f-i}	54.67^{ab}	7.04^{a-e}
IRAQ	89.11^{b-f}	40.21^{a}	46.91^{de}	381.55^{b-g}	2.75^{ab}	49.84^{abc}	49.88^{def}	6.87^{b-e}
Al Mahmodia	78.88^{h}	36.70^{abc}	48.74^{a-d}	335.11^{g}	2.60^{b-f}	41.77^{hi}	52.06^{b-e}	6.55^{c-f}
Al Diyar	90.02^{b-f}	33.07^{b-e}	49.70^{abc}	370.81^{d-g}	2.57^{b-f}	42.37^{ghi}	53.56^{bc}	6.54^{c-f}
$LSD_{(0.05)}$	0.72	0.70	0.32	7.36	0.03	0.62	0.42	0.17

Different letters beside means refer to significant differences between means ($P < 0.05$). Chl. – chlorophyl index.

of the genotypes can be categorized as stay-green genotypes but it does not necessarily correlate with considerable yield, and this was proved by Hashem and Al-Issawi (2023). The number of spikes in each squared meter ranged between 335.11 that were recorded by Al Mahmodia and 457.04 that recorded by G-7. Although, genotypes varied in this trait among the three seasons, 8 of which were won across the environments confirming the GE interaction. As for fertility ratio [%], 11 out of 24 genotypes were superior in this trait. The fertility ratio did not indicate good yield and other components seem to have more contribution to it than FR such as grain count in spike (GN), and this was consistent with what has been indicated by Bancal (2008). Seven genotypes were superior in counts of grains in a spike, of which four were also superior in yield [t/ha] and that was confirmed by the strong positive correlation between the two traits ($P<0.001$) (Figure 2). The genotype G-4 recorded the highest number of grains per spike (52.65) and G-25 recorded the lowest mean of this trait (41.74) (Table 3). Grain weight (GW) also did not seem to have a big contribution to the yield as only two genotypes (G-18 and G-41) were superior in this trait and only G-41 was also superior in yield. Figure 1 shows a non-significant correlation between GW and all traits under investigation ($P>0.05$). Yield is considered the most important trait that indicates stability for specific genotypes, although other traits cannot be neglected as they all in one way or another contribute to the yield. Table 4 highlights 8 genotypes that indicated considerable and significant yield namely G-3, G-4, G-7, G-9, G-19, G-29, G-32, and G-41. The lowest amount of yield was recorded by G-25 [5.3 t/ha] which did not show significance for all eight traits examined in this study.

In the current study, a simple correlation coefficient was also calculated to describe the nature of the relation among the studied traits (Figure 2). Plant height (PH) was positively correlated with chlorophyll index (Chl.) and flag leaf area (FLA) ($P<0.001$) while the negative correlation with fertility ratio (FR) and yield (YLD) ($P<0.001$ and $P<0.05$ respectively) was recorded. It has been found that the increase in flag leaf area increased

