

GENOTYPIC STABILITY FOR SOME BREAD WHEAT PURE LINES

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ABSTRACT

The objective of this research to evaluate a genotypic stability for new developed wheat pure lines (*Triticum aestivum* L.). A crossing program among six wheat genotypes; Alfateh, A.3031, M2, IPA99, A4.10 and Abu-Ghraib3, were crossed during 2001-2002, using half diallel method and developed 15 crosses. A single plant selection was used during six seasons. The parents and some selected crosses (S12, S52, S76, S83, S94, S97, S102, S118, S123, S130, S148, S152, S155, S175, S177), were evaluated during five years (2009-2014), using randomized complete block design. The results were analyzed using analysis of variance and some statistic parameters SD, SE and CV, joint regression method also, adopted to evaluate the stability of genotypes through five environments, for grain yield and it's components. A significant differences were found among genotypes, environments and GxE interaction in all the traits. The highest grain yield 5981 kg.ha⁻¹ produced from the genotype S123. The statistical analysis revealed that S155 had highest grain yield stability. While joint regression method showed that, S130 had higher stability and S155, S152, and S118 were a promising stable and high productive genotypes and the genotype S123 was more adapted to favorable environment.

Key words: grain yield, adaptability, crossing, genotypes.

بكتاش

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الثبات الوراثي لبعض الخطوط النقية من حنطة الخبز

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المستخلص

يهدف البحث الى تقييم الثبات الوراثي لبعض الخطوط النقية من حنطة الخبز. أجريت تضرّيبات تبادلية بين ستة تراكيب وراثية: Alfateh, A.3031, M2, IPA99, A4.10 and Abu-Ghraib3 في الموسم 2001-2002 واستنبطت 15 تضرّيبا. تم تنفيذ برنامج انتخاب نبات - خط لستة مواسم. تم تقييم الاباء و بعض التراكيب الوراثية (S12, S52, S76, S83, S94, S97, S102, S118, S123, S130, S148, S152, S155, S175, S177) في خمس سنوات (2009-2014) باستعمال تصميم القطاعات الكاملة المعشاة وبأربعة مكررات. حلت النتائج حسب تحليل التباين وتم استعمال بعض الطرائق الاحصائية SD, SE, CV بالإضافة الى طريقة Joint regression. وجدت فروقات معنوية بين التراكيب الوراثية والبيئات والتداخل بينهما. انتج التركيب الوراثي S123 اعلى حاصل للحبوب 5891 كغم.ه⁻¹. أثبت التحليل الاحصائي بأن التركيب الوراثي S155 تميز في الثبات الوراثي في حاصل الحبوب، بينت طريقة Joint regression بأن التركيب الوراثي S130 لها اعلى ثبات وراثي، والتراكيب الوراثية S155, S152, S118 تميزت بالثبات الوراثي و الحاصل العالي، والتركيب الوراثي S123 ملائمة في البيئات المناسبة للحنطة.

كلمات مفتاحية: حاصل الحبوب، ملائمة، تضرّيبات، تراكيب وراثية.

INTRODUCTION

The reliability of cultivar performance across locations and years can be an important consideration in plant breeding. Some cultivars are adapted to a broad range of environmental conditions, while others are more limited in their potential distribution. There are cultivars that perform similarly regardless of the productivity level of the environment, and others whose performance is directly related to the productivity potential of the environment (3). The stability of cultivar performance across environments is influenced by the genotype of individual plants and the genetic relationship among plants of the cultivar. The terms of homeostasis and buffering have been used to describe the stability in performance of individual plants or groups of plants over different environments (17). Genetic homeostasis and population buffering have been used to describe the stability of groups of plants that exceeds of its individual members (7). Phenotypic stability is the important ideal for the genotypes which release to commercial cultivation at a wide range of environment in the future, the yield and its components could be varies due to local environment for those genotypes (8, 30, 31). Generally the phenotypic stability will be estimate by the interaction of genotypes X environment (GXE), when study at different locations or and different years (26, 28, 33, 34). After statistical analysis, when GXE significant, this mean that tested genotypes differ in their response across environments, but when not significant this reveal that studied genotypes react similarity across environments. For studying phenotypic stability, the genotypes must be grown in multi locations, or multi years or using different agricultural managements and seeding dates within the study (11, 12, 18). The field crops grown under a wide range of the environments, like temperatures, moisture, soil properties cultivation and managements, all those influences become under classification of environments (1, 2, 14, 15). Stress tolerance of a plant genotype is a product of many physiological and morphological characters for which effective selection criteria have not yet been developed (22). Therefore, grain yield and its components remain the major selection

