

## **STABILITY ANALYSIS FOR SOME WHEAT GENOTYPES AND GENOTYPE X ENVIRONMENT INTERACTION**

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### **ABSTRACT**

Three field experiments at a randomized complete block design with three replications in two successive seasons of 2009/2010 and 2010/2011 at the Agricultural Research and Experimental Station of the Fac. of Agric., Moshtohor, Benha Univeristy.

The first was nitrogen fertilization at rate of 25 Kg N/fed., the second was at 50 Kg N/fed and the third experiment was at 75 Kg N/fed with ten genotypes five lines produced by using pedigree method (Line No. 1, 5, 7, 8 and 10) and three lines produced by Single Seed Descent SSD (Line No. 2, 4 and 9) and one produced by Bulk method (line No. 6) as well as cultivar Giza 168 were evaluated. Ten genotypes, environments and their interaction were evaluated on grain yield (ard/fed), number of spikes/m<sup>2</sup>, number of grains/spike and 1000-kernel weight. The aim of this study also, to estimate of phenotypic and genotypic stability parameters. The studied traits were number of spikes/m<sup>2</sup>, number of grains/spike and 1000-kernel weight and grain yield (ard/fed). The obtained results could be summarized as follows:

- 1- Significant mean squares due to environments (two seasons and three nitrogen fertilizer rates), genotypes and genotypes x environment interaction were detected for the four studied traits. The environment No. 6 (N75 kg N/fed in the second season 2010/2011) gave the highest mean for all traits. However, the Environments No. 1 and No. 4 expressed the lowest values for the studied traits.
- 2- The line No. 6 (M37Bulk) gave significant highest No. of spikes/m<sup>2</sup>, 1000-kernel weight and grain yield ard/fed followed by genotype No. 3 (G.168) for No. of spikes/m<sup>2</sup> and grain yield ard/fed.
- 3- The significance of genotype-environment (Linear) mean squares was detected for all traits except 1000-kernel weight.
- 4- For grain yield (ard/fed), the genotypes No. 3, 5 and 6 gave mean values above grand mean and their regression coefficients ( $b_i$ ) did not differ significantly from unity. Also, minimum deviation mean squares  $S^2d_i$  were detected, revealing that these genotypes were more phenotypic stable than others under the environmental studies for this trait. The lines No. 2, 9 and 6 showed average genetically stable for grain yield. Line number 6 was promising genotype, where gave superior yield and some of its components. This promising genotype No. 6 is likely to be candidate to replace the present alternative varieties whereas gave superior grain yield ard/fed.

### **INTRODUCTION**

Wheat is one of the most important cereal crops in the world. In Egypt, wheat is the main winter cereal crop used as a staple food grain for

human and the major source of straw fodder for animal feeding. Egypt imports about 45% of its wheat requirements. This reflects the size of the problem and the efforts needed to increase wheat production. Thus, increasing production per unit area appears to be one of the most important factors for narrowing the gap between wheat production and consumption. Increasing wheat production per unit area could be possible by adopting higher yielding varieties rather than increasing the area devoted for wheat production under the limitations of arable land and irrigation water. The main goal of the Egyptian National Wheat Program is to develop high yielding wheat genotypes. This can be achieved through, genetic studies of stability and genetic components for wheat genotypes from which wheat breeder could select the best lines which characterized by stability and higher yield .

Identification of a genotype with higher yielding ability and least seasonal fluctuation over a wide range of environments is of prime important in any improvement program. Finlay and Wilikinson (1963) proposed that the average yield of all cultivars grown at a particular season could be regarded as a measure of that environment. They used regression and variance analysis in their study. However, they used "b" value as a measure of both stability and adaptation. Cultivar with "b>1" was considered above average in stability and especially adapted to unfavorable environment. Cultivar with "b<1" was considered below average in stability and specially adapted to favorable environments, and cultivar with "b=1" was considered average in stability. They added that either poor or well adaptation of a genotype to all environments depends upon the cultivar mean yield. Eberhart and Russell (1966) reported that an ideal cultivar is the one that has the highest yield over a broad range of environments. They defined a stable cultivar as the one that has regression coefficient,  $b_i$  equal to 1 and mean square deviation from regression  $S^2_{di}$  equal to zero. Tai (1971) suggested portioning the genotype x environment interaction effects of a genotype into two components,  $\alpha$  statistic that measures the linear response to environmental effects and  $\lambda_i$  statistic that measures the deviation from linear.