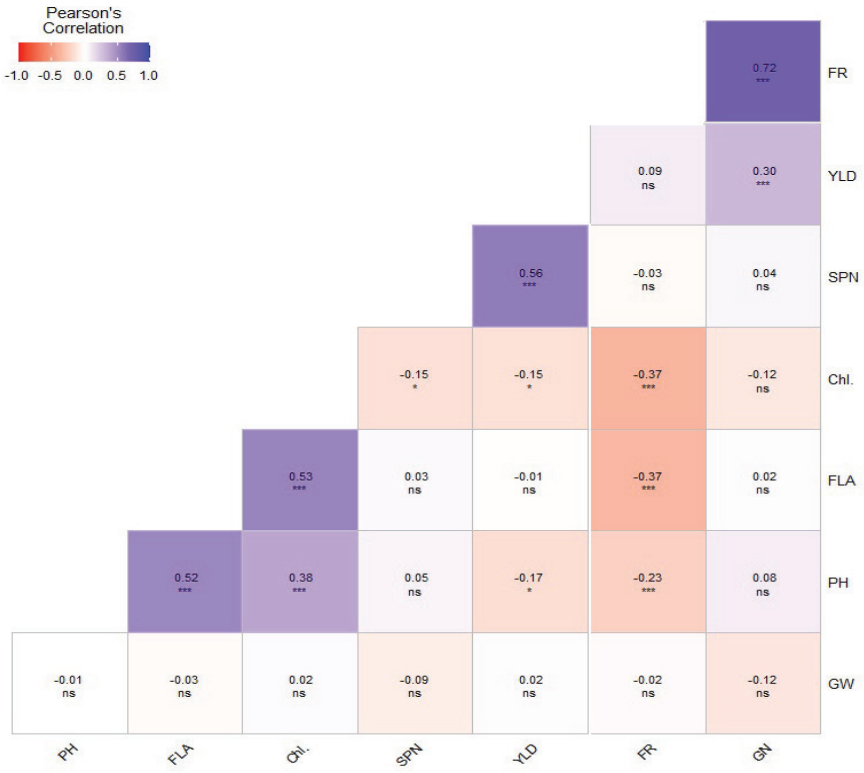


Figure 2. The linear simple correlation among the studied traits across environments.
Note: PH – plant height; FLA – flag leaf area; Chl. – chlorophyll content; SPN – spike number per square meter; YLD – yield; FR – fertility ratio; GN – grain number per spike; GW – grain weight. ns $P>0.05$, $^{+}P<0.05$, $^{++}P<0.01$ and $^{+++}P<0.001$.

chlorophyll index (Chl.) and a reduction in fertility ratio (FR) ($P<0.001$). The chlorophyll index had a negative and significant correlation with fertility ratio ($P<0.001$), yield ($P<0.05$) and spike count per square meter ($P<0.05$). The number of spikes per square meter had a positive and significant correlation with yield only ($P<0.001$) while yield in turn had a positive significant correlation with grain numbers per spike only ($P<0.001$). It is clear that some of the traits were linearly correlated either positively or negatively (Afonnikov *et al.* 2022), and this requires further investigation to figure out the non-linear correlation among the studied traits.

Based on the pooled ANOVA (Table 2) and mean performances of the traits under investigation which indicated GE interaction between genotypes and environments (Geneti *et al.* 2022). The data presented in Table 5 indicates the winner genotype in different environments. It is worth mentioning that G-4 was superior in yield in environment ReSt12021 as well as to fertility ratio grain number per spike in other environments. It had been found that genotypes winning in yield were not superior in other traits. Winning genotypes across different environments should have high yield potential and be stable (Yan & Tinker 2011).

Stability according to additive main effect and Multiplicative Interaction (AMMI) analysis

The analysis offered in this study demonstrated that wheat genotypes were strongly affected by the genotype (G), Environment (E) and their interaction (GEI). Table 6 indicated that 91.68% of the variation of plant height (PH) belongs to the environment while genotype contributed only 3.93% only. It is obvious that Environmental Contribution to the total variation was more than both genotype and GEI except in grain number per spike (GN) and grain weight (GW) where the genotype (30.32 and 50.83%) had more effect than environment (35.54 and 12.39%) for the two traits respectively. However, between 80 to 99% of the total variation was explained by the effect of either G, E or GEI.

The AMMI analysis of the variance for the eight traits of the 24 wheat genotypes was determined in three consecutive environments (Table 6 and Figures 3–4) which explained the total variation of either genotypes, environments, or their interactions. It is obvious that AMMI analysis explained 67.9, 65.2, 77.4, 64.3, 56.6, 63.8, 78.6, and 87.4% for PH, Chl., FLA, SPN, GN, FR, GW and YLD respectively (Figure 2). The AMMI2 was plotted between the first two components (PC1 and PC2) which explained the GEI, which PC1 and 2 were PH (67.9, 32.1%), FLA (65.2, 34.8%), Chl. (77.4, 22.6%), SPN (64.3, 35.7%), FR (56.6, 43.4%), GN (63.8, 36.2%), GW (78.6, 21.4%), and YLD (87.4, 12.6%) for the two components respectively (Figure 4) (Krishnamurthy *et al.* 2021).

