

STABILITY ANALYSIS FOR GRAIN YIELD IN BREAD WHEAT GENOTYPES

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Received: Feb. 14 , 2019

Accepted: Feb. 27, 2019

ABSTRACT: *Wheat breeders have to determine the new cultivars and lines responsive to the environmental changes for grain yield and yield components. Therefore, this study was conducted to evaluate 20 bread wheat (*Triticum aestivum* L) genotypes including 9 registered cultivars and 11 promising lines for their stability grown in five different locations (EL-Gemmeiza, Sakha , Nubaria, Sids and Shandaweel Agricultural Research Station) for three growing seasons (2009-2010, 2010-2011 and 2011-2012), and to select genotypes having desirable traits to be used in twenty bread wheat genotypes. Field trials were conducted in a randomized complete block design with three replications at each location. Number of spikes per square meter, number of kernels per spike, 1000-kernel weight and grain yield of the genotypes were evaluated in each location. The AMMI analysis showed that (73.79,57.28,47.27 and 22.51%) of the total squares were due to environmental impacts (1.72, 4.96, 4.01 and 20.37) to genetic effects (13.65, 24.44, 27.76, and 32.4%) of the effects GEI on the grain yield, the number of spikes / m², number of kernels / spike and 1000- kernel weight, respectively.*

The genetics (GEI) were divided into three axes for the analysis of the reaction components (IPCA) of the grain yield and its components.

The results showed that IPCAs were of great importance. Three IPCAs (55.77,63.76,61.45 and 67.38%) represented the interaction variation of the grain yield, the number of spikes / m², the number of kernels / spike and the weight of 1000 -grain, respectively.

The most stable genotypes were Giza 168, G18, G13, Gemmeiza11 and G10 with high yield potential. For grain yield.

The best genotypes with respect to E5 and E14 were Sids12 and Masr1. For E13, E3, E2 and E7 as well as for G20 and G 17. For E6, E1 and E15, were G11. The E4 had Sids13 and shandaweel1. E9, E11, E8 and E12 were the G12. E1, E9 and E13 were also the most distinct environments. For grain yield. The most stable genotypes were G18, G16, Masr2, G13and G20 with high production potential,

For recorded Gemmeiza 11 genotypes at environments E15, E10, E8, E3, E9, E5, E13, E4 and E12. For E6, E2, E1, E7 and E11 were Sids13. It also shows that E1 and E6 are the most distinct environments. For Number of spike/m²

The most stable genotypes were G19, G13, G15 Sids13and G14 with high production potential for Number of kernels/spike. The best genotype namely G20 were E7, E12, E2, E8. and G10 for E1, E13, E3 and E10. For E5, E15 and E4, they were G1. For E9, E6 and E14 were Shandaweel1. It also shows that E14, E15, E5 and E4 were the most distinctive environments. for Number of kernels/spike.

The most stable genotypes were Masr2, Sids12, Sids13 G12 and G13 with high potential, The best genotypes with respect at environment number E4, E5, E7, E10, E14 and E15 were Gemmeiza11. For environment number E6 and E1were genotype number G17.At environment number E3, E19 and E13 were genotypes number G19.The best distinct environment number E1 and E9 for the 1000 kernel-weight.

INTRODUCTION

Wheat (*Triticum aestivum* L) is one of the most important crops and is a stable food for large parts of the world population including Egypt. Information about phenotypic stability is useful for selection of crop varieties in a breeding program. Plant breeders encounter genotype \times environment interaction (G \times E) when testing varieties across a number of environments. The magnitude of the interaction or the differential genotypic responses to environments differs greatly across environments (Kaya *et al.*, 2002).

Environmental conditions are known to have significant influence on yield of wheat. But relative magnitude of environmental, genetic, and G \times E effects on grain yield is unclear, and development of a selection strategy for grain yield requires knowledge of the magnitude of the genotype and environment (G \times E) interaction. Plant breeders carry out performance tests at different locations in different years in target areas, and data obtained from these tests are used to determine the magnitude of G \times E interactions. In the presence of G \times E interactions, stability parameters are estimated to determine the superiority of individual genotypes across the range of environments

Wheat production can be boosted up through cultivars having broader genetic base and better performance under various agro-climatic conditions. In wheat, genetic improvement is a slow process in nature however, the selective process of man can speed it up through appropriate management of environmental factors. Improvement gets complicated when a trait is environment-driven and selection gets more complex (Mohammad *et al.*, 2011.).

Multi-environment trials (METs) are used to accurately estimate and predict yield based on limited experimental data, determine yield stability and the pattern of response of genotypes across environments and provide reliable assistance for selecting the best genotypes for planting in future years and at new sites (Crossa, 1990).

The additive main effects and multiplicative interaction (AMMI) model consists of the analysis of variance for the genotype and environment main effects with the principle components analysis (PCA) of the genotypes-environments interaction. It uses the standard analysis of variance (ANOVA) procedure, where after the AMMI model separates the additive variance from the multiplicative variance (interaction), and then applies PCA to the interaction (residual) portion from the ANOVA to extract a new set of coordinate axes which account more effectively for the interaction patterns (Shafii *et al.* (1992)).

The objectives of this study are aimed to:

- 1- Estimate the stability yield and its components for twenty bread wheat genotypes across fifteen variable environments.
- 2- Identified the promising genotypes with high yield ability and stability.
- 3- Apply multivariate techniques AMMI statistical model for determination of the magnitude and pattern of GE interaction effects and performance stability of grain yield in selected wheat genotypes.

MATERIALS AND METHODS

The field experiment was carried out using 20 bread wheat genotypes which are (9 commercial cultivars (Gemmeiza 9-

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Gemmeiza11-Giza168-Sakha94-Shandaweel 1- 1 Sids 12-Sids 13-Masr 1 and Masr2) and 11 promising lines) field experiments were conducted for three successive seasons (2009/2010-2010/2011- 2011/2012). The environments were represented by five locations (EL-

Gemmeiza, Sakha ,Nubaria, Sids and Shandaweel Agricultural Research Station). 20 genotypes of bread wheat were evaluated over 15 environments.