criteria for improved adaptation to environmental stresses in many breeding programs (23, 24). Grain yield stability is one of the most important needs of agriculture, especially in the sub-tropical environment. The ideal wheat genotype should be high yielding under any environmental conditions, but as genetic effects are not independent of environmental effects, most genotypes do not perform satisfactorily in all environments (2, 9, 19, 21). When interaction between genotype and environment occur, the relative ranking of cultivars for yield often differs when genotypes are compared over a series of environments and/or years. This poses a serious problem for selecting genotypes significantly superior in grain yield (32, 33). Various statistical techniques have been developed to identify systematic variation in individual genotypic responses. Among these, Eberhart and Russell model (12) has been widely used in studies of adaptability and stability of plant materials (7, 9, 13, 16). Joint regression proposed by Finlay and Wilkinson (18), statistical analysis of adaptation was widely used for stability estimation, some times descriptive statistical analysis SD, SE and CV used for stability analysis. The effectiveness of each method depends on the proportion of the genotype by environment interaction that each analysis can explain (29). Therefore, the choice of an adequate model to measure the stability of different genotypes is a question to be resolved by researchers. According to Crossa et al. (10), the selection of superior genotypes in a plant-breeding program is based mainly on their yield potential and stable performance over a range of environments (25). This study was conducted to evaluate a phenotypic stability for new developed wheat pure lines.

MATERIALS AND METHODS

A crossing program among six wheat (*Triticum aestivum* L.) pure lines; Alfateh, A.3031, M2, IPA99, A4.10 and Abu-Ghraib3, were started during 2001-2002, using half diallel method. The crosses and parents were evaluated (4, 6). A single plant selection was used during six seasons. The parents and some promising selected lines (S12, S52, S76, S83, S94, S97, S102, S118, S123, S130, S148, S152, S155, S175, S177), were evaluated

during five years (2009-2014), using randomized complete block design with 4 replications, (Table1). The soil and plants management used as recommended by the researchers. The nitrogen fertilizer as urea (46% N) used as nitrogen sources, of rate of 200kg.ha⁻¹, splitted in three applications; during third leaves initiation, stem nodes discover and booting stage. Superphosphate fertilizer (45 % P₂O₅), was added at 100 kg.ha⁻¹ during soil preparation. The genotypes planted during the second half of November in

each year. During growing seasons hand weeding and irrigation were applied when needed. The results were analyzed using analysis of variance and the means were compared by LSD (27). The genotype environmental interaction (GxE) was analyzed using parametric statistic, Standard deviation (SD), Standard error (SE), Coefficient of variation (CV) and joint regression method adopted by Finlay and Wilkinson (18) used to evaluate their phenotypic stability across environments.

