

Genotype by Environment Interactions and Its Implications in Stability of Wheat Genotypes

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ABSTRACT

Twenty-four genotypes of wheat (*Triticum aestivum* L) include twenty promising genotypes and four commercial cultivars were evaluated at three Agricultural Research Stations, Etay-El-Baroud, Mallawy and Nubaria, for two growing seasons 2004/2005 and 2005/2006 (six environments) for their phenotypic stability. Using several parameters of stability included modified superiority index and three different indexes. The results can be summarized as follows:-

1-Highly significant differences among wheat genotypes were detected at each environment. Analysis of variance for combined data across environments showed that genotypes, environments and genotypes X environments were highly significant for all the studied traits.

2- There were 12 wheat genotypes had grain yield higher than grand mean over all environments.

3- Generally, mean grain yield at Nubaria region was lower than other two regions.

4- In the selection process a genotype were selected when recorded score of 50% or more in each index. The tested wheat genotypes based on four indexes of stability classified into four groups.

5- This classification of wheat genotypes allows choice of genotypes which have a low probability to produce poor yield under harsh environments condition, and provide knowledge of the magnitude and cause of the environmental effects in wheat breeding program.

INTRODUCTION

A major problem in selection of genotypes with wide adaptability is the absence of phenotypic stability across environments as a result of occurrence of genotype - environment interaction (Ghaderi *et al* 1981). Several authors (Eisemann, 1981; Romagosa and Fox, 1993) indicated that the success of wheat breeding in combining high yield potential and wide adaptation involved large numbers of crosses, testing advanced lines internationally, and continuous alternating selection cycles in various environments. These environments which differed in altitude, latitude, temperature, photoperiod, rainfall, soil type or other a biotic environmental situations and disease situations or other biotic environmental conditions allowed the expression of high yield potential.

Before selecting desirable genotypes many potential genotypes are usually evaluated in different environments, (in this case, environment

refers to locations, years or the combination of both). However, the relative ranking of genotypes for yield often differs when genotypes are compared over series of environments. This poses a serious problem for selecting stable genotypes significantly superior in grain yield and reduces the progress from selection in any one environment (Yau, 1995).

A number of different approaches have been suggested by plant breeders to describe the performance of genotypes over different environments. Plant breeders generally agree on the importance of high yield and stability, but there is less accord on the most appropriate definition of stability and the methods to measure and to improve yield stability (Baker and Leon, 1988). However, no single method can be adequately describe genotype stability.

The objectives of this study were 1- To evaluate 24 wheat genotypes under multi-location trials and select the genotypes with superior grain yield 2- Study the adaptation of different wheat genotypes using stability parameters and 3- Utilization of the stability analysis including grain yield and measures the most suitable method for identifying high yield genotype with wide adaptation.

MATERIALS AND METHODS

Twenty-four wheat (*Triticum aestivum* L) genotypes include twenty promising genotypes and four commercial cultivars (names and pedigree of those wheat genotypes are presented in Table 1). They were evaluated at three research stations representing different ecological environments, i.e., Nubaria (North West Delta), Etay EL-Baroud (North Delta) and Mallawy (South Egypt) for two growing seasons, 2004/2005 and 2005/2006 (six environments referring to the combination of locations and years). The experimental layout for all locations was a randomized complete block design (RCBD) with three replications. Seeds were drilled in the rows by hand, because genotypes under study are differed in their kernel weight the seeding rate was calculated to achieve a density of 400 seed /m² according to each genotype kernel weight. The plot in each locations consists of six rows with 3 meter long and 20 cm apart. All other cultural practices were applied as recommended for each location.

At harvest time, the central (guarded) four rows of each plot with 2.5 meter long were cut by hand and mechanically threshed. Data were recorded for grain yield, number of spikes /m², number of kernels / spike, and 1000-kernel weight. Grain yield (ton ha⁻¹) was expressed in ton ha⁻¹.

Statistical analysis:

Data from each location for one season (single environment) were analyzed using PROC ANOVA (Statistical Analysis System SAS 6.12 software, 1996) according to Steel and Torrie, (1980) then the data were subjected to combined analysis of variance over all environments. Genotype effect was considered fixed and environment effect was random.