The pedigree of the studied bread wheat genotypes is presented in Table (1).

Table (1): pedigree of the studied bread wheat genotypes used in this study

| no | Genotypes | Pedigree |
|----|--------------|----------------------------------------------------------------------------------------------------------|
| 1 | Gemmeiza 9 | ALD "S" / HUAC // CMH 74A. 630 / SX CGM 4583-5GM-1GM-0GM |
| 2 | Gemmeiza11 | BOW"S"/KVZ"S"//7C/SER182/3/GIZA168/SAKHA61 GM7892-2GM-1GM-2GM-1GM-0GM |
| 3 | Giza168 | MRL/BUE/SERI CM93046-8M-0Y-0M-2Y-0B |
| 4 | Sakha94 | OPATA/RAYON//KAUZ CMBW90Y3180-0TOPM-3Y-010M-010M-010Y-10M015Y-0Y-0AP-0S. |
| 5 | Shandaweel 1 | SITE/MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC CMSS93B00567S-72Y-010M-010Y-010M-3Y-0M-0HTY0SH |
| 6 | Sids 12 | BUC//7C/ALD/5/MAYA74/ON//1160.147/3/BB/GLL/4/CH AT"S"/6/MAYA/VUL//CMH74A.630/4*SX SD7096-4SD-1SD-1SD-0SD |
| 7 | Sids 13 | KAUZ"S" //TSI / SNB"S" ICW94-0375-4AP-2AP-030AP-0APS-3AP-0APS-050AP0AP-0SD |
| 8 | Masr 1 | OASIS / SKAUZ // 4*BCN /3/ 2*PASTOR CMSS00Y01881T-050M-030Y-030M-030WGY-33M-0Y0S |
| 9 | Masr 2 | SKAUZ / BAV92 CMSS96M03611S-1M-010SY-010M-010SY-8M-0Y-0S |
| 10 | Line 1 | GEMMEIZA/GIZA168. s-15647-8s-0sy-1s-0s. |
| 11 | Line 2 | PFAU/SERI.IB//AMAD/3/WAXING. CGSS02-Y00153S-099M-099Y-099M-46Y-0B. |
| 12 | Line 3 | F6031478/MRL//CN079/3/KA-NAC/4/STAR. |
| 13 | Line 4 | KAUZ//PASTOR//BAV92/3/RAYON. CMSS00M02400S-030M-030WGY-030M-13M-0Y-0NUB. |
| 14 | Line 5 | CHAM-6//GHURAB"s" /3/REGRAG-1 ICW98-0042-12AP-0APS-030AP-19AP-2AP-0AP-0SD. |
| 15 | Line 6 | SERI/RAYON |
| 16 | Line 7 | HD2687 |
| 17 | Line 8 | SAKHA93/GEMMEIZA9. S-6-1GZ-4GZ-1GZ-2GZ-OS |
| 18 | Line 9 | OTUS/3/SARA/THB//VEE. CMSS97YOO2275-5Y-010M-010Y-010M-2Y-1M-0Y-0GM |
| 19 | Line 10 | ALMAZ-8. ICW94-0375-2AP-1AP-030AP-0APS-6AP-0APS |
| 20 | Line 11 | BOW"s"/VEE"s"//BOW"s"/TST/3/BANI/SUEFI. SD294-1SD-25D-4SD-0SD |

The experimental layout at each environment was randomized complete

block design with three replications. Plot size (4.2m²) contain six rows was 20cm between rows long at 3.5m.

Studied characters

- 1- Number of spikes/ m²: Number of fertile tillers/ m² were calculated by counting all spikes per square meter
- 2-Number of kernels /spikes: Average number of kernels in ten randomly chosen spikes.
- 3- 1000- kernel weight: A random sample of 1000- kernel were taken from each plot, hand counted and weighted in grams.
- 4- Grain yield (Ard/Fed.): It was calculated from the grain weight the four middle rows in each plot

Statistical analysis.

AMMI combines analysis of variance (ANOVA) and principal component analysis (PCA) into a single model with additive and multiplicative.

The eigen vector is scaled as unit vectors and are unit less, whereas, λ has the units of yield. A convenient scaling for the multiplicative parameters is $\lambda 0.5 \gamma$ and $\lambda 0.5 \delta e$, termed the 'genotype IPCA scores' and 'environment IPCA scores' because their product gives the expected interaction value. There are at most min (G-1, E-1) axes, but usually the number of axes N retained in the model is smaller, producing a reduced model denoted AMMI1 or AMMI2 if retaining 1 or 2 IPCAs [Gauch and Zobel (1996)].

Genotypes with first principal-component axis value close to zero indicate general adaptation to environments.

A genotype is regarded as stable if its first and second correspondence analysis scores are near to zero Lopez (1990).

AMMI stability value

The AMMI Stability Value (ASV) proposed by Purchase (1997) and Purchase *et al.* (2000) because AMMI does not make provision for quantitative stability measure, they developed their own test based on the AMMI model's IPCA1 and IPCA2 values for each genotype. This ASV is in effect, the distance from the coordinate point to the origin in a two-dimensional scatter plot of IPCA1 scores against IPCA2 scores. Because the IPCA1 score contributes more to G \times E sum of squares, a weighted value is needed. This weighted value is calculated according to the relative contribution of IPCA1 to IPCA2 to the interaction sum of square.

RESULTS AND DISCUSSION

Additive main effects and multiplicative interaction (AMMI) for grain yield character.

The additive main effects and multiplicative interaction (AMMI) model consists of the analysis of variance for the genotype and environment main effects with the principle components analysis (PCA) of the genotypes-environments interaction. It uses the standard analysis of variance (ANOVA) procedure, where after the AMMI model separates the additive variance from the multiplicative variance (interaction), and then applies PCA to the interaction (residual) portion from the ANOVA to extract a new set of coordinate axes which account more effectively for the interaction patterns (Shafii *et al.* (1992)). A genotype is regarded as stable if its first and second correspondence-analysis (PCA) scores are near zero (Lopez (1990)).