Table1. Genotype symbols , pedigree and origin

Genotypes	Symbols	Pedigree	Origin
Alfateh	P1	(CI-82-24/C168-3/3Cn02 /711C / Tob-Swm6828-6AP-3-AP-OAP) xMexipak	Iraq
A3103	P2	Kanz/'S'/Kanz/S/xICW-91-0493-OTS-SAP-OTS-IAP-OAP	Australian
M.2	P3	Ns732Hcr/shix4414/Crolj'S'	Germany
IPA99	P4	Ures/Bows/3/Jup/B/2S1//Ures	CIMMYT
A4.10	P5	Kanz/3/S/ x ICW-91-0157-OBR-12AP-OTS-OAP	Australian
Abu-Graib3	P6	Ajeepa x Inia66R x Mexico24	Iraq
S12	G1	5x4	A4.10 x IPA99
S52	G2	4x1	IPA 99 x Alfateh
S76	G3	6x3	Abu-Graib3 x M. 2
S83	G4	4x2	IPA99 x A3103
S94	G5	4x3	IPA99 x M.2
S97	G6	5x3	A4.10 x M.2
S102	G7	2x1	A3103 x M.2
S118	G8	6x1	Abu-Ghraib3 x Alfateh
S123	G9	6x5	Abu-Ghraib3 x A4.10
S130	G10	5x4	A4.10 x IPA99
S148	G11	5x2	A4.10 x A3101
S152	G12	6x2	Abu-Ghraib3 x A3103
S155	G13	4x3	IPA99 x M.2
S175	G14	5x1	A4.1 x Alfateh
S177	G15	6x1	Abu-Ghraib3 x Alfateh

RESULTS AND DISCUSSION

Estimation of genotype x environment interaction obtained with selected genotypes may be higher or lower than those with be obtained with random individual plants(13).

1-Number of spikes.m⁻²

In wheat plant cultivars spikes population depend on the tillering processes, more of wheat plants produce tillers with higher number of barren spikes. Tillering activity in wheat continue to the end of booting stage, at this stage the highest number of fertile tillers could be found (5). A significant differences were found among genotypes through different environments in number of spikes. M² (Table 2). The genotype G7 produced the higher number of spikes (465 spikes), while the lowest number of spikes (364 spikes) were produced from the plants of G11. We can conclude that the G11 could be adequate to

highest seeding rates. Also a significant differences were found among environments and genotypes x environment interaction (GxE). The GxE interaction reflect ranking difference among genotypes a cross environments. The phenotypic stability estimates by another statistical parameters indicated that the G5 had lowest values for SD, SE and CV in comparison to the other genotypes, (27.3 , 12.2 , 6.22), respectively, (Table 3) . So, G5 considered as more stable than the others by using those parameters for the number of spikes. M². The phenotypic stability analysis by the joint regression adopted by Finlay and Wilkinson (18) method showed that the G1, G8 and G15 more stable and there regression coefficient values (b) are close to unity (1.04, 1.0, 1.07, respectively) and there values located at the desirable region from rectangular at the right site from the

means of genotypes (Fig.1). So, they produced higher number of spikes $.m^{-2}$ and more stability. We can conclude, when the plant breeder aimed higher number spikes. m^{-2} could be use the genotypes G1, G2, G15, will

be satisfied but when he targeted for lowest number of spikes. m^{-2} and lowest number of tillers, due to use higher seeding rates, the G2 and G11 could be used, (8).

Table2.Genotypes mean number of spikes. m^{-2} for different environments.

Genotypes		E1	E2	E3	E4	E5	Means
G1	S12	342	458	453	498	539	458
G2	S52	299	440	411	436	453	408
G3	S76	369	477	438	453	472	442
G4	S83	246	488	420	443	466	412
G5	S94	409	472	412	445	455	439
G6	S97	343	485	365	457	457	421
G7	S102	402	523	425	484	491	465
G8	S118	339	496	430	448	483	439
G9	S123	229	496	390	434	461	402
G10	S130	298	496	487	405	446	426
G11	S148	215	419	376	400	409	364
G12	S152	376	516	390	457	453	438
G13	S155	346	470	425	444	449	427
G14	S175	444	566	408	446	412	455
G15	S177	361	557	436	431	459	449
LSD		10.11					4.52
Means		335	490	418	445	460	
LSD		2.61					

Table3.Some statistical analysis of genotypes number of spikes . m^{-2} for different environments .