Based on Figures (3 and 4), that indicate crossover patterns of the biplots that refer to the interaction between genotypes and environments. Yet, it is necessary to determine whether the crossover is repeatable across years or not. This in turn leads to the division of the target environment into different mega environments and the studied genotype can be evaluated individually in each mega environment to exploit the GEI (Yan & Tinker 2005). Figure 4 shows the correlation between genotypes under adverse environments and PC1 for the eight traits investigated in this study. The environments ReSt1 2021 and ReSt2 2022 had stronger interaction compared to Hit 2020 which had a shorter vector than the other two environments for the trait of PH and Chl. As for the other traits, it had been found that

Table 5

Winner genotype in each environment for each trait

Environments	PH	FLA	Chl.	FR	GN	GW	YLD
Hit 2020	G-6	IRAQ	G-30	G-20	G-6	G-18	G-3
ResSt1 2021	G-11	G-24	Al Diyar	G-4	G-4	G-18	G-4
ResSt2 2022	G-19	G-39	G-4	G-39	G-39	G-18	G-32

Based on function ge_winners() using R packages (METAN). Note: PH, FLA, Chl., FR, GN, GW, YLD – see Figure 3.

the three environments had approximately the same force of the interaction as they had longer vectors from the origin (Figure 4). For all the eight parameters e.g., PH, Chl. and FLA, SPN, GN, FR, GW, and YLD, it had been noticed that most of the genotypes were distributed close to the origin point, which makes them insensitive to the environments according to the AMMI stability analysis compared to the further distributed genotypes which were indicated as environment sensitive. Genotypes such as G-11, G-3 G-7, G-19, Al Mahmodia and G-36 for the plant height and the chlorophyll index, genotypes viz., G-5, G-25, G-31, G-9, G-32, G-4 and G-19 were further from the origin which indicates that those genotypes were affected by environments in comparison with the closer genotypes to the origin. In addition, genotypes viz., IRAQ, G-29, G-24, G-7, G-4, G-G-25, G-39, and Al Mahmodia were sensitive to the environments in terms of flag leaf area.

GGE BiPlots

The use of GGE biplot model analysis was performed to find the high-yielding genotypes besides their stability (Kebede *et al.* 2023). GGE analysis, as shown in the polygon view of the 24 wheat gen-

T a b l e 6

The contribution of Genotypes (G), Environments (E) and their interaction (GEI) to the total variation of the eight traits under the study

Traits	G	E	GE	% (G+E+GE)
PH	3.93	91.68	2.21	97.82
FLA	0.81	96.62	1.10	98.53
Chl.	0.85	97.54	0.59	98.98
SPN	6.06	73.12	5.73	84.91
FR	5.59	87.79	2.72	96.10
GN	30.32	35.54	16.44	82.31
GW	50.83	12.39	13.08	76.30
YLD	0.51	97.98	0.50	98.99

Note: PH – plant height; Chl. – chlorophyll content; FLA – flag leaf area; SPN – spike number per square meter; GN – grain number per spike; FR – fertility ratio; GW – grain weight; YLD – yield.