On the other hand, stability may, in fact, depends on holding certain morphological and physiological attributes steady and allowing others to vary, resulting in predictable G x E interaction quantitatively inherited and is greatly influenced by the environment (Mahak *et al.* 2006, Letta *et al.* 2008, Sakin, *et al.* 2011 and Beyen *et al.* 2011).

The objectives of this study were aimed to observe genotypic stability (with respect to grain yield) of 10 spring wheat genotypes across six environments, to select genotypes combining a high level of grain yield with yield stability and to group the genotypes having similar response pattern over all environments.

## **MATERIALS AND METHODS**

The experimental work of this study aimed to evaluate ten wheat genotypes under three nitrogen fertilization rates, i.e., 25, 50 and 75 Kg N/fed

during the two successive seasons of 2009/2010 and 2010/2011. These genotypes comprised five lines developed by pedigree method (Line No. 1, 5, 7, 8 and 10) and three lines produced by Single Seed Descent SSD (Line No. 2, 4 and 9) and one produced by Bulk method ( line No. 6), beside cultivar Giza 168.

The nine lines were produced by Dr. M. E. El-Badawy from three crosses namely, (R.C.B.38 x Giza 170), (Sakha 93 x Gamiza 7) and (Giza 170 x Sakha 93 which were made in 2002/2003 season. Plants of F<sub>1</sub> were grown in 2003/2004 season and plants of F<sub>2</sub> to F<sub>6</sub> were grown from 2004/2005 to 2008/2009 where three methods of breeding were done (Bulk, Pedigree and SSD). The code number, names, pedigree and origin of the tested genotypes are presented in Table (1).

**Table 1: The code number, pedigree and origin of all genotypes used in the study.**

Code No.	Genotype	Pedigree	Origin
1	M43-3-5-276	(Giza 170 x Sakha 93) produced by using pedigree method	Moshtohor-Egypt
2	M43-ssd13	(Giza 170 x Sakha 93) produced by Single Seed Descent SSD	Moshtohor-Egypt
3	G168	(MRL/Buc//SERICM93046-8M-0Y-0M-2Y-0B0GZ)	Egypt
4	M43-ssd	(Giza 170 x Sakha 93) produced by Single Seed Descent SSD	Moshtohor-Egypt
5	M37-11-6-3-261	(R.C.B.38 x Giza 170) produced by using pedigree method	Moshtohor-Egypt
6	M37Bulk	(R.C.B.38 x Giza 170) produced by Bulk method	Moshtohor-Egypt
7	M37-7-2-1-198	R.C.B.38x Giza 170) produced by using pedigree method(	Moshtohor-Egypt
8	M37-15-402-353	(R.C.B.38 x Giza 170) produced by using pedigree method	Moshtohor-Egypt
9	M45-20-205ssd	(Sakha 93 x Gamiza 7) produced by Single Seed Descent SSD	Moshtohor-Egypt
10	M37-9-604-199	(R.C.B.38 x Giza 170) produced by using pedigree method	Moshtohor-Egypt

The nine lines along with cultivar Giza 168 were evaluated at a randomized complete block design with three replications in two successive seasons of 2009/2010 and 2010/2011 under the three nitrogen fertilizer rates at the Agricultural Research and Experimental Station of the Fac. of Agric., Moshtohor, Benha Univeristy.