Stability analysis:

The regression method suggested by Eberhart and Russell (1966) has been widely used in studies of adaptability and stability of crops as follows.

$$Y_{ij} = U_i + b_i l_j + S_{ij},$$

Y_{ij} = mean of the i^{th} genotype at the j^{th} environment,

U_i = mean of the i^{th} genotype over all environments,

b_i = regression coefficient for the response of the i^{th} genotype on the environmental index,

l_j = environmental index obtained as the mean of all genotype at each environment – the grand mean,

S_{ij} = the deviation from regression of the i^{th} genotype and j^{th} environment.

The stability of a genotype was defined by two parameters; a regression coefficient (b_i) = 1 and deviations from regression as small as possible ($S^2_d = 0$), a third estimate of stability was introduced by Francis and Kannenburg, the coefficient of variability of a genotype across environment (Francis and Kannenburg, 1978). The analyses of the stability model were performed using SAS software 1996.

Kang (1998) used index includes mean yield and stability parameters to select the best stable genotypes. Shehata *et al* (2005) suggested another index which combined the mean grain yield and two parameters of stability (b_i and S^2_{yx}) of the regression of genotype mean on environmental index. Habliza and Khalifa (2006) developed modified superiority index which includes three different stability parameters include regression coefficient (b_i), variance of deviations from regression (S^2_{yx}) and coefficient of variation (C.V) in addition to mean grain yield to select the most desirable stable genotypes. Because the correlation coefficient is very highly between the variance of deviations from regression (S^2_{yx}) and

deviation from regression (S^2_d) they prefer use variance of deviation from regression (S^2_{yx}).

The stability index developed by Habliza and Khalifa (2006) included three stability parameters an addition to yield, a score was given for each component as follow:

- 1- The distance of a genotype from the overall mean using LSD from the ANOVA at $p=$ (not significant, 0.10, 0.05, 0.01, 0.001) and a yield score was given (score= 0,2,4,6,8 + if above mean or – if below) as coded value for mean yield.
- 2- Regression coefficient estimated in the usual manner as $b_i = \frac{\sum_j Y_{ij}}{\sum_j 1}$ the distance of genotype regression coefficient (b) from 1 divided by the $(S_b * t_a)$ represented a regression score of 4,3,2,1,0 for probability \leq ns,0.1,0.05,0.01,0.001, respectively. Pooled S^2_b was calculated from S^2_e divided by S.S. for environmental index. The pooled standard error of the regression coefficient was the square root of the pooled S^2_b .
- 3- The variance of deviations from regression (S^2_{yx}) divided by the pooled MS error (S^2_e) with a score of 4,3,2,1,0 corresponding to ns,0.1,0.05,0.01,0.001 probability levels according to its F value.
- 4- The coefficient of variation (C.V) for each genotype. The C.V values were classified for four groups corresponding to 4,3,2,1 for CV values of $\leq 5, \leq 10, \leq 15$ and 20% respectively.

In the present study we used modified superiority index with combination of different stability parameters to make three indexes each of them includes two parameters of stability to describe the performance of wheat genotypes over environments. The three stability indexes were $(b_j + S^2_{yx})$, $(b_j + C.V)$, and $(S^2_{yx} + C.V)$.

Table (1): Name and pedigree of twenty four genotypes of bread wheat used in the study

Genotype	Pedigree
1	B1/3/Bow's/Vee's//Bow's/Vee's'
2	B1/5/Skh8/4/Rtu/Ww15/3/Bi's'
3	B2/3/Bow's/Vee's//Bow's/Tsi
4	B2/3/Bow's/Vee's//Bow's/Vee's'
5	B2/5/Skh8/4/Rtu/Ww15/3/Bi's'
6	B4/4/Maya's/Mon's//CMH 74A/592/3/Sakha 8
7	B3/3/Bow's/Vee's//Bow's/Tsi
8	B3/5/Skh8/4/Rtu/Ww15/3/Bi's'
9	B3/4/Maya's/Mon's//CMH 74A/592/3/Sakha 8
10	B4/Sids1
11	B4/Sakha 61
12	B4/3/Bow's/Vee's//Bow's/Vee's'
13	B4/5/Skh8/4/Rtu/Ww15/3/Bi's'
14	B4/4/Maya's/Mon's//CMH 74A/592/3/Sakha 8
15	B5/Giza 164
16	B5/3/Bow's/Vee's//Bow's/Vee's'
17	Sids4/3/Bow's/Vee's//Bow's/Vee's'
18	Sids4/5/Skh8/4/Rtu/Ww15/3/Bi's'
19	Sids5/3/Bow's/Vee's//Bow's/Vee's'
20	Sids 6/Sakha 61
21	Giza 168
22	Sakha 93
23	Gemmiza 7
24	Gemmiza 9