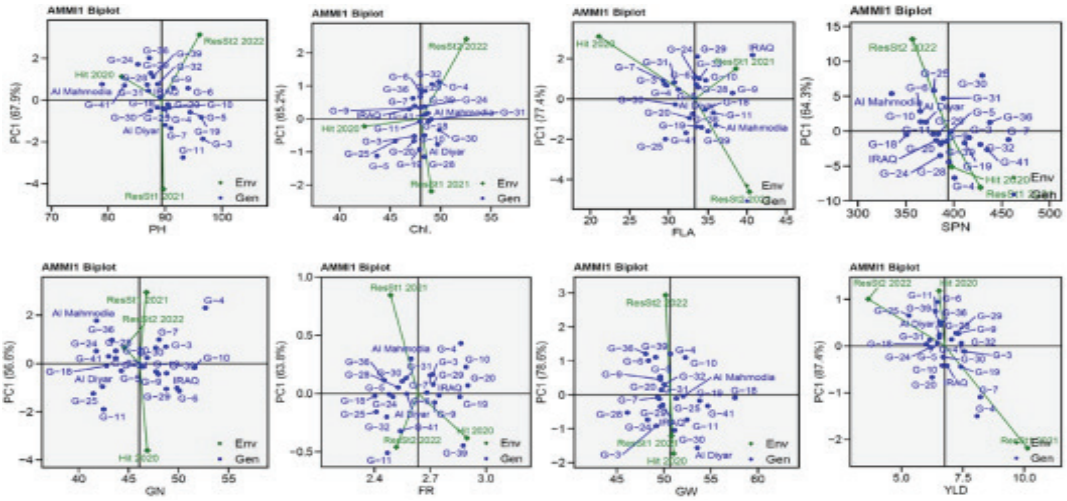


Figure 3. AMMI (1) analysis for the eight traits under the study.
Note: PH – plant height; Chl. – chlorophyll content; FLA – flag leaf area; SPN – spike number per square meter; GN – grain number per spike; FR – fertility ratio; GW – grain weight; YLD – yield.

otypes (Figure 5), indicated significant scores of the two main components (PC1 and PC2). The scores of those two components varied among the traits under the study; however, PC1 explained the variation of 68.17, 54.89, 57.26, 47.38, 49.69, 56.17, 69.53, and 75.17% for the traits of PH, Chl., FLA, SPN, GN, FR, GW, and YLD respectively. On the other hand, PC2 explained 21.94, 26.79, 29.57, 29.89, 28.89, 26.93, 24.94, and 16.61% for the aforementioned traits respectively. It is worth mentioning that the two principal components explained 91.78% of the variation in the yield trait. In Figure 5, the genotype in the section with a specific environment performed well in the specified environments, while the genotype close to the centre did not respond very well to either changes/changes in genotypes or environments. Based on what has been aforementioned, genotypes that are located on the vertex of the polygon showed more stability than others the ones located beside the polygon e.g., for the yield trait, G-20, G-4, G-7, G-32, G-9, G-11, and G-18 recorded highest mean of yield in ResSt1&2. On the other hand, genotypes