The experimental plot comprised of 3.5 meter and 1.2 meter wide (4.2 m<sup>2</sup>). The soil was clay in texture with a pH value of 7.81, 7.79 and an organic matter content of 1.69, 1.71% and available N of 43, 48 ppm during the two growing seasons, respectively. In the two seasons, the preceding crop was maize. The planting date was 25<sup>th</sup> November in both seasons. Nitrogen rates as form Ammonium nitrate (33.5% N) were applied in two equal doses before the first and second irrigations. The dry method of planting was used and the rest of cultural practices were followed as used for ordinary wheat area. At maturity, the plots area 3.5x1.2 m<sup>2</sup> were harvested. For each plots grain yield (ard/fed), number of spikes m<sup>-2</sup>, number of grains spike<sup>-1</sup> and 1000-kernel weight were recorded in this study.

A regular analysis of variance of a randomized complete block design of separate environment was carried out for each trait according to Snedecor and Cochran (1967). Combined analysis of the six experiments carried out whenever homogeneity of variance was detected. The stability analysis was computed according to Eberhart and Russel (1966) and Tai (1971) to detect the phenotypic and genotypic stability parameter for the previous three traits. In the analysis of the data, the genotypes and nitrogen fertilization were considered as fixed variables while, years were considered as random variables.

## **RESULTS AND DISCUSSION**

Combined analysis of variance for No. of spikes/m<sup>2</sup>, No. of kernels/spike, 1000-kernel weight (g) and grain/yield (ard/fed) of wheat genotypes is presented in Table (2). The analysis of variance for the combined analysis over six environments (Three nitrogen rates and two seasons) was made for the four studied traits. Bartlett's test of homogeneity of variance showed that the variance estimates of error were homogenous.

Mean squares of environments, genotypes and genotypes by environments interaction for the four traits were significant (Table 2). Significant mean squares due to environments (three nitrogen rates and two growing seasons) were detected for the traits under study, indicating that the performance of these traits differed from one environment to another. Significant mean squares due to genotypes and genotypes x environment interaction were detected for the four studied traits, revealing that genotypes carried genes with different additive and additive x additive effects which seemed to be inconstant from environment to another. These results emphasize that the environments had stress and non stress conditions. The significant of genotypes x environments interaction is in agreement with Hassan (1997), El-Morshidy (2000), Abdel-Karim and Salem (2003), Dawwam *et al.* (2007), Hamada *et al.* (2007), Letta *et al.* (2008), El-Hosary *et al.* (2011) and Sakin, *et al.* (2011).

**Table 2: Combined analysis of variance for number of spikes/m<sup>2</sup>, Number of kernels/spike, 1000-grain weight and grain yield (ard/fed) of wheat genotypes.**

Sources of variation	d.f	Number of spikes/m <sup>2</sup>	Number of kernels/spike	1000 –Grain weight	Grain yield (ard/fed)
Environments	5	26109.600**	808.1125**	42.2135**	315.8969**
Replication within / Environments	12	121.6667	0.5833	29.3594**	0.2728
Genotypes	9	18546.22**	11.0903**	5.1172**	10.2196**
Environments x Genotypes	45	1326.5780**	1.6736**	16.9181**	3.3394**
Error	108	145.037	0.5764	2.115	0.1841

The significant ExG effects demonstrated that genotypes responded differently to the variation in environmental conditions of nitrogen fertilization and year indicated the necessary of testing wheat genotypes at multiple environments. This shows the difficulties encountered by breeders in selecting new genotypes for release. These difficulties arise mainly from the

masking effects of variable environments. Thus, it is important to study adaptation patterns of genotypes response and their stability in multi-environments. This may lead to the conclusion that it is essential to determine the degree of stability of each genotype. The environment No. 6 (N75 kg N/fed in the second season 2010/2011) gave the highest mean values for all traits Table (3), followed by environment No. 3 for these traits, However, the Environments No. 1 and No. 4 expressed the lowest values for the studied traits.

