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STABILITY ANALYSIS FOR GRAIN YIELD IN BREAD GENOTYPES

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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 / m 2, 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.

Key words: ***Bread Wheat, Grain Yield, Ammi Stability Value***

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 × environment interaction (G × 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 x 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 x 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 x E interactions. In the presence of G x 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-

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-OY-OGM
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 (4.2m^2) contain six rows was 20cm between rows long at 3.5m.

Studied characters

1- Number of spikes/ m^{-2}: Number of fertile tillers/ m-² 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 λ0.5 γg and λ0.5 δe, 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) andPurchase *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 IPCAI scores against IPCA2 scores. Because the IPCA1 score contributes more to G × 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 twenty bread wheat genotypes across fifteen environments. The AMMI analysis of variance revealed that environments (E), genotypes (G) and the Genotypes × Environments interaction (GEI) mean squares were highly significant for grain yield.

Also, the AMMI analysis of variance showed that (73.79,57.47.27.45and 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× 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.**

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.

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, Gemmeiza11and G10 with high yield potential, where genotypes G12, G20, Sids13 and Sids12 unstable and

more responsive to the environmental changes.

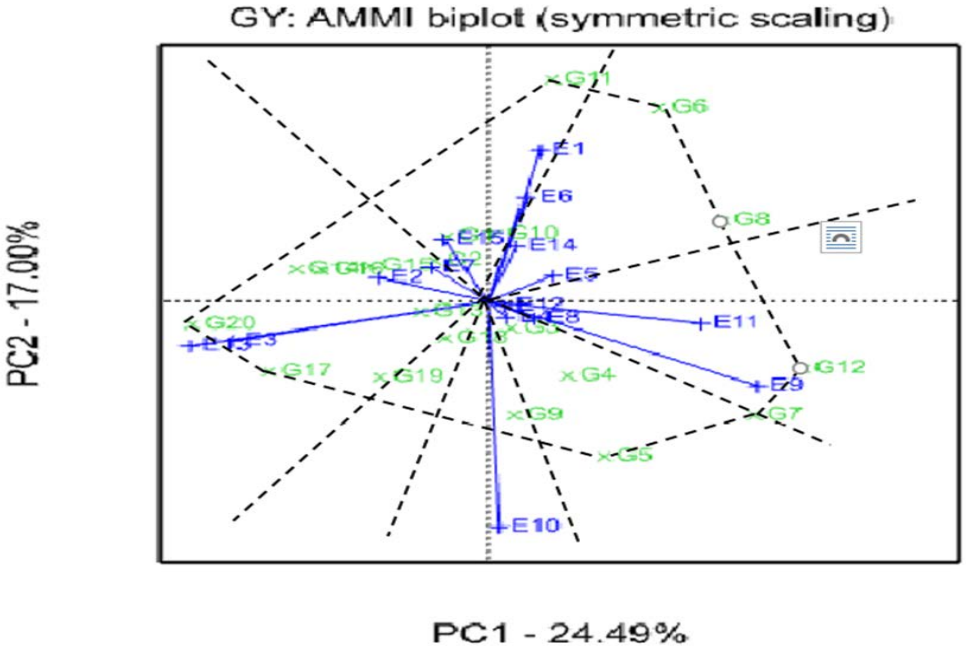

Figure 1: Additive mean multiplicative interaction (AMMI) scatter plot for grin yield (GY), + Environment sign and × genotype sign.

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.