The combined analysis of variance showed that there is highly significant difference for environments, genotypes and their interaction, combining analysis of variance and AMMI analysis is shown in (Table (2, 3, 4 and 5) mean squares (MS) from AMMI analysis for grain yield of

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twenty bread wheat genotypes across fifteen environments. The AMMI analysis of variance revealed that environments (E), genotypes (G) and the Genotypes \times Environments interaction (GEI) mean squares were highly significant for grain yield.

Also, the AMMI analysis of variance showed that (73.79, 57.47, 27.45 and 22.51%) of the total sum of squares were attributable to environmental effects, (1.72, 4.96, 4.01 and 11.38%) to genotypic effects (13.65, 24.44, 27.76 and 32.4%) to GEI effects for grain yield, number of spikes/m², number of kernels/spike and 1000-kernel weight respectively. A large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variations in these characters. The magnitude of the GEI sum of squares was larger than that for genotypes, indicating that there were substantial differences in genotypic response across environments. Crossa (1990) Reported that, AMMI analysis first fits the additive main effects of genotypes and environments by the usual analysis of

variance and then describes the non-additive part, genotype-environment interaction, by principal components analysis. Bradu and Gabriel (1978) and Gauch (1988) reviewed that, (AMMI) method integrates analysis of variance and principal components analysis into a unified approach. The recent results match with the previous findings. Kendal and Dogan (2015).

The genotypes \times environment interaction (GEI) was portioned three interaction principle components analysis axis (IPCA) for grain yield and its components. The results showed that three IPCAs were highly significant. IPCA1, IPCA2 and IPCA3 accounted for (24.5, 17.00 and 14.27%) from grain yield, (38.98, 14.63 and 10.15%) from number of spikes/m², (24.29, 23.51 and 13.65%) from number of kernel/ spike and (30.98, 22.40 and 14.00%) from 1000-kernel weight, respectively. Three IPCAs represent (55.77, 63.76, 61.45 and 67.38%) of interaction variation for grain yield, number of spikes/m², number of kernels/spike and 1000-kernel weight respectively.

Table (2): Combined and AMMI analysis of variance for grain yield (ardab/fed.) of twenty genotypes across fifteen environments

| Source | df | ss | % ss | MS |
|--------------|-----|-------|-------|---------|
| Genotypes | 19 | 277 | 1.72 | 14.6** |
| Environments | 14 | 11892 | 73.79 | 849.4** |
| Block | 30 | 198 | 1.23 | 6.59** |
| Interactions | 266 | 2200 | 13.65 | 8.27** |
| IPCA 1 | 32 | 539 | 24.5 | 16.84** |
| IPCA 2 | 30 | 374 | 17 | 12.47** |
| IPCA 3 | 28 | 314 | 14.27 | 11.2** |
| Residuals | 176 | 973 | 44.23 | 5.53 |
| Error | 570 | 1549 | | 2.72 |

* and ** indicates significance at 0.05 and 0.01 level.

Table (3): Combined and AMMI analysis of variance for no. of spikes/m² of twenty genotypes across fifteen environments

| Source | df | ss | % ss | MS |
|--------------|-----|---------|-------|---------|
| Genotypes | 19 | 119689 | 4.96 | 6299** |
| Environments | 14 | 1381186 | 57.28 | 98656** |
| Block | 30 | 17520 | 5.72 | 584 |
| Interactions | 266 | 589381 | 24.44 | 2216** |
| IPCA 1 8 | 32 | 229757 | 38.98 | 7180** |
| IPCA 2 | 30 | 86217 | 14.63 | 2874** |
| IPCA 3 | 28 | 59818 | 10.15 | 2136** |
| Residuals | 176 | 213589 | 36.24 | 1214 |
| Error | 570 | 303355 | | 532 |

* and ** indicates significance at 0.05 and 0.01 level.

Table (4): Combined and AMMI analysis of variance for No. of kernels/spike of twenty genotypes across fifteen environments

| Source | df | ss | % ss | MS |
|--------------|-----|-------|-------|----------|
| Genotypes | 19 | 2061 | 4.01 | 108.5** |
| Environments | 14 | 24286 | 47.27 | 1734.7** |
| Block | 30 | 1482 | 2.88 | 49.4** |
| Interactions | 266 | 14259 | 27.76 | 53.6** |
| IPCA 1 | 32 | 3463 | 24.29 | 108.2** |
| IPCA 2 | 30 | 3353 | 23.51 | 111.8** |
| IPCA 3 | 28 | 1946 | 13.65 | 69.5** |
| Residuals | 176 | 5498 | 38.56 | 31.2 |
| Error | 570 | 9285 | | 16.3 |

* and ** indicates significance at 0.05 and 0.01 level.

Table (5): Combined and AMMI analysis of variance for 1000-Kernel weight of twenty genotypes across fifteen environments

| Source | df | ss | % ss | MS |
|--------------|-----|------|-------|----------|
| Genotypes | 19 | 3866 | 20.37 | 203.49** |
| Environments | 14 | 4271 | 22.51 | 305.08** |
| Block | 30 | 388 | 2.04 | 12.95 |
| Interactions | 266 | 6155 | 32.4 | 23.14** |
| IPCA 1 | 32 | 1907 | 30.98 | 59.6** |
| IPCA 2 | 30 | 1379 | 22.40 | 45.97** |
| IPCA 3 | 28 | 862 | 14.00 | 30.8** |
| Residuals | 176 | 2006 | 32.53 | 11.4 |
| Error | 570 | 4296 | | 7.54 |

* and ** indicates significance at 0.05 and 0.01 level.

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The presented results are in according with the results of Mohamed (2009), Najafian *et al.*, (2010), Farshadfar *et al.*, (2011), Hagos and Abay (2013) and Mohamed *et al.*, (2013).

IPCA scores of genotypes and environments displayed positive and negative values are presented in (Tables 6, 7, 8 and 9). A genotype with large

positive IPCA score in some environments must have large negative interaction in some other environments. Thus, these scores presented a disproportionate genotype response, which was the major source of variation for any crossover (quantitative) interaction. This disproportionate genotype response is referred to as crossover GE interaction.