**Table 3: Means of number of spikes/m<sup>2</sup>, Number of kernels/spike, 1000-grain weight and grain yield as affected by environments (combined analysis of the six environments).**

Environments	Number of spikes/m <sup>2</sup>	Number of kernels/spike	1000 –Grain weight	Grain yield (ard/fed)
N25 2010/2011 E1	383.870	50.910	37.050	18.280
N50 2010/2011 E2	433.070	60.090	36.280	22.910
N75 2010/2011 E3	448.270	61.870	37.500	25.170
N25 2011/2012 E4	422.130	52.720	37.210	19.430
N50 2011/2012 E5	450.270	61.370	38.37	24.440
N75 2011/2012 E6	469.070	63.170	39.050	26.350
over all mean	434.447	58.355	37.58	22.763
L.S.D 0.05	6.095	0.384	1.145	0.217
L.S.D 0.01	8.010	0.505	1.504	0.285

These results indicating that increasing nitrogen rate to 75kg N/fed increased all traits under study in both seasons. The line No. 6 (M37Bulk) gave significant highest No. of spikes/m<sup>2</sup>, 1000-kernel weight and grain yield ard/fed followed by genotypes No. 3 for No. of spikes/m<sup>2</sup> and grain yield ard/fed. Table (4). While, line No. 1 (M43-3-5-276) gave the lowest 1000-kernel weight and grain ard/fed. Such results are in agreement with those obtained by Sharma *et al.* (1987), El-Morshidy *et al.* (2000) Salem *et al.* (2000) and Ammar *et al.* (2003) they found differences among genotypes over all environments in their studies.

**Table 4: Mean values of number of spikes/m<sup>2</sup>, Number of kernels/spike, 1000-grain weight and grain yield as affected by genotypes (combined analysis of six environments).**

Code No.	Genotypes	Number of spikes/m <sup>2</sup>	Number of kernels/spike	1000 –Grain weight	Grain yield (ard/fed)
1	M43-3-5-276	432.220	58.030	36.070	21.720
2	M43-ssd13	421.330	57.960	37.400	23.120
3	G168	456.890	58.140	35.620	23.830
4	M43-ssd	409.330	58.830	38.120	22.540
5	M37-11-6-3-261	464.440	58.470	39.360	22.330
6	M37Bulk	504.670	58.660	40.700	24.040
7	M37-7-2-1-198	417.780	57.880	37.160	22.260
8	M37-15-402-353	401.110	58.010	37.080	22.080
9	M45-20-205ssd	428.890	57.300	37.800	23.120
10	M37-9-604-199	407.780	60.210	36.450	22.590
Mean		434.444	58.349	37.576	22.763
L.S.D 0.05		7.868	0.496	1.478	0.280
L.S.D 0.01		10.341	0.652	1.942	0.368

**The stability analysis**

Results in pooled analysis of variance in Table (5) showed that the genotypes mean squares were highly significant for the all the traits studied. Mean squares due to genotype, environment (Env.) + GxEnv.), environ. (Linear), (genotype x environ.) linear and pooled deviation were significant for all traits except (genotype x environ) linear for 1000-kernel weight and pooled deviation for No. of kernel spike<sup>-1</sup> indicating that the genotypes interact considerably with the varying environments. The significance of genotype-environment (Linear) mean squares was detected for all traits except 1000-kernel weight, indicating that genotypes differ genetically in linear.

**Table 5: Mean squares of variance for G x E interaction for number of spikes/m<sup>2</sup>, 1000-grain weight, Number of kernels/spike and grain yield for combined data.**

Source of variance	d.f	Number of spikes/m <sup>2</sup>	Number of kernels/spike	1000-Grain weight	Grain yield (ard/fed)
Total	59	2017.88**	23.82**	7.28**	10.29**
Genotypes	9	6182.55**	3.69**	14.07**	3.41**
Env. X (Genotypes x Env.)	50	1268.24**	27.44**	6.05**	11.53**
Env. (Linear)	1	43522**	1346.91**	48.92**	526.50**
(Genotype x Env.) Linear	9	607.29**	1.98**	2.94	4.42**
Pooled deviation	40	360.0**	0.18	5.69**	0.257**
Genotype 1 (L1)	4	58.41	0.32	3.66	0.45**
2	4	292.44**	0.26	5.75**	0.26**
3	4	579.89**	0.11	1.56	0.36**
4	4	303.02**	0.17	1.46	0.17*
5	4	156.1*	0.05	20.84**	0.12
6	4	106.05	0.11	17.16**	0.17*
7	4	790.06**	0.18	1.70	0.34**
8	4	455.23**	0.03	1.18	0.18*
9	4	108.70	0.14	1.06	0.19*
10	4	757.23**	0.45	2.46	0.32**
Pooled error	120	47.57	0.19	1.64	0.06