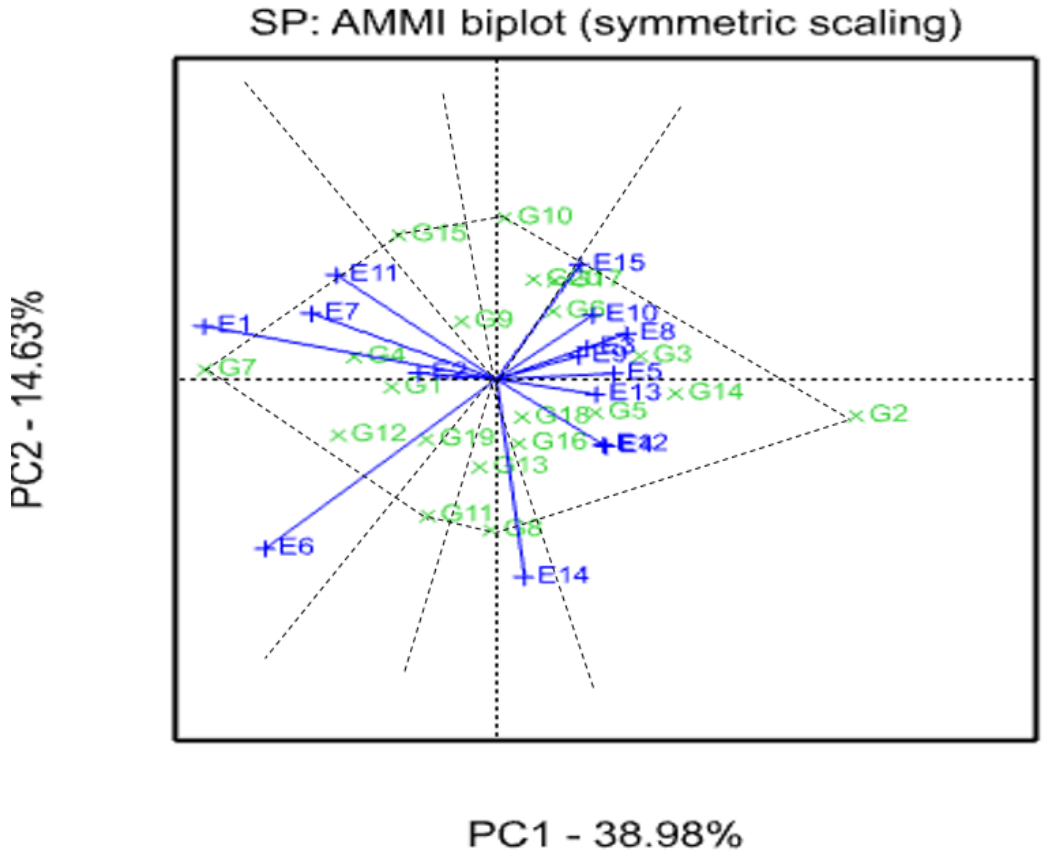

Figure 2: Additive mean multiplicative interaction (AMMI) scatter plot for no.of spikes/m²(SP), + Environment sign and × genotype sign.

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.

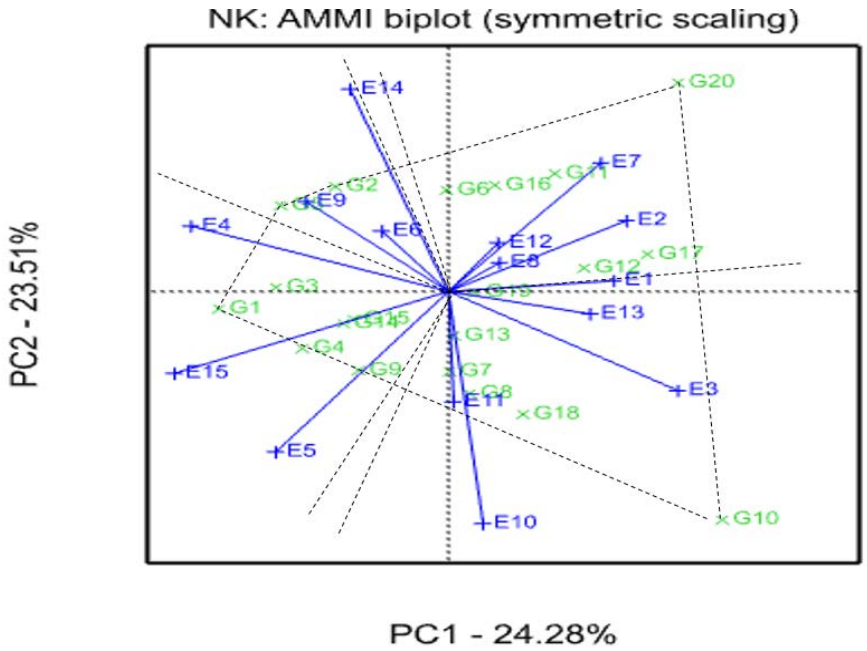

Figure 3: Additive mean multiplicative interaction (AMMI) scatter plot for No. of kernel/spike (NK), + Environment sign and × genotype sign.