RESULTS AND DISCUSSION

Analysis of variance for yield and its components at each environment showed highly significant differences among wheat genotypes for all characters under study except the grain yield at Mallawi, 2004/2005 and kernel number per spike at Nubaria, 2005/2006. Analysis of variance of combined data across environments are presented in Table (2). The results showed that environmental effects were highly significant for all the studied traits indicating that all environments have differed conditions. Highly significant differences were also observed between wheat genotypes indicated that the mean performance of genotypes across the six environments were different. The presence of genotypes X environments

interactions indicated that wheat genotypes under study tended to rank differently at different locations for the four traits under study.

Grain yield and its components:

Table (3) showed the mean values of grain yield of tested wheat genotypes under different environments and over all environments. Mean grain yield at Etay, 2004/05 ranged from 5.28 to 9.27 t ha⁻¹ with an average of 7.20 t ha⁻¹, while at Nubaria 2005/06 ranged from 3.83 to 8.15 t ha⁻¹ with an average of 5.92 t ha⁻¹. The overall mean for grain yield of the 24 wheat genotypes was 6.87 t ha⁻¹, with 12 genotypes had grain yield higher than grand mean. The highest grain yield was obtained from genotypes No. 18, 21, 17 and 24 (7.98, 7.85, 7.82 and 7.62 t ha⁻¹ respectively). It is possible that selection of stable wheat genotypes would be different if tested in wider range of environments. Generally, mean grain yield at Nubaria region (E5 and E6) was lower than at Etay El-Baroud (E1 and E2) and Mallawy (E3 and E4) Table (3).

Concerning yield components .i.e. number of spikes/m², number of kernels/spike and 1000-kernel weight the results showed that there were significant differences between wheat genotypes in all different environments and over all environments (Table 5). For number of spikes/m² the data showed that genotype No. 24 (Gemmiza 9) produced the highest number of spike/m² over all environments.

Table (2): Mean square values for grain yield (GY), number of spikes / m² (SPN), number of kernels / spike (KN), and 1000-kernel weight (KW) for combined data over six environments.

S.O.V	d.f	GY	SPN	KN	KW
Environment (Env)	5	24.55**	353428**	4679.8**	236.2**
Rep / Env.	12	4.16	1527.6	18.05	12.6
Genotypes (Gen)	23	8.72**	11610.9**	267.3**	151.6**
Env X Gen	115	1.94**	2303.6**	86.77**	38.96**
Combined error	276	0.82	563.8	25.8	5.79
C.V		13.2	5.5	8.9	5.0

** Significant at the 0.01 level of probability.

Table (3): Mean of grain yield (t ha⁻¹) for twenty four wheat genotypes evaluated at six environments (three locations X two growing seasons).

Genotype	Etay 2004/05	Etay 2005/06	Mallawy 2004/05	Mallawy 2005/06	Nubaria 2004/05	Nubaria 2005/06	Mean	Rank
1	7.32	8.00	6.88	7.04	8.95	6.64	7.47	5
2	7.23	7.55	7.49	6.51	8.31	3.83	6.82	13
3	6.39	6.43	7.13	7.33	6.75	4.16	6.36	18
4	6.30	7.26	7.31	6.33	8.23	5.52	6.82	14
5	5.28	6.94	6.65	6.25	6.58	4.83	6.09	21
6	7.69	7.29	7.20	6.83	8.71	4.93	7.11	9
7	6.67	7.48	7.96	7.74	6.61	6.73	7.20	8
8	8.25	8.28	7.13	6.65	7.63	6.54	7.41	7
9	6.95	7.48	7.34	7.20	6.61	6.37	6.99	12
10	5.75	7.74	5.63	6.75	5.55	5.29	6.12	20
11	7.69	7.93	5.60	6.77	6.05	6.08	6.69	17
12	6.67	7.74	6.76	7.10	6.15	6.35	6.79	16
13	6.76	5.76	6.11	5.82	6.10	4.63	5.86	22
14	5.65	6.78	6.76	6.14	6.05	5.41	6.13	19
15	5.74	6.36	4.64	6.99	4.33	4.89	5.49	24
16	5.56	5.44	5.33	7.03	5.66	5.41	5.74	23
17	8.71	8.67	7.03	7.04	8.20	7.29	7.82	3
18	7.87	8.22	7.49	9.54	8.00	6.77	7.98	1
19	8.89	8.76	6.31	6.74	6.73	4.85	7.04	10
20	7.23	7.42	7.20	5.78	6.53	6.62	6.80	15
21	8.15	9.56	6.86	7.53	7.83	7.16	7.85	2
22	8.34	7.84	6.33	5.84	7.68	6.23	7.04	11
23	8.43	9.18	6.07	6.31	6.68	8.14	7.47	6
24	9.27	9.31	6.41	6.24	7.26	7.23	7.62	4
Mean	7.20	7.64	6.65	6.81	6.96	5.91	6.87	
Max.	9.27	9.56	7.96	9.54	8.95	8.14	7.98	
Mini.	5.28	5.44	4.64	5.78	4.33	3.83	5.49	
LSD0.05	0.87	0.61	1.94	0.91	1.46	2.31	0.59	