Response to different environments when they were tested with pooled deviations. On the other hand, the highly significant of pooled deviation for all traits except No. of kernels spike<sup>-1</sup>, indicated that the major components of differences for stability were due to deviation from the linear function. These results lead to the conclusion that it is necessary to determine degree of stability of each genotypes under study. These results confirmed with those previously reached by Fox *et al.* (1990), Salem *et al.* (1990), Mevlut *et al.* (2005) and Amin (2006). In addition, Mishrs and Chandraker (1992), Kheirall and Ismail (1995), Abbel-Karim and Salem (2003), Hamada *et al.* (2007), El-Hosary *et al.* (2011) and Sakin, *et al.* (2011) who found in their studies highly significant differences among the studied genotypes, environments and genotypes x environments interaction for number of spikes/m<sup>2</sup>, 1000-kernel weight and grain yield (ard/fed).

**Phenotypic and genotypic stability parameters:**

The phenotypic stability of the studied genotypes was measured by the three parameters i.e., mean performance over environments, the linear regression and the deviations from regression function. Phenotypic stability parameters of the four studied traits are presented in Table (6). The results showed clearly that regression coefficient ( $b_i$ ) of all genotypes were significantly differed from zero in these traits.

**Table 6: Estimates of phenotypic stability for number of spikes/m<sup>2</sup>, Number of kernels/spike, 1000-grain weight and grain yield (ard/fed) of ten wheat genotypes.**

Code No.	Genotypes	Number of spikes/m <sup>2</sup>		Number of kernels/spike		1000 –Grain weight		Grain yield (ard/fed)	
		$b_i$	$S^2d_i$	$b_i$	$S^2d_i$	$b_i$	$S^2d_i$	$b_i$	$S^2d_i$
1	M43-3-5-276	1.0789	5299.25	0.9688	127.705	2.2168	38.693	1.4112	106.634
2	M43-ssd13	0.7541	3644.5	1.021	141.447	1.6743	36.706	0.7804	33.118
3	G168	0.3784	2942.625	1.0175	139.891	1.8458	22.907	0.4939	14.29
4	M43-ssd	0.9267	4949.313	0.8791	104.787	1.2206	13.125	1.2134	78.2
5	M37-11-6-3-261	0.7807	3276.875	0.9058	110.711	-0.018	83.374	1.1709	72.678
6	M37Bulk	1.1822	6505.75	1.0534	149.9	0.2219	68.884	0.8324	37.192
7	M37-7-2-1-198	1.7841	17012.25	1.012	138.654	1.3716	15.991	1.2647	85.59
8	M37-15-402-353	1.2497	8616.75	1.1854	189.355	0.3495	5.313	1.1981	76.28
9	M45-20-205ssd	1.055	5278.875	1.643	183.162	0.315	4.732	0.7729	32.21
10	M37-9-604-199	0.8103	5885.875	0.7925	86.393	0.802	13	0.8621	40.403
SE		<b>0.11</b>		<b>0.09</b>		<b>0.3</b>		<b>0.18</b>	

The distribution of  $\alpha_i$  and  $\lambda_i$  values (genotypic stability parameters of genotypes are presented in graphics and it should be noticed that the vertical axis is  $\alpha_i$  which ranges from -1 to 1. The curves are prediction limits for  $\alpha_i = 0$  at levels of probability of 0.90, 0.95 and 0.99 and the horizontal axis is  $\lambda_i$  otherwise, the two vertical lines are the confidence intervals for  $\lambda_i = 1$ . The area between the two vertical lines and inside curve ( $\alpha_i = 0$  and  $\lambda_i = 1$ ) includes the average stable genotypes and the area between the two vertical lines and under the curve  $\alpha_i < 0$  and  $\lambda_i = 1$  includes above average stable genotype. Also Fig.1 gives a graphic summary that useful in identifying the genetically stable genotypes.