Genotypes		Means	SD	SE	CV	b
G1	S12	458	73.6	32.9	16.09	1.01
G2	S52	408	62.8	28.1	15.39	1.00
G3	S76	442	43.4	19.4	9.82	0.72
G4	S83	412	96.4	43.1	23.38	1.59
G5	S94	439	27.3	12.2	6.22	0.41
G6	S97	421	63.1	28.2	14.96	0.97
G7	S102	465	49.8	22.3	10.71	0.79
G8	S118	439	62.3	27.9	14.18	1.04
G9	S123	402	104.0	46.5	25.87	1.75
G10	S130	426	80.4	35.9	18.86	1.14
G11	S148	364	84.7	37.9	23.30	1.37
G12	S152	438	56.5	25.3	12.90	0.85
G13	S155	427	47.9	21.4	11.23	0.80
G14	S175	455	64.4	28.8	14.14	0.49
G15	S177	449	70.4	31.5	15.70	1.07

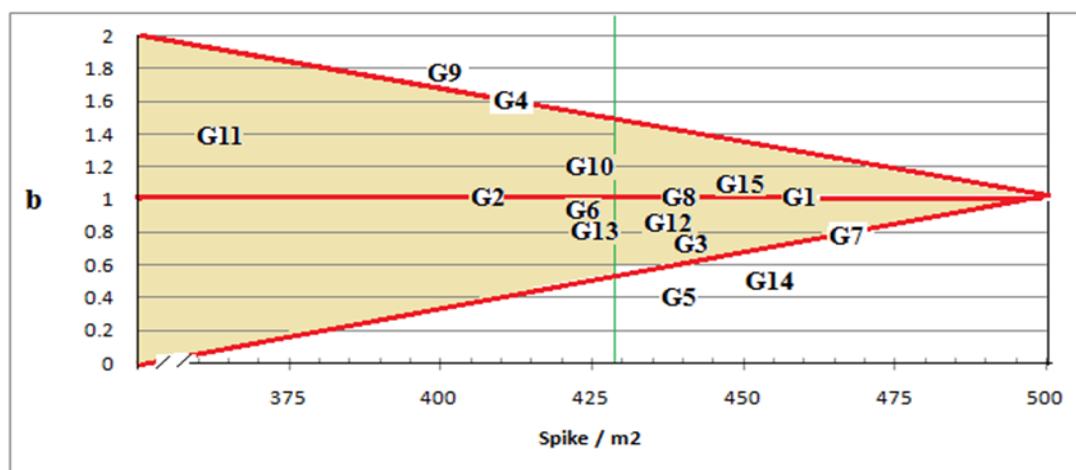


Fig.1 .Regression of genotypes number of spikes $.m^{-2}$ to different environments.

Numer of grains .spike⁻¹:

There are a significant correlation between number of fertile flowers and number of grains formation at maturity period, under a wide range of genotype and environmental effects (5, 6, 25). The grains formation and development depends to the genetic materials, environmental effects and their interaction (G x E), (11). A significant differences were found among genotypes through different environments in number of grains .spike⁻¹ (Table 4). The genotype G2 produced the highest number of grains .spike⁻¹ (75 grains), and didn't differ significantly from both genotypes G9 and G10 . Also, a significant differences were found among environments and genotypes x environments interaction

(GxE), (Table 4).The parametric phenotypic stability indices revealed that G14 had low SD (4.30) , SE (1.92) and CV (7.24) and considered as more stable genotype , (Table5).According to the joint regression adopted by Finlay and Wilkinson (18), analysis indicated that G2 , G9 , G10 , G11 were located at the desirable region from rectangular, (Fig. 2). Those location revealed that the Genotypes G2, G9, G10, G11, were highly stable in comparison to other genotypes in number of grains . spike⁻¹ . The genotype G2 which produced highest number of grains . spike⁻¹, (Table 4) within the higher stable , could be use in the future to produce cultivars with the highest number of grains .spike⁻¹, which one of the essential grain yield components, (26).

Table4. Genotypes mean number of grains. spike⁻¹ for different environments.