Table (4): Mean of number of spikes / m², number of kernels / spike and 1000-kernel weight (g) for twenty four wheat genotypes over all environments.

Genotype	Number of spikes / m ²		number of kernels / spike		1000-kernel weight (g)	
	Mean	Rank	Mean	Rank	Mean	Rank
1	424.9	12	62.5	3	49.8	5
2	418.5	14	59.5	8	47.2	17
3	406.8	21	60.8	5	48.8	10
4	402.1	24	56.7	13	48.8	11
5	411.6	19	60.2	6	49.9	4
6	411.9	18	62.4	4	47.5	15
7	428.9	11	55.2	17	49.5	6
8	464.2	3	57.0	11	47.3	16
9	479.2	2	51.0	23	47.9	13
10	409.2	20	60.1	7	46.6	20
11	454.6	5	53.1	22	46.9	19
12	418.2	15	63.2	2	51.9	3
13	415.8	17	53.2	21	47.9	14
14	406.2	23	59.2	9	47.2	18
15	406.5	22	57.1	10	43.4	23
16	436.4	10	57.0	12	43.3	24
17	450.9	6	55.6	15	48.9	9
18	424.9	13	65.0	1	46.5	21
19	461.0	4	50.8	24	56.4	1
20	445.1	8	54.5	19	49.0	8
21	446.3	7	53.5	20	44.8	22
22	444.6	9	55.1	18	48.0	12
23	416.6	16	55.4	16	54.0	2
24	490.3	1	56.1	14	49.4	7
Mean	433.0		57.3		48.4	
Max.	490.3		65.0		56.4	
Mini.	402.1		50.83		43.3	
LSD0.05	15.58		3.3		1.6	

(490.3), and there were genotypes produced number of spikes/m² more than the grand mean (Table 4).

The differences among wheat genotypes in number of kernels/spike showed that genotype No. 18 had the best record for this trait (65.0) and

there were nine genotypes produced number of kernels/spike more than the grand mean. For the 1000-kernel weight genotype No. 19 gave the highest mean value (56.4) and there were 11 genotypes exceeded the grand mean. These findings revealed that the tested wheat genotypes possess different means across the 6 environments.

Stability Analysis:

Three stability parameters for the tested 24 genotypes were summarized in Table (5) to judge the phenotypic stability of a particular genotype. Generally, the ideal genotype as proposed by Eberhart and Russell (1966) is considered to be stable if it would have a high mean performance over a range of environments, with a regression coefficient = 1 and its response to environments is parallel to the grand mean, if the residual mean square from the regression model on the environmental index (S^2_{yx}) is small.

The regression coefficients of the wheat genotypes ranged from 0.01 to 4.01 for grain yield. The large variation in the regression coefficients indicated that genotypes had different environmental responses. Genotypes with regression coefficient greater than one would be adapted to more favorable environment, while those with coefficient less than one would be relatively better adapted to less favorable growing conditions.

Coefficient of variation (C.V) measure relative variation of genotypes across environments weighted by the genotype mean and it reflects homeostasis or buffering ability of genotypes. The low C.V values would indicate that the genotypes were the consistent, therefore had relatively better buffering ability. The high C.V value of a genotype indicated that genotype were unstable across environments.