It could be noticed that the average stability in the figure contained one line No. 2 (M43-ssd13) where  $\alpha_i$  stability value was not significantly differed from 0 at all the probability levels at  $p = 0.90$ . Also, the estimated  $\lambda_i$  statistics were not significantly differed from  $\lambda_i = 1$  for this line. While, the two lines No. 10 and No.1 showed above stable and it gave relatively high mean values, indicating that both genotypes were more genetic stability over all environments under study.

For number of kernel/spike regression coefficient ( $b_i$ ) for all genotypes was significant from zero. However,  $b_i$  was significantly differed than unity for lines No.4 and 10. With respect to the second stability parameter ( $S^2d_i$ ) the all genotypes had insignificant from regression. These results suggests that the genotypes No. 10, 3, 5 and 4 was stable for No. of kernel spike<sup>-1</sup>.

Results presented in Table (7) and fig (2) showed that the stability parameter  $\alpha_i$  was not significant differed from zero for lines 1, 9, 5 and 6. The estimated  $\lambda_i$  statistics were significant differed from  $\lambda_i = 1$  for the above genotypes. These results indicated that wheat line No.1 showed below average degree of stability. While, line No. 9 showed the average degree of stability and line No.5 showed above degree of stability and it gave the highest mean value compared with grand mean.

**Table 7: Parameters of genotypic stability for number of spikes/m<sup>2</sup>, Number of kernels/spike, 1000-grain weight and grain yield (ard/fed) of ten wheat genotypes.**

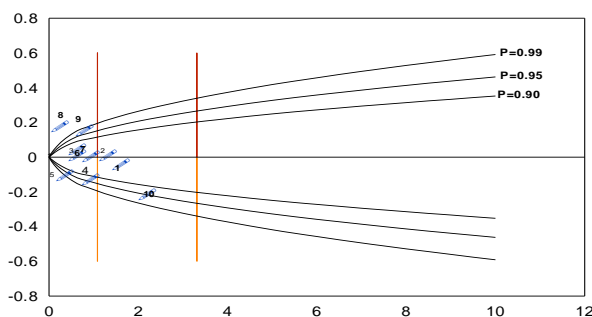
Code No.	Genotypes	Number of spikes/m <sup>2</sup>		Number of kernels/spike		1000 –Grain weight		Grain yield (ard/fed)	
		$\alpha_i$	$\lambda_i$	$\alpha_i$	$\lambda_i$	$\alpha_i$	$\lambda_i$	$\alpha_i$	$\lambda_i$
1	M43-3-5-276	0.0793	1.0737	-0.031	1.4834	1.361	1.7975	0.4116	6.4264
2	M43-ssd13	-0.2471	5.3713	0.0211	1.1904	0.7542	2.9623	-0.2198	3.8078
3	G168	-0.6246	10.6269	0.0175	0.5064	0.9461	0.7589	-0.5065	5.1912
4	M43-ssd	-0.0736	5.5714	-0.121	0.8006	0.2468	0.7569	0.2136	2.4664
5	M37-11-6-3-261	-0.2204	2.868	-0.0943	0.2326	-1.1381	10.7881	0.171	1.7988
6	M37Bulk	0.183	1.947	0.0535	0.5047	-0.8703	8.9009	-0.1677	2.5713
7	M37-7-2-1-198	0.7578	14.468	0.012	0.8124	0.4156	0.8743	0.265	4.9706
8	M37-15-402-353	0.2508	8.363	0.1855	0.1143	-0.7276	0.5825	0.1983	2.5288
9	M45-20-205ssd	0.0553	1.9985	0.1644	0.6681	-0.7662	0.5178	-0.2273	2.7365
10	M37-9-604-199	-0.1906	13.9198	-0.2076	2.0722	-0.2215	1.2812	-0.1381	4.6162