Genotypes		E1	E2	E3	E4	E5	Means
G1	S12	96	67	56	59	59	67
G2	S52	108	78	64	64	61	75
G3	S76	91	61	60	62	57	66
G4	S83	106	68	64	62	60	72
G5	S94	92	59	53	53	54	62
G6	S97	100	61	54	52	52	64
G7	S102	99	62	61	62	60	69
G8	S118	107	62	54	54	52	65
G9	S123	108	64	68	66	67	74
G10	S130	107	69	64	62	63	73
G11	S148	104	66	66	63	62	72
G12	S152	106	65	59	58	53	68
G13	S155	106	67	59	59	52	69
G14	S175	53	64	62	60	59	59
G15	S177	93	59	56	57	59	65
LSD		5.52					2.47
Means		98	65	60	60	58	
LSD		1.43					

Table5. Some statistical analysis of genotypes number of grains spikes⁻¹ for different environments

Genotypes		Means	SD	SE	CV	b
G1	S12	67	16.51	7.38	24.57	0.96
G2	S52	75	19.68	8.80	26.27	1.13
G3	S76	66	14.20	6.35	21.52	0.82
G4	S83	72	19.50	8.72	27.15	1.14
G5	S94	62	16.85	7.54	27.12	0.99
G6	S97	64	20.59	9.21	32.32	1.20
G7	S102	69	16.74	7.49	24.41	0.97
G8	S118	65	23.30	10.40	35.68	1.37
G9	S123	74	18.57	8.30	24.96	1.06
G10	S130	73	19.44	8.69	26.68	1.14
G11	S148	72	17.78	7.95	24.75	1.04
G12	S152	68	21.26	9.51	31.15	1.24
G13	S155	69	21.35	9.55	31.18	1.24
G14	S175	59	4.30	1.92	7.24	0.20
G15	S177	65	15.78	7.06	24.43	0.92

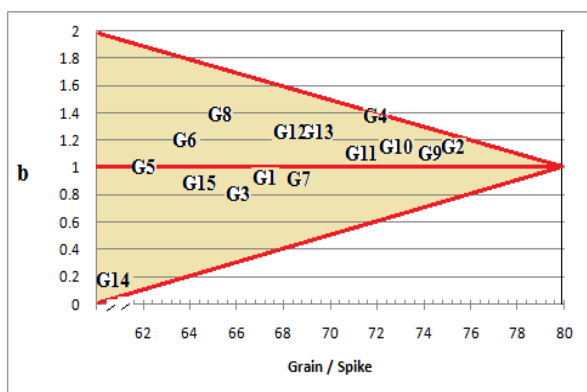


Fig.2.Regression of genotypes number of grains .spike⁻¹ to different environments.

3-Weight of 1000 grains.gms⁻¹:

Grains weight influenced by the genetic materials, anatomical and environmental factors, before and after fertilization. Genetically depends to the very complicated gene action which depend to the nature of the DNA , which control this trait, anatomically size of the embryo sac and number of endosperm cell division and relation between source and sink , while environmental effect , include successes photosynthesis and grain filling duration. The weight of 1000 grains. gm⁻¹ which produced from the plants of the genotypes through environments used in this experiment, differed significantly (Table 6).

The highest grain weight 42 gms were produced from G11, with no significant differences from G2, for the same trait. The differences among environments and genotype x environments interaction (G x E) for weight of 1000 grains . gms⁻¹ were significant (Table 6). The descriptive statistical analysis values SD , SE and CV , shows differences among genotypes, (Table 7). The genotype G6 had lowest values as the above statistics (1.15, 0.52, 2.82, respectively). This revealed that this genotype considered as more stable genotype in grain weight .The results showed in Figure 3, revealed G4 , G5 , G2 , and G9 were above average mean of 1000 grains weight and regression coefficient close to unity , and therefore considered as most stable genotypes. Similar inconsistency is ranking genotypes by using different unvaried approach was previously recorded, (9), the reason for that , grain weight was highly influenced by the environments especially during grain filling duration and before that mitosis in the endosperm tissue . It was concluded that the breeder couldn't depend to the 1000 weight. gms⁻¹ for detecting stability in weight, (22) .

Table6.Genotypes mean of 1000 grains weight .gms⁻¹ for different environments.