Modified superiority index:

The modified superiority index (Habliza and Khalifa 2006) was calculated, using accumulated score for each of mean grain yield, regression coefficient (b_j), variance of deviation from regression (S^2_{yx}) and the coefficient of variability (CV). Because the importance of grain yield of each genotypes across the environments, it was given a double weight

ranging from -8 to + 8 , while the other stability parameters were given a single weight.

In order to describe the performance of wheat genotypes over environments and allow a proper selection criteria for broadly adapted wheat genotypes the modified superiority index and another three different indexes of stability were used in the present study. Each index included two parameters of stability ($b_i + S^2_{yx}$), ($b_i + C.V$), and ($S^2_{yx} + C.V$) in addition to mean grain yield to judging the phenotypic stability of a particular genotype. The selected wheat genotypes had a score of 50 % or more in each index. According to the different stability indexes the tested wheat genotypes were classified into four groups (Table 6):

1- Group A: included four genotypes, No 8, 17, 18 and 21 selected by the four indexes with high stability and wide adaptation.

2- Group B: included two genotypes, No 1 and 24 selected by three indexes and showing broader adaptability.

3- Group C: included four genotypes, No 9, 12, 20 and 23 selected by two indexes.

4- Group D: included fourteen genotypes No 2,3,4,5,6,7,10,11,13,14,15,16,19 and 22 were not selected for any index or one index only.

In the selection process a genotype must be selected for its superiority in grain yield, but high mean yield alone is not necessarily indicative of high stability and wide adaptation. This classification of wheat genotypes allows choice of genotypes which have a low probability to produce poor yield under harsh growth conditions.

Table (5): Mean of grain yield (t ha⁻¹) and various stability measurements and their scores of 24 wheat genotypes evaluated at six environments (three locations X two growing seasons).

Gen. No.	Grain yield			Regression coefficient			deviation from regression			Coefficient of variation		
	Mean	I	Select	bi	I	Select	S^2_{yx}	I	Select	C.V	I	Select
1	7.47	4	Yes	0.86	4	Yes	0.62	1	No	10.49	2	No
2	6.82	0	Yes	2.13	2	No	1.20	0	No	16.08	1	No
3	6.36	-2	No	1.18	4	Yes	1.05	0	No	16.02	1	No
4	6.82	0	No	0.87	4	Yes	0.83	0	No	13.36	2	No
5	6.09	-4	No	0.90	4	Yes	0.55	1	No	12.13	2	No
6	7.11	0	Yes	1.52	4	Yes	0.96	0	No	13.75	2	No
7	7.20	0	Yes	0.15	4	Yes	0.44	3	Yes	9.26	3	Yes
8	7.41	2	Yes	1.14	4	Yes	0.19	4	Yes	5.89	3	Yes
9	6.99	0	Yes	0.50	4	Yes	0.13	4	Yes	5.22	3	Yes
10	6.12	-4	No	1.15	4	Yes	0.54	2	No	12.10	2	No
11	6.69	0	Yes	1.22	4	Yes	0.51	2	No	10.68	2	No
12	6.79	0	Yes	0.62	4	Yes	0.24	4	Yes	7.24	3	Yes
13	5.86	-8	No	0.82	4	Yes	0.34	4	Yes	9.95	3	Yes
14	6.13	-4	No	0.52	4	Yes	0.28	4	Yes	8.54	3	Yes
15	5.49	-8	No	0.79	4	Yes	1.12	0	No	19.24	1	No
16	5.74	-8	No	0.01	4	Yes	0.52	2	No	12.47	2	No
17	7.82	6	Yes	4.01	0	No	0.36	4	Yes	7.62	3	Yes
18	7.98	8	Yes	0.79	4	Yes	0.79	0	No	11.12	2	No
19	7.04	0	Yes	2.49	1	No	0.37	4	Yes	8.70	3	Yes
20	6.80	0	Yes	0.43	4	Yes	0.39	4	Yes	9.20	3	Yes
21	7.85	8	Yes	1.37	4	Yes	0.35	4	Yes	7.54	3	Yes
22	7.04	0	Yes	1.25	4	Yes	0.67	0	No	11.66	2	No
23	7.47	4	Yes	0.77	4	Yes	1.81	0	No	18.01	1	No
24	7.62	4	Yes	1.50	4	Yes	1.35	0	No	15.28	1	No
Mean	6.86			1.12			0.65			11.30		
	LSD			$S_b \times t_a$			$S^2_e \times F_a$			Value		
				0.10 = 0.50			0.10 = 0.84			0.10 = 0.38		≤ 5 = 4
				0.05 = 0.59			0.05 = 1.00			0.05 = 0.43		≤ 10 = 3
				0.01 = 0.78			0.01 = 1.31			0.01 = 0.53		≤ 15 = 2
				0.001= 0.99			0.001= 1.68			0.001= 0.57		≤ 20 = 1

Table (6): Comparison of superiority index based on mean grain yield in addition to $(bi + S^2_{yx})$, $(bi + C.V)$, $(S^2_{yx} + C.V)$ and $(bi + S^2_{yx} + C.V)$ for 24 wheat genotypes evaluated at six environments.

