# GESTAB: A BASIC PROGRAM FOR CALCULATING SOME STATISTICAL MODELS FOR ESTIMATING STABILITY IN MAIZE

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#### **ABSTRACT**

The need for determining the stability of performance of genotypes across a range of environments has been recognized by many successful breeders and geneticists working with quantitative traits. A DOS-version computer program (GESTAB) was designed for stability models (Tai's,1971), (Eberhart and Russell's,1966), (Perkins and Jinks',1968) and (Freeman and Perkins,1971). GESTAB operates on IBM-PCs or compatible microcomputers with a BASIC, GBASIC or QBASIC. Application, five field experiments were carried out during 2002 and 2003 growing seasons; each experiment included 12 three -way crosses (310, 320, 321, 322, 323, 324, 325, 326, 327, 352, Wataneia 1 and Nefertety).

Phenotypic stability parameters were calculated according to Eberhart and Russell (1966), Perkins and Jinks'(1968), and Freeman and Perkins(1971), results indicated that all hybrids were characterized by high general and specific stability except hybrids T.W.C.321, T.W.C.352 and Nefertety for grain yield (ard/fed). Concerning genotypic stability as estimated by Tai (1971), hybrids T.W.C.323, T.W.C.324, and T.W.C.325 had grain yield above average of stability. On the other hand the hybrids T.W.C.310, T.W.C.320, T.W.C.321, T.W.C.322, T.W.C.326, T.W.C.327, T.W.C.352, Wataneia 1 and Nefertety were not stable.

Key words: Stability, GESTAB, Maize, Three-Way crosses, Sowing dates.

#### MATERIALS AND METHODS

GESTAB was written in BASIC (DOS version) and will operate on an IBM-PC or compatible computers with a BASIC, GBASIC OR QBASIC interpreter. This program was designed and tested, available to calculate the following stability models:

### Tai model for estimating genotypic stability.

This technique was performed according to Tai (1971), who separated genotype x environment interaction effect of the  $i^{th}$  genotypes into two statistical parameters namely  $\alpha$  and  $\lambda$ . These statistics  $\alpha$  and  $\lambda$  measure the

linear response to environmental effects and the deviation from linear response in terms of the magnitude of the error variance, respectively, as follow:

$$\alpha = \frac{S_i(gL)_i}{(MSL - MSB/mp)}$$

$$\lambda = \frac{S^2(gL)_i - \alpha s_i.(gL)_i}{(m-1)MSE/mp}$$

Where

 $S_i(\xi_i)_i$  is the simple covariance between the environment and interaction effects,  $S^2(\xi_i L)_i$  is the sample variance of the interaction effects of the i th var ety to the menvironments. MSL, MSB, MSE, m and p are the mean squares of environmental effects, the replicates within environments, the error deviates, number of varieties and number of replications, respectively. A perfectly stable variety has values ( $\alpha = -1$  and  $\lambda = 1$ ) a variety with average stability has values ( $\alpha = 0$  and  $\lambda = 1$ ), a genotype with above average stability has values of ( $\alpha < 0$  and  $\alpha <$ 

A prediction interval for  $\alpha = 0$  at the probability level P can be obtained by considering the correlation between the pairs of effects  $I_j$  and  $(gI)_{ij}$  for the  $i^{th}$  variety. It is known that  $\rho_{1,(g1)i}=0$  if and only if  $\alpha_i=0$ . The observed correlation (r) between  $I_j$  and  $(gI)_i$ , (j=1,2,...,n). Then  $[(n-2)r^2/(1-r^2)]^{1/2}$  follows the t-distribution with (n-2) degrees of freedom. Denoting the tabulated t value at the probability level a=1-p with (n-2) degrees of freedom as  $t_a$  the two predication limits for  $\alpha_i$