Genotypes		E1	E2	E3	E4	E5	Means
G1	S12	42	40	36	34	34	37
G2	S52	41	40	41	42	31	39
G3	S76	40	41	38	36	36	38
G4	S83	35	54	37	37	37	40
G5	S94	43	39	38	39	37	39
G6	S97	43	40	41	41	40	41
G7	S102	37	35	38	30	34	35
G8	S118	39	40	36	36	36	37
G9	S123	41	41	38	38	37	39
G10	S130	40	38	38	40	37	39
G11	S148	46	44	40	40	39	42
G12	S152	47	39	36	36	36	37
G13	S155	39	40	38	37	37	38
G14	S175	53	36	36	36	36	39
G15	S177	41	39	36	36	36	38
LSD		4.62					2.06
Means		41	40	38	37	36	
LSD		1.19					

4-Grain yield kg.ha⁻¹: The scientist and farmers are wants successful new wheat cultivars , that show high performance for grain yield and other essential agronomic traits .This superiority could be reliable over a wide range of environmental conditions , but also over years (20). The grain yield production of wheat as a sink of their components. So, the grain yield control by few genes more than it's

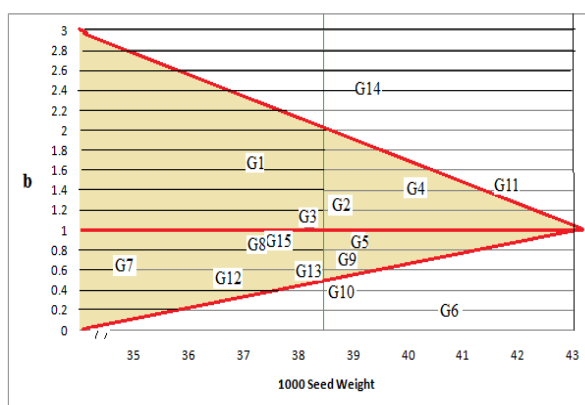
components and influenced highly environments , and one expect that it's stability less than yield components, (3 , 4). A significant differences were found among genotypes in grain yield , (Table 8). The highest grain yield 5981 kg.ha⁻¹ produced from genotypes (G9),(Fig. 4). However, this may be attributed to a posses higher number of grains.spike⁻¹, (Table 4).

Table 7. Some descriptive statistics of genotypes 1000 grains weight (gms) for different five environments

Genotypes		Means	SD	SE	CV	b
G1	S12	37	3.55	1.59	9.53	1.68
G2	S52	39	4.64	2.07	11.97	1.26
G3	S76	38	2.43	1.09	6.37	1.06
G4	S83	40	8.00	3.58	19.95	1.40
G5	S94	39	2.31	1.03	5.91	0.90
G6	S97	41	1.15	0.52	2.82	0.24
G7	S102	35	3.31	1.48	9.51	0.63
G8	S118	37	1.88	0.84	5.02	0.86
G9	S123	39	1.51	0.67	3.87	0.72
G10	S130	39	1.39	0.62	3.58	0.33
G11	S148	42	3.12	1.39	7.47	1.46
G12	S152	37	1.41	0.63	3.84	0.52
G13	S155	38	1.44	0.65	3.78	0.60
G14	S175	39	17.66	3.43	19.50	2.43
G15	S177	38	2.04	0.91	5.44	0.92

Table 8. Genotypes mean of grain yield (kg.ha⁻¹) for different environments.

Genotypes		E1	E2	E3	E4	E5	Means
G1	S12	4927	4488	5513	5794	5955	5335
G2	S52	4904	4319	6148	6584	6412	5673
G3	S76	4773	3873	5960	6120	5924	5330
G4	S83	3149	3890	6209	6146	6158	5110
G5	S94	5101	3690	5287	6166	5388	5126
G6	S97	5210	3743	5155	6200	6024	5266
G7	S102	4311	3996	6432	6555	6394	5538
G8	S118	5059	4872	5765	5823	6072	5518
G9	S123	5178	4507	6630	6832	6757	5981
G10	S130	5674	4518	6198	6208	6388	5797
G11	S148	4114	4180	6201	6299	6166	5392
G12	S152	6128	4425	5063	6238	6136	5598
G13	S155	4641	4766	5531	5586	5282	5161
G14	S175	5410	4104	5219	5425	5286	5089
G15	S177	4843	4906	6209	6108	5712	99.02
LSD		221.41					99.02
Means		4895	4285	5835	6139	6003	
LSD		57.17					