Genotype	Mean Grain Yield +								Selection Group
	$(bi + S^2_{yx})$		$(bi + C.V)$		$(S^2_{yx} + C.V)$		$(bi + S^2_{yx} + C.V)$		
	Score	select	Score	select	Score	select	Score	select	
1	9	Yes	10	Yes	7	No	11	Yes	B
2	2	No	3	No	1	No	3	No	D
3	2	No	3	No	-1	No	3	No	D
4	4	No	6	No	2	No	6	No	D
5	1	No	2	No	-1	No	3	No	D
6	4	No	6	No	2	No	6	No	D
7	7	No	7	No	6	No	10	Yes	D
8	10	Yes	9	Yes	9	Yes	13	Yes	A
9	8	Yes	7	No	7	No	11	Yes	C
10	2	No	2	No	0	No	4	No	D
11	6	No	6	No	4	No	8	No	D
12	8	Yes	7	No	7	No	11	Yes	C
13	0	No	-1	No	-1	No	3	No	D
14	4	No	3	No	3	No	7	No	D
15	-4	No	-3	No	-7	No	-3	No	D
16	-2	No	-2	No	-4	No	0	No	D
17	10	Yes	9	Yes	13	Yes	13	Yes	A
18	12	Yes	14	Yes	10	Yes	14	Yes	A
19	5	No	4	No	7	No	8	No	D
20	8	Yes	7	No	7	No	11	Yes	C
21	16	Yes	15	Yes	15	Yes	19	Yes	A
22	4	No	6	No	2	No	6	No	D
23	8	Yes	9	Yes	5	No	9	No	C
24	8	Yes	9	Yes	5	No	9	Yes	B

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الملخص العربي مضاعفات التداخل بين البيئة والوراثة على ثبات التراكيب الوراثية في القمح

أحمد محمد جادالله و ماهر عبد المنعم المغربي وهانى سعد البرهامي
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- تم تقييم 24 تركيب وراثي لقمح الخبز شملت 20 تركيب وراثي مبشر واربع أصناف تجارية وذلك لثباتها المظهرى فى 6 بيئات مختلفة هى عبارة عن 3 مواقع مختلفة هى محطة بحوث إيتاي البارود و محطة بحوث ملوى ومحطة بحوث النوبارية لمدة موسمين زراعيين 2004/ 2005 و 2005 / 2006 ، وقد أستخدمت عدة تقديرات لحساب الثبات ويمكن تلخيص أهم النتائج المتحصل عليها فيما يلى :
- 1- أظهر تحليل التباين وجود أختلافات معنوية بين التراكيب الوراثية للقمح فى كل بيئة على حدة ، كما أظهر تحليل التباين المشترك وجود أختلافات عالية المعنوية بين التراكيب الوراثية والبيئات وكذلك التفاعل بين البيئة والوراثة.
 - 2- سجلت بعض التراكيب الوراثية محصول حبوب أكبر من المتوسط العام لكل البيئات. وكان محصول الحبوب كمتوسط عام لكل التراكيب الوراثية فى الموقع الثالث (النوبارية) هو الأقل بالنسبة للمواقع الأخرى.
 - 3- تم انتخاب التراكيب الوراثية التى سجلت 50 % فأعلى فى كل دليل للثبات وتبعاً لذلك قسمت التراكيب الوراثية تحت الدراسة إلى 4 مجموعات وذلك بأستخدام عدة تقديرات لحساب الثبات ، وقد أظهر هذا التقسيم أنه يعطى الفرصة لانتخاب التراكيب الوراثية ذات الأحتمال الأقل فى أنتاج محصول حبوب منخفض عند تعرضها لظروف بيئية معاكسة، كما يساعد فى تقدير مدى مساهمة البيئات المختلفة وتأثيرها على برامج التربية لمحصول القمح.