For 1000-kernel weight, regression coefficients ( $b_i$ ) for line No. 4 and 7 were not significantly differed from unity. Also, the minimum deviation mean squares ( $S^2d_i$ ) were detected for both lines, revealing that both genotypes were more stable than others under the environments studied for this trait. Fig (3) gives a graphic summary that was useful in identifying the genetically stable genotypes .It could be noticed that the average stability was in the figure contained the two lines number 10 and 2 where  $\alpha$  stability values were not significantly differed from 0 at all the probability levels. Also, the estimated  $\lambda_i$  statistics were not significantly differed from  $\lambda_i = 1$  for both genotypes indicating that both lines were average stable under environments studies. While, line No.1 showed below average degree of stability. Roy and Romagosa (1988), Kheiralla *et al.* (1997) Hamada *et al.* (2007) and El-Hosary *et al.* (2011) indicated that thousand kernel weights was the most stable component.

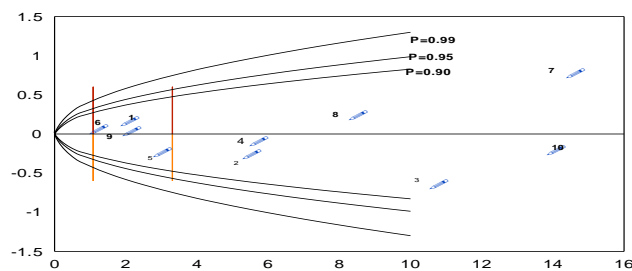
Results presented in Table (7) present mean grain yield (ard/fed),  $b_i$  and  $S^2d_i$  parameters for the ten genotypes. The genotypes were differentially response at different environments. According to parameters stability (Mean performance over environments, the linear regression and the deviation from regression function) genotypes No. 3, 5 and 6 gave mean values above grand mean and their regression coefficients ( $b_i$ ) did not differ significantly from unity. Also, the minimum deviation mean squares  $S^2d_i$  were detected, revealing that these genotypes were more phenotypic stable than others under the environmental studies for this trait.



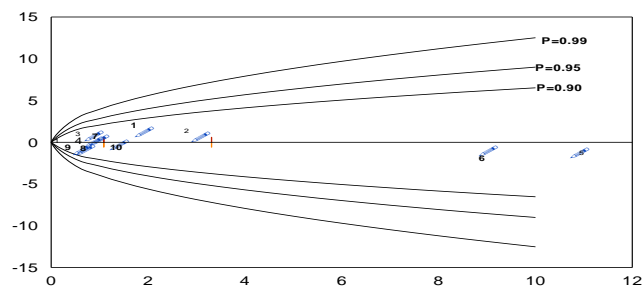
Results illustrated in Fig (4) indicated a graphic summary that could be useful in identifying the genetically stable genotypes for grain yield ard/fed. It could be noticed that the average stability area in the figure contained lines No. 4, 5 and 8 had below average stability. While lines No. 2, 9 and 6 showed above average stable and it gave the highest mean values compared with grand mean, indicating that the three lines were more genetic stability over all environments under study. The lines No. 4, 5 and 8 were genetically stable for grain yield and it gave the lowest mean values compared with grain yield. The previous genotypes can be used as a source for stability where they can be crossed with high yielding genotypes and practice selection for genotypes with high yield and good stability. The pure line No. 6 may be recommended to be released for commercial wheat production, which it performed better under all environments. It could be stated that, only of the high yielding promising line No. 6 that had satisfactory stability. Line number 6 was promising genotype, where gave superior yield and some of its components. This promising line No. 6 is likely to be candidate to replace the present alternative varieties where it gave superior grain yield ard/fed.