**Fig. 3. Regression 1000 grains weight (gms). to different environments**

A significant differences were found among environments and genotype environments interaction of Gx E (Table 8). This revealed the genotypes through different environments

had more elasticity. The results of descriptive statistics, SD, SE and CV, are presented in Table 9. G13 had lower SD, SE and CV value (436, 195 and 8, respectively), which indicated that the G13 most stable genotype for grain yield in this study. The phenotypic stability analysis by joint regression adopted by Finlay and Wilkinson (18) method showed that G10 more stable genotype, because of possessing high yielding capacity (5797 kg.ha⁻¹), (Figure 5), and regression coefficient (b) values to unity (0.90). The conclusion; stable genotypes G10 and promising pure lines G12, G15 and G8. Moreover, the genotype G9 was more adapted to favorable environments and possesses high yielding potential (5981 kg.ha⁻¹).

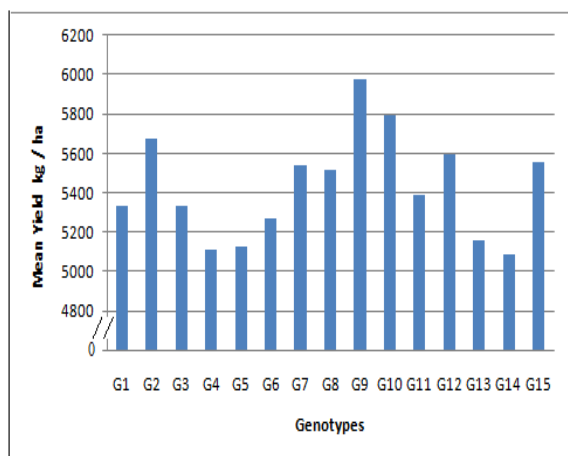


Fig.4. Genotypes grain yield $\text{kg}\cdot\text{ha}^{-1}$ for different environments.

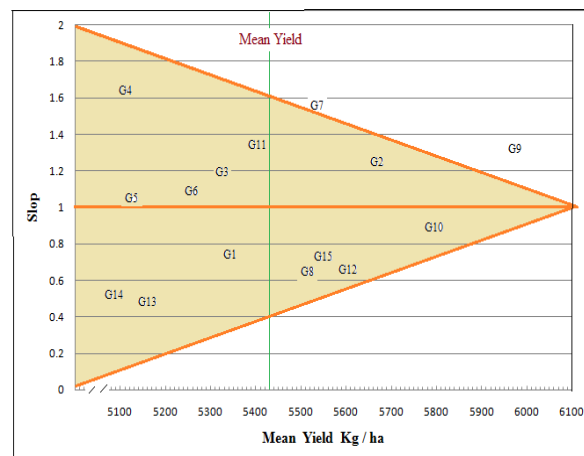


Fig.5. Regression grain yield $\cdot\text{kg}^{-1}$ to different environments.

Table 9. Some statistical analysis of genotypes grain yield $\text{kg}\cdot\text{ha}^{-1}$ for different environments

Genotypes	Means	SD	SE	CV	b	
G1	S12	5335	615	275	12	0.75
G2	S52	5673	1003	449	18	1.24
G3	S76	5330	975	436	18	1.20
G4	S83	5110	1476	660	29	1.63
G5	S94	5126	900	402	18	1.01
G6	S97	5266	972	435	19	1.09
G7	S102	5538	1270	568	23	1.54
G8	S118	5518	522	233	10	0.62
G9	S123	5981	1068	478	18	1.32
G10	S130	5797	763	341	13	0.90
G11	S148	5392	1138	509	21	1.34
G12	S152	5598	813	363	15	0.62
G13	S155	5161	436	195	8	0.48
G14	S175	5089	557	249	11	0.52
G15	S177	99.02	649	290	12	0.72

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