Table (6): Grain yield means, interaction principle component analysis scores and AMMI stability value of twenty genotypes across fifteen environments.

| Genotype | AR/FED | IPCAg[1] | IPCAg[2] | IPCAg[3] | ASV | rank |
|-------------|--------|----------|----------|----------|----------|------|
| Gemmeiza9 | 22.7 | -0.20854 | -0.51075 | 1.44234 | 0.592614 | 6 |
| Gemmeiza11 | 22.56 | -0.27373 | -0.3211 | 0.64677 | 0.508655 | 4 |
| Giza168 | 22.4 | 0.1207 | 0.21224 | 0.90688 | 0.274417 | 1 |
| Sakha94 | 22.98 | 0.40586 | 0.58699 | -1.54507 | 0.828664 | 7 |
| Shandaweel1 | 23.03 | 0.59522 | 1.22033 | 0.35376 | 1.491662 | 13 |
| Sids12 | 22.52 | 0.87272 | -1.52417 | 0.11251 | 1.976111 | 17 |
| Sids13 | 22.79 | 1.35849 | 0.8949 | 0.6621 | 2.152654 | 18 |
| Masr1 | 23.73 | 1.19279 | -0.63635 | 0.13781 | 1.833023 | 16 |
| Masr2 | 24.07 | 0.13434 | 0.89553 | 0.02997 | 0.916219 | 9 |
| G10 | 22.62 | 0.03746 | -0.52875 | -1.30475 | 0.531499 | 5 |
| G11 | 23.79 | 0.32936 | -1.74369 | -0.37436 | 1.807142 | 15 |
| G12 | 22.88 | 1.60238 | 0.53003 | -0.04039 | 2.369358 | 20 |
| G13 | 23.39 | -0.34397 | 0.08129 | -0.46429 | 0.502342 | 3 |
| G14 | 22.81 | -0.97561 | -0.25321 | 0.36984 | 1.428644 | 12 |
| G15 | 22.53 | -0.60319 | -0.28016 | 0.15423 | 0.913333 | 8 |
| G16 | 22.71 | -0.85084 | -0.24667 | -0.48735 | 1.250775 | 11 |
| G17 | 23.11 | -1.11544 | 0.55376 | 0.46992 | 1.700251 | 14 |
| G18 | 22.34 | -0.22192 | 0.29056 | -0.2691 | 0.432104 | 2 |
| G19 | 22.9 | -0.54897 | 0.59698 | -1.05128 | 0.991122 | 10 |
| G20 | 21.53 | -1.50709 | 0.18225 | 0.25045 | 2.179615 | 19 |

(IPCA) interaction principle component analysis and (ASV) AMMI stability value.

Table (7): No. of spikes/m²mean, interaction principle component analysis scores and AMMI stability value of twenty genotypes across fifteen environments.

| Genotype | number | IPCAg[1] | IPCAg[2] | IPCAg[3] | ASV | rank |
|-------------|--------|----------|----------|----------|----------|------|
| Gemmeiza 9 | 383.3 | -2.89265 | -0.27564 | -3.52452 | 7.71346 | 13 |
| Gemmeiza11 | 353.9 | 9.9358 | -1.26877 | -3.07084 | 26.50799 | 20 |
| Giza168 | 387.3 | 3.97113 | 0.81117 | -1.84054 | 10.61358 | 16 |
| Sakha94 | 391.5 | -3.92082 | 0.78061 | -0.39597 | 10.47759 | 15 |
| Shandaweel1 | 375.2 | 2.73019 | -1.16486 | 2.27774 | 7.368258 | 12 |
| Sids12 | 366.9 | 1.57422 | 2.36807 | 4.26649 | 4.817316 | 6 |
| Sids13 | 398.6 | -8.03965 | 0.33615 | 0.40207 | 21.42725 | 19 |
| Masr1 | 378.9 | -0.15771 | -5.25717 | 2.6593 | 5.273942 | 7 |
| Masr2 | 399.9 | -0.96888 | 2.01741 | -2.8616 | 3.276637 | 3 |
| G10 | 379.5 | 0.22352 | 5.62053 | -3.93441 | 5.652005 | 10 |
| G11 | 386.3 | -1.89496 | -4.74451 | -2.38553 | 6.929001 | 11 |
| G12 | 389.8 | -4.36878 | -1.94959 | 0.29812 | 11.80433 | 17 |
| G13 | 400.4 | -0.45747 | -3.05921 | -2.59895 | 3.293169 | 4 |
| G14 | 385.4 | 4.94678 | -0.49825 | -0.41829 | 13.19193 | 18 |
| G15 | 389.1 | -2.70641 | 5.02311 | -1.58329 | 8.789076 | 14 |
| G16 | 386.9 | 0.61855 | -2.23283 | 0.2918 | 2.775356 | 2 |
| G17 | 369.9 | 1.61462 | 3.43924 | 2.66015 | 5.50836 | 8 |
| G18 | 391.1 | 0.70433 | -1.32521 | 2.50534 | 2.297632 | 1 |
| G19 | 388.3 | -1.93011 | -2.09629 | 1.81538 | 5.554271 | 9 |
| G20 | 369.9 | 1.0183 | 3.47605 | 5.43756 | 4.409846 | 5 |

(IPCA) interaction principle component analysis and (ASV) AMMI stability value.

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Table (8): No. of kernels/ spike mean interaction principle component analysis scores and AMMI stability value of twenty genotypes across fifteen environments.

| Genotype | Number | IPCAg[1] | IPCAg[2] | IPCAg[3] | ASV | Rank |
|-------------|--------|----------|----------|----------|----------|------|
| Gemmeiza9 | 57.71 | -2.17257 | -0.22608 | -1.62523 | 2.255205 | 18 |
| Gemmeiza11 | 58.67 | -1.07019 | 1.36899 | 0.163 | 1.759494 | 14 |
| Giza168 | 57.65 | -1.63429 | 0.05508 | 0.47086 | 1.688804 | 12 |
| Sakha94 | 54.47 | -1.38217 | -0.74055 | 0.53812 | 1.60817 | 11 |
| Shandaweel1 | 58.63 | -1.58534 | 1.12101 | -2.01163 | 1.984333 | 16 |
| Sids12 | 58.93 | -0.01668 | 1.3214 | -0.4779 | 1.321512 | 6 |
| Sids13 | 57.94 | 0.01111 | -1.04113 | 0.14271 | 1.041193 | 4 |
| Masr1 | 54.87 | 0.20334 | -1.32746 | -1.03448 | 1.34397 | 7 |
| Masr2 | 57.72 | -0.84891 | -1.02943 | 0.83606 | 1.352196 | 8 |
| G10 | 55.62 | 2.59517 | -2.97304 | -0.10882 | 4.002876 | 20 |
| G11 | 55.08 | 1.00702 | 1.53649 | 1.87595 | 1.855403 | 15 |
| G12 | 57.43 | 1.28379 | 0.30731 | -0.65564 | 1.361054 | 9 |
| G13 | 54.68 | 0.05187 | -0.57723 | -0.74453 | 0.579711 | 2 |
| G14 | 54.56 | -0.99554 | -0.41704 | 3.10666 | 1.109558 | 5 |
| G15 | 55.25 | -0.90299 | -0.36019 | -0.1835 | 0.999753 | 3 |
| G16 | 57.13 | 0.4398 | 1.3846 | 0.22151 | 1.457203 | 10 |
| G17 | 55.32 | 1.88581 | 0.48491 | -1.17588 | 2.007133 | 17 |
| G18 | 55.71 | 0.70681 | -1.59972 | -0.14297 | 1.758409 | 13 |
| G19 | 55.43 | 0.2483 | -0.00887 | 0.75376 | 0.256599 | 1 |
| G20 | 57.77 | 2.17567 | 2.72097 | 0.05193 | 3.528866 | 19 |

(IPCA) interaction principle component analysis and (ASV) AMMI stability value.

Table (9): 1000-Kernel weight mean, interaction principle component analysis scores and AMMI stability value of twenty genotypes across fifteen environments.

| Genotype | Gram | IPCAg[1] | IPCAg[2] | IPCAg[3] | ASV | Rank |
|-------------|-------|----------|----------|----------|------|------|
| Gemmeiza 9 | 48.58 | -1.019 | 0.463 | -0.727 | 1.66 | 12 |
| Gemmeiza11 | 52.2 | 1.687 | 2.419 | 0.671 | 3.34 | 19 |
| Giza168 | 46.65 | 0.152 | -1.055 | -1.563 | 1.50 | 7 |
| Sakha94 | 46.35 | 0.389 | 1.495 | 0.560 | 1.53 | 8 |
| Shandaweel1 | 45.92 | -0.175 | -0.142 | 0.431 | 1.61 | 11 |
| Sids12 | 49.53 | -0.754 | 0.135 | -0.609 | 1.26 | 4 |
| Sids13 | 43.48 | -0.527 | -0.078 | 1.589 | 1.33 | 5 |
| Masr1 | 48.32 | -0.031 | 1.430 | -0.431 | 1.48 | 6 |
| Masr2 | 45.2 | -0.856 | -0.250 | 0.963 | 1.20 | 2 |
| G10 | 49.31 | 0.580 | 0.298 | -0.690 | 2.02 | 16 |
| G11 | 48.8 | 1.568 | 0.109 | -0.633 | 2.37 | 17 |
| G12 | 47.19 | 0.804 | -0.387 | 0.055 | 1.07 | 1 |
| G13 | 48.14 | -0.977 | 0.268 | 0.091 | 1.21 | 3 |
| G14 | 48.63 | -0.305 | -2.112 | 2.023 | 1.78 | 14 |
| G15 | 48.32 | -1.394 | 0.275 | 1.021 | 1.89 | 15 |
| G16 | 46.4 | 0.415 | -1.258 | -0.471 | 1.53 | 9 |
| G17 | 51.27 | 2.646 | -1.500 | -0.243 | 4.48 | 20 |
| G18 | 46.24 | 0.916 | -0.159 | 0.089 | 1.68 | 13 |
| G19 | 46.24 | -1.902 | -0.734 | -1.541 | 2.93 | 18 |
| G20 | 50.4 | -1.217 | 0.786 | -0.586 | 1.53 | 10 |

(IPCA) interaction principle component analysis and (ASV) AMMI stability value

The AMMI stability value measure was proposed by Purchase, (1997) and Purchase *et al.*, (2000). ASV is the distance from zero in a two-dimensional scatter gam of IPCA 1 score against IPCA 2. A genotype with least ASV is the most stable, in respect to grain yield as given in

Table (6) and illustrated in Figure (1), the most stable genotypes were Giza168, G18, G13, Gemmeiza11 and G10 with high yield potential, where genotypes G12, G20, Sids13 and Sids12 unstable and more responsive to the environmental changes.

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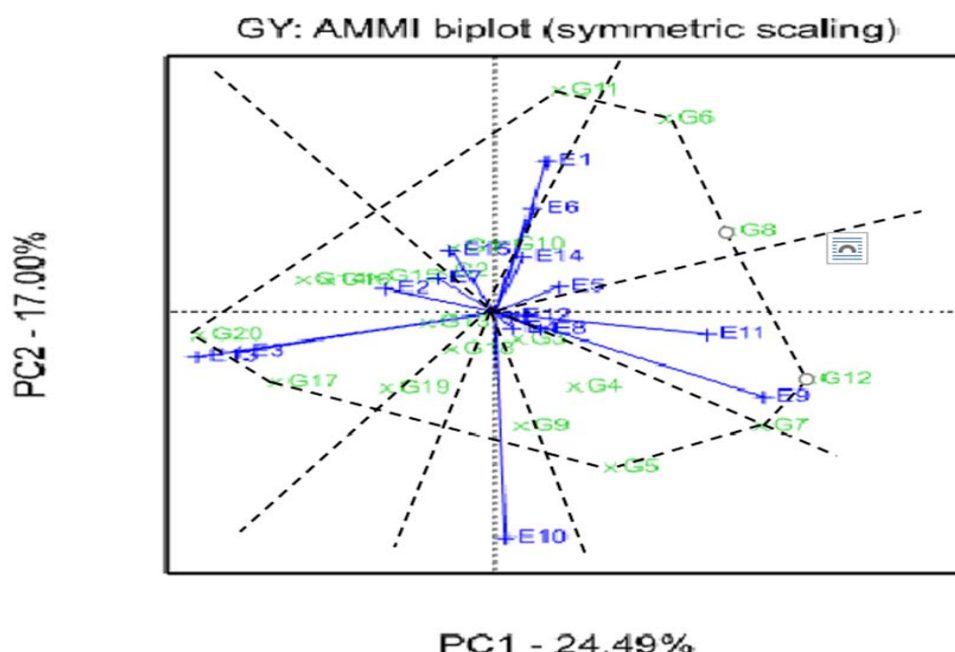


Figure 1: Additive mean multiplicative interaction (AMMI) scatter plot for grain yield (GY), + Environment sign and x genotype sign.

| code | genotypes | code | genotypes | code | environment | code | environment |
|------|--------------|------|-----------|------|-----------------------|------|-----------------------|
| G1 | Gemmeiza 9 | G11 | Line 2 | E1 | Sakha year 9/10 | E11 | Sakha year 11/12 |
| G2 | Gemmeiza11 | G12 | Line 3 | E2 | Gem.year 9/10 | E12 | Gem.year 11/12 |
| G3 | Giza168 | G13 | Line 4 | E3 | Nubariayear 9/10 | E13 | Nubariayear 11/12 |
| G4 | Sakha94 | G14 | Line 5 | E4 | Sidsyear 9/10 | E14 | Sidsyear 11/12 |
| G5 | Shandaweel 1 | G15 | Line 6 | E5 | Shandaweel year 9/10 | E15 | Shandaweel year 11/12 |
| G6 | Sids 12 | G16 | Line 7 | E6 | Sakha year10/11 | | |
| G7 | Sids 13 | G17 | Line 8 | E7 | Gem.year 10/11 | | |
| G8 | Masr 1 | G18 | Line 9 | E8 | Nubariayear 10/11 | | |
| G9 | Masr 2 | G19 | Line 10 | E9 | Sidsyear 10/11 | | |
| G10 | Line 1 | G20 | Line 11 | E10 | Shandaweel year 10/11 | | |

The best genotypes with respect to E5 and E14 were Sids12 and Masr1. For E13, E3, E2 and E7 as well as G20 and G 17. For E6, E1 and E15 were G11. for E4 was Sids13and shandaweel1 fore E9, E11, E8 and E12 were G12; also show that E1, E9 and E13 were the most discriminative environments as indicated by the longest distance between its mark and the origin and accounted the most part of G x E interaction.

Concerning number of spikes/m² Table (7) and Figure (2) the most stable genotypes were G18, G16, Masr2, G13 and

G20 with high yield potential, where genotypes Gemmeiza11, Sids13, and G14 unstable and more responsive to the environmental changes.

The best genotypes with respect to E15, E10, E8, E3, E9, E5, E13, E4 and E12 were Gemmeiza11. for E6, E2, E1, E7 and E11 were Sids13.; also show that E1 and E6 were the most discriminative environments as indicated by the longest distance between its mark and the origin and accounted the most part of G x E interaction.

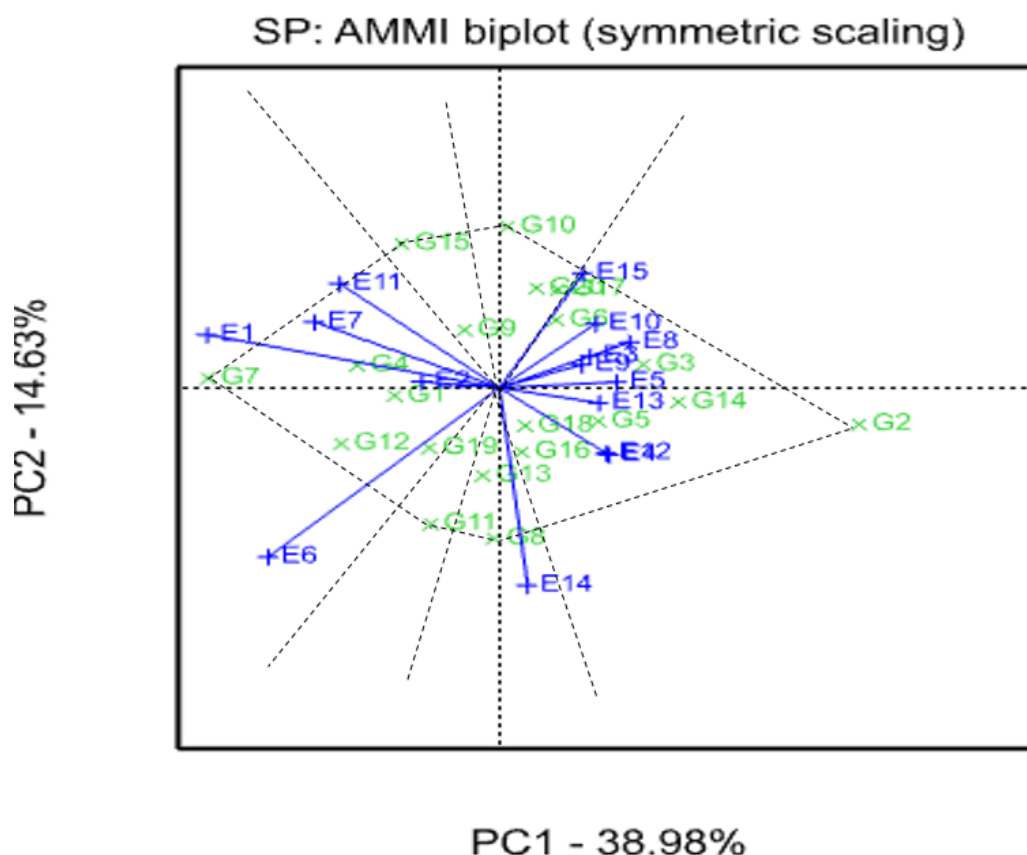


Figure 2: Additive mean multiplicative interaction (AMMI) scatter plot for no.of spikes/m²(SP), + Environment sign and x genotype sign.

With regarded to number of kernels/ spike Table (8) and Figure (3) the most stable genotypes were G19, G13, G15, Sids13and G14 with high yield potential, while the genotypes G10, G20, and Gemmeiza 9 unstable and more responsive to the environmental changes.

The best genotypes with respect to E7, E12, E2 and E8 were G20. for E1, E13, E3, E10 and E11 as well as G10.for E5, E15 and E4 were G1. for E9, E6 and E14 were Shandaweel 1 the results show that E14, E15, E5 and E4 were the most discriminative environments as indicated by the longest distance between its mark and the origin and accounted the most part of G x E interaction.

For 1000-kernel weight Table (9) and Figure (4) the most stable genotypes were G12, Masr2, G13, Sids12and Sids13 with high yield potential, where genotypes G17, Gemmeiza11, and G19 unstable and more responsive to the environmental changes. Gemmeiza11 was the best genotypes at E10, E15, E5, E7, E14 andE4, while G17 the best genotypes at E1 and E6. G19 the best genotypes at E3, E9, and E13.

The most discriminative environments as indicated by the longest distance between its mark and the origin and accounted the most part of G x E interaction.

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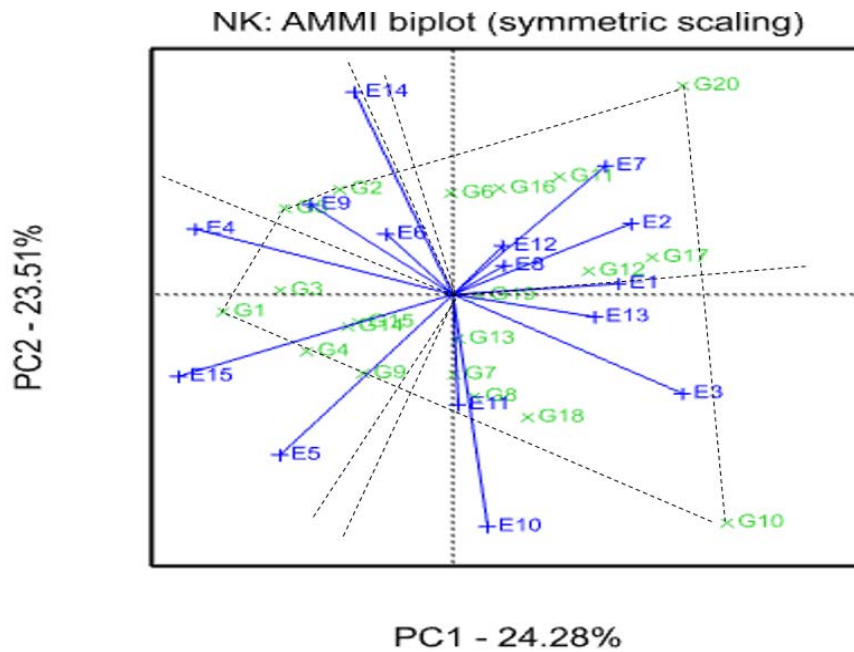


Figure 3: Additive mean multiplicative interaction (AMMI) scatter plot for No. of kernel/spike (NK), + Environment sign and x genotype sign.

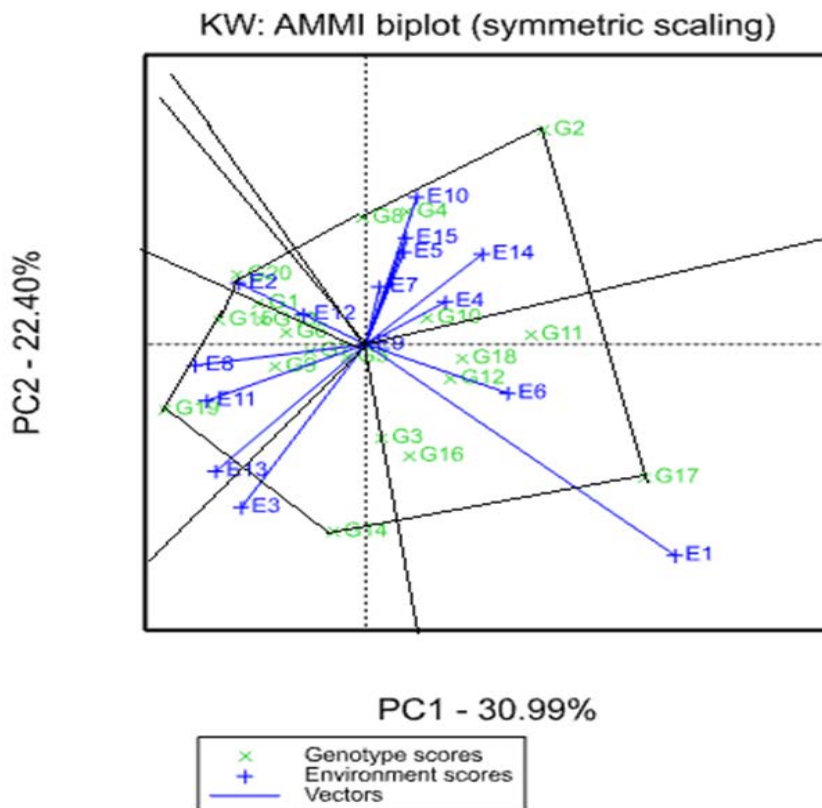


Figure 4: Additive mean multiplicative interaction (AMMI) scatter plot for 1000-Kernel weight (KW), + Environment sign and x genotype sign.

Conclusion

- 1- The results Indicated that genotypes the most stable genotypes were Giza168, G18, G13, Gemmeiza11 and G10 with high yield potential. The best genotypes with respect to E5 and E14 were Sids12 and Masr1. for E13, E3, E2 and E7 as well as G20 and G 17. for E6, E1 and E15 were G11. for E4 was Sids13 and shandaweel1 fore E9, E11, E8 and E12 were G12; also show that E1, E9 and E13 were the most discriminative environments for grain yield.
- 2- The most stable genotypes were G18, G16, Masr2, G13 and G20 with high yield potential and the environments number (E15, E10, E8, E3, E9, E5, E13, E4 and E12) were Gemmeiza11. For E6, E2, E1, E7 and E11 were Sids13.; also show that E1 and E6 were the most discriminative environments for number of spikes/m².
- 3- With regarded to number of kernels/ spike the most stable genotypes were G19, G13, G15, Sids13 and G14 with high yield potential, where genotypes G10, G20. The best genotypes with respect to E7, E12, E2 and E8 were G20. for E1, E13, E3, E10 and E11 as well as G10. for E5, E15 and E4 were G1. for E9, E6 and E14 were Shandaweel1; also show that E14, E15, E5 and E4 were the most discriminative environments.
- 4- For 1000-kernel the most stable genotypes were G12, Masr2, G13, Sids12 and Sids13 with high yield potential, where genotypes G17, Gemmeiza11, and G19 unstable and more responsive to the environmental changes. Gemmeiza11 was the best genotypes at E10, E15, E5, E7, E14 and E4, while G17 the best genotypes at E1 and E6. G19 the best genotypes at E3, E9, and E13.

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تحليل الثبات لمحصول الحبوب في بعض التراكيب الوراثية لقمح الخبز

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الملخص العربى

يتعين على مربى القمح تحديد الأصناف والسلالات الجديدة التي تستجيب للتغيرات البيئية للتعرف على التراكيب الوراثية المتفوقة في منطقة ما. لذلك أجريت هذه الدراسة لتقييم 20 تركيباً وراثياً من قمح الخبز (*Triticum aestivum* L) تتضمن 9 أصناف منزرعة و 11 سلالة واعدة لتقييمها في خمسة مواقع مختلفة (سحا - الجميزة - النوبارية - سدس - ومحطة بحوث شندويل)، خلال ثلاثة مواسم زراعية (2009-2010 ، 2010-2011 و 2011-2012) ، واختيار التراكيب الوراثية ذات الصفات المرغوبة لاستخدامها في برنامج تربية القمح في المستقبل. أجريت التجارب في تصميم قطاعات كاملة العشوائية بثلاثة مكررات في كل موقع. تم اخذ القراءات التالية عدد السنابل لكل متر مربع ، وعدد الحبوب لكل سنبل ، و وزن 1000 حبة/جم ومحصول الحبوب اردب/الفدان) من التراكيب الوراثية في كل موقع وتم تحليل النبات الوراثي بطريقتي AMMI والمحاور الثنائية للتفاعل بين البيئة والتركيبة الوراثي (GE- Biplot) ويمكن تلخيص اهم النتائج فيما يلى:

- 1- اظهرت النتائج ان التراكيب الوراثية جيزة 168 ، G18 ، G13 ، جميزة 11 و G10 اكثر ثباتا مع الانتاجية العالية للمحصول. كانت افضل التراكيب الوراثية فيما يتعلق بالبيئات رقم E5 و E14 هي سدس 12 و مصر 1. اما بالنسبة للتراكيب الوراثية G20 و G17 فكانت البيئات رقم E13 و E3 و E2 و E7 افضل البيئات ها. وبالنسبة للتراكيب الوراثية G11 فكانت افضل البيئات له هي E6 و E1 و E15 . البيئه رقم E4 كانت بيئه مثالية للتراكيب الوراثية سدس 13 و شندويل 1. وكان التركيب الوراثي G12 مميز فى البيئات رقم E9 و E11 و E8 و E12 ؛ اوضحت النتائج ان البيئات رقم E1 و E9 و E13 كانت البيئات الأكثر تميزاً بالنسبة لصفة محصول الحبوب اردب/الفدان.
- 2- كانت التراكيب الوراثية G18 و G16 و مصر 2 و G13 and G20 اكثر ثباتا مع زيادة الانتاجية بالنسبة لصفة عدد السنابل/م². كانت أفضل التراكيب الوراثية هي جميزة 11 فيما يتعلق بالبيئات رقم E15 ، E10 ، E8 ، E3 ، E9 ، E5 ، E13 ، E4 و E12. والتركيبة الوراثية سدس 13 فى البيئات رقم E6 و E2 و E1 و E11. E7 . تبين أيضاً أن E1 و E6 هما أكثر البيئات تميزاً بالنسبة لصفة عدد السنابل /م².
- 3- اوضحت النتائج ان التراكيب الوراثية الأكثر ثباتا هي G19 و G13 و G15 و سدس 13 و G14 . و أفضل التراكيب الوراثية G20 بالنسبة للبيئات رقم E7 ، E12 ، E2 ، والبيئة رقم E8. للتركيب الوراثي G10. وان البيئات E14 و E15 و E5 و E4 كانت الأكثر تميزاً بالنسبة لصفة عدد الحبوب / السنبل
- 4- كانت التراكيب الوراثية الأكثر ثباتا هي G12 ، و مصر 2 ، و G13 ، و سدس 12 و سدس 13 بالنسبة لصفة وزن 1000 حبة وكانت افضل التراكيب الوراثية هي جميزة 11 فى البيئات رقم E10 ، E15 ، E5 ، E7 ، E14 ، E4. و اظهرت النتائج ان التركيب الوراثي G17 يعطى اعلى انتاجية فى للبيئات رقم E6 و E1. ايضا كان التركيب الوراثي G19 بالنسبة إلى البيئات رقم E9 و E13 و E3. وكانت البيئات رقم E1 و E9 كانت أكثر البيئات تميزاً بالنسبة لصفة وزن 1000 حبة.

أسماء السادة المحكمين

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