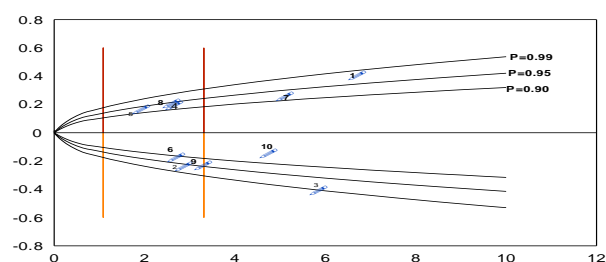
**Fig. 1: Distribution of stability statistics of no of kernel/spike in wheat.**  
 $X= \alpha_i$  and  $Y= \lambda_i$



**Fig. 2: Distribution of stability statistics of no of spike/m<sup>2</sup> in wheat.**  
 $X= \alpha_i$  and  $Y= \lambda_i$



**Fig. 3: Distribution of stability statistics of 1000-kernel weight in wheat.  $X = \alpha_i$  and  $Y = \lambda_i$**



**Fig. 4: Distribution of stability statistics of grain yield ard/fed in wheat.  $X = \alpha_i$  and  $Y = \lambda_i$**

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### تحليل الثبات لبعض التراكيب الوراثية في القمح و التفاعل بين التراكيب الوراثية و البيئة

محمود الزعبلوى البدوى

قسم المحاصيل – كلية الزراعة – جامعة بنها

أقيمت ثلاث تجارب حقلية علي التسميد النيتروجيني بمعدل ٢٥ ، ٥٠ ، ٧٥ كجم / فدان علي التوالي لعشرة تراكيب وراثية من قمح الخبز منها ٥ سلالات منتخبة بطريقة سجل النسب ( ١ ، ٥ ، ٧ ، ٨ ، ١٠ ) وثلاثة منتخبة بطريقة الانحدار من بذرة واحدة ( ٢ ، ٤ ، ٩ ) وواحدة منتخبة بطريقة التجميع ( ٦ ) علاوة علي الصنف التجاري المنزرع جيزة ١٦٨ ونفذت التجارب في تصميم قطاعات كاملة العشوائية في موسم ٢٠٠٩ / ٢٠١٠ ، وكررت في موسم ٢٠١٠ / ٢٠١١ بمركز البحوث والتجارب الزراعية بكلية الزراعة بمشتهر جامعة بنها. تهدف الدراسة الي دراسة التفاعل بين التراكيب الوراثية والبيئة وتقدير قيم الثبات المظهري والوراثي حسب طريقة (Eberhart and Russell (1966), Tai (1971) لمحصول الحبوب أردب/فدان وعدد السنابل /م<sup>٢</sup> وعدد الحبوب / لسنبلة ووزن الألف حبة وكانت أهم النتائج المتحصل عليها ما يلي:

- ١- كان التباين الراجع الي البيئات والتراكيب الوراثية والتفاعل بينهما معنويا في جميع الصفات المدروسة وحقت البيئة رقم ٦ أعلى متوسط لجميع الصفات بينما حقق البيئتين ١ ، ٤ اقل متوسط للقيم.
- ٢- أظهر السلالة رقم ٦ معنوية عالية لصفات عدد السنابل /م<sup>٢</sup> ، وزن الألف حبة ومحصول الحبوب للفدان تلاها في الترتيب الصنف التجاري جيزة ١٦٨ في صفة عدد السنابل / م<sup>٢</sup> ومحصول الحبوب للفدان.
- ٣- أظهر التفاعل بين التراكيب الوراثية والبيئات معنوية وانحراف عن خط الانحدار في كل الصفات تحت الدراسة ماعدا وزن الألف حبة.
- ٤- أظهرت التراكيب الوراثية ٣،٥،٦ ثباتا مظهريا لمحصول الحبوب للفدان بينما كانت السلالة ٦،٩،٢ هي الأكثر ثباتا وراثيا لصفة محصول الحبوب للفدان بينما كان التركيب الوراثي ٦ ثابتا وراثيا للمحصول مع بعض مكوناته بالإضافة الي ارتفاع متوسط محصول الحبوب لذلك يعتبر هذا التركيب الوراثي مبشرا ويوصي بزراعته في تجارب مكبره وعند ثباته يمكن استخدامه كصنف تجاري متميز.

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