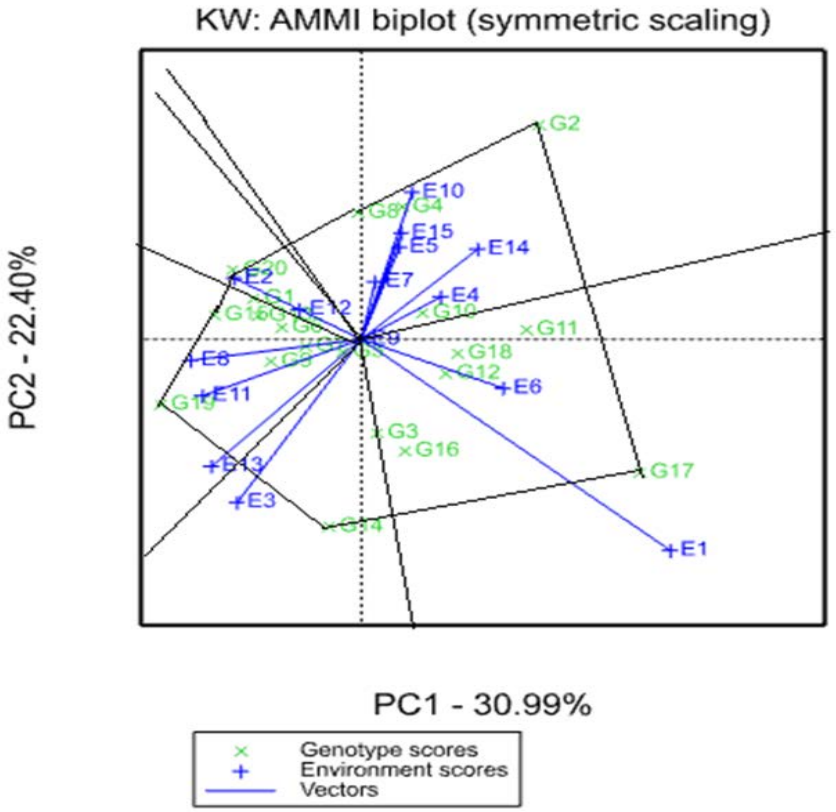

Figure 4: Additive mean multiplicative interaction (AMMI) scatter plot for 1000-Kernel weight (KW), + Environment sign and × genotype sign.

Conclusion

1- **The results Indicated that genotypes the most stable genotypes were Giza168, G18, G13, Gemmeiza11and 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 andE15 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 for grain yield.**

2- **The most stable genotypes were G18, G16, Masr2, G13and 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, Sids13and 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 andE4 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, 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.**

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تحليل الثبات لمحصول الحبوب في بعض التراكيب الوراثية لقمح الخبز

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الملخص العربى

يتعين على مربي القمح تحديد الأصناف والسلالات الجديدة التي تستجيب للتغيرات البيئية للتعرف علي التراكيب الوراثية المتفوقة في منطقة ما. لذلك أجريت هذه الدراسة لتقييم 20 تركيبا وراثيا من قمح الخبز (*Triticum aestivum* L) تتضمن 9 أصناف منزرعة و 11 سلالة واعدًة لتقيمها في خمسة مواقع مختلفة (سخا -الجميزة – النوبارية- سدس -ومحطة بحوث شندويل)، خلال ثلاثة مواسم زراعية (2009-2010 ، 2010-2011 و2011-2012) ، 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 االسنابل لكل متر مربع ، وعدد الحبوب لكل سنبلة ، 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 والتركيب الوراثي (GE- Biplot)

ويمكن تلخيص اهم النتائج فيما يلى:

1- اظهرت النتائج ان التراكيب الوراثية جيزة 168 ، G18، G13، جميزة11 و G10 اكثر ثباتا مع الانتاجية العالية للمحصول.كانت افضل التراكيب الوراثية فيما يتعلق بالبيئات رقم5E و E14 هى سدس12 و مصر1. اما بالنسبة للتراكيب الوراثيةG20 و G 17 فكانت البيئات رقمE13 و E3 و E2 و E7 افضل البيئاتل ها. وبالنسبة للتركيب الوراثيةG11 فكانت افضل البيئات له هى E6 و E1 و E15 . البيئه رقم E4 كانت بيئة مثالية للتراكيب الوراثية سدس13 و شندويل.1 وكان التركيب الوراثىG12 مميز فى البيئات رقم E9 و E11 و E8 و E12 ؛ اوضحت النتائج ان البيئات رقمE1 و E9 و E13 كانت البيئات الأكثر تميزًا بالنسبة لصفة محصول الحبوب اردب/الفدان.

2- كانت التراكيب الوراثية G18وG16 ومصر2و G13and G20 اكثر ثباتا مع زيادة الانتاجية بالنسبة لصفة عدد السنابل/م2.كانت أفضل التراكيب الوراثية هى جميزة 11فيما يتعلق بالبيئات رقمE15 ، E10 ، E8 ، E3 ، E9 ، E5 ، E13 ، E4و .E12 والتركيبة الوراثية سدس 13 فى البيئات رقم E6 و E2 و E1 و .E11 E7 . تبين أيضًا أن E1و E6 هما أكثر البيئات تميزًا بالنسبة لصفة عدد السنابل /م2.

3- اوضحت النتائج ان التراكيب الوراثية الأكثر ثباتا هي G19 و G13 و G15 و سدس 13و G14 . و أفضل االتراكيب الوراثية G20 بالنسبة للبيئات رقم E7، E12، E2 والبيئة رقم E8.للتركيب الوراثى G10.وان البيئاتE14 و E15 و E5 و E4 كانت الأكثر تميزًا بالنسبة لصفة عدد الحبوب / السنيلة

4- كانت التراكيب الوراثية الأكثر ثباتا هي G12 ، و مصر2 ، و G13 ، و سدس12 وسدس13 بالنسبة لصفة وزن 1000 حبة وكانت افضل التراكيب الوراثية هى جميزة 11 فى البيئات رقم E10، E15، E5، E7، E14 و E4. واظهرت النتائج ان التركيب الوراثىG17 يعطى اعلى انتاجية فى للبيئات رقم .E6 و E1. ايضا كان التركيب الوراثىG19 بالنسبة إلى البيئات رقمE9 و E13 و E3. وكانت البيئات رقم E1 وE9 كانت أكثر البيئات تميزًا بالنسبة لصفة وزن 1000 حبة.

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