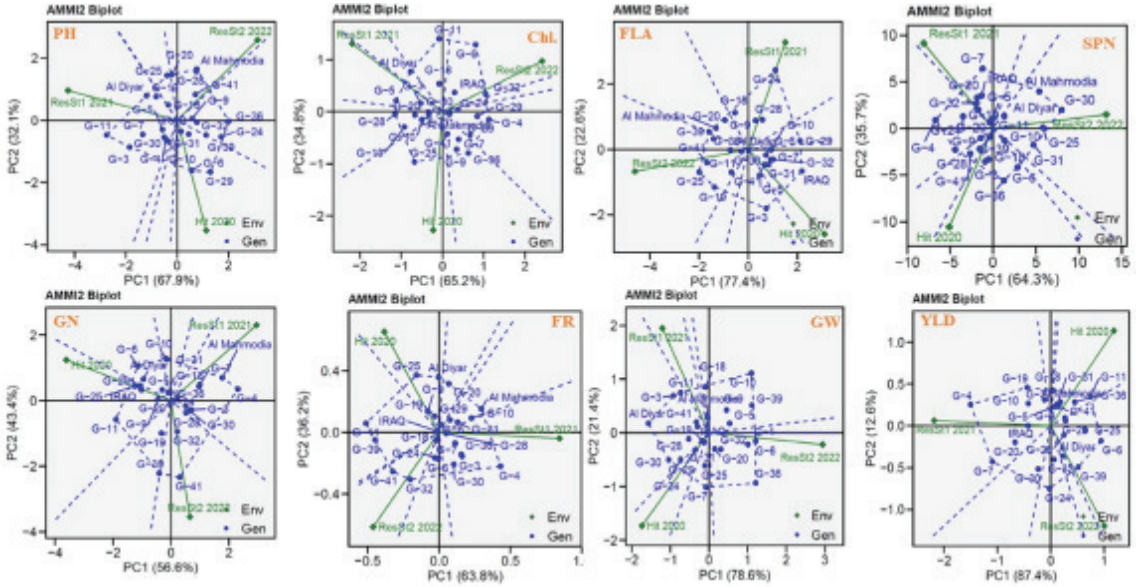


Figure 4. AMMI (2) analysis for the eight traits under the study.
Note: PH – plant height; Chl. – chlorophyll content; FLA – flag leaf area; SPN – spike number per square meter; GN – grain number per spike; FR – fertility ratio; GW – grain weight; YLD – yield.

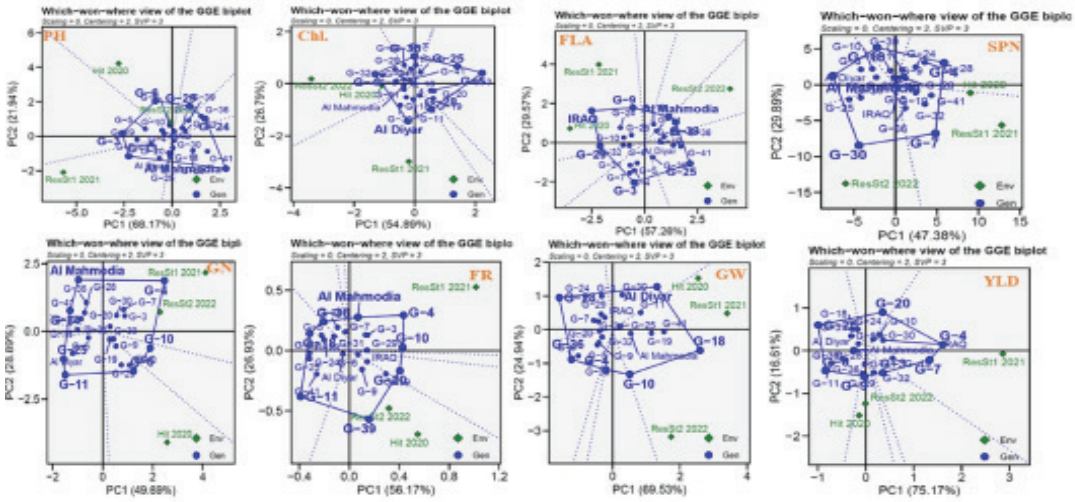


Figure 5. A "which won where" biplots based on PH – Plant height, Chl. – Chlorophyll content, FLA – flag leaf area, SPN – spike number per square meter, GN – grain number per spike, FR – fertility ratio, GW – grain weight, YLD – yield of the 24 wheat genotypes evaluated in the three seasons in different locations.

that are located close to the plot origin were more adaptable to record a lower yield in comparison with those appearing on the vertex.

CONCLUSIONS

METAN analysis showed that the 24 genotypes included in this study varied according to their agronomical performance as well as according to the changes in the environment. Moreover, the eight traits included in this study differently contributed to the yield including grain number per spike and number of spikes per square meter. The experiments that have been done during three seasons in different locations confirmed the significance of METAN analysis in deciphering the GE interactions based on data of traits other than yield. AMMI analysis showed that the environment had more effect on the 7 traits out of 8 included in this study. Grain weight has been affected by genotype in comparison with the change in the environment. GE interactions were found to be significant only for grain weight and grain number per spike. Furthermore, grain weight was the most stable trait that won in the three locations. ResSt1 2021 seems to be the best environment that showed the potential performances of the 24 genotypes during the growing seasons of 2020-2021. Genotypes such as G-20, G-10, G-30, G-4, and IRAQ showed higher stability than the rest of the genotypes while genotypes such as G-24, G-3, G-29, G-28, and G-7 showed high performances in terms of yield. Overall, genotypes that showed high stability and productivity can serve as performant resources for arid and semi-arid areas. Finally, METAN analysis has the potential to be extremely effective in identifying wheat genotypes that exhibit high and consistent yields in a variety of settings and climate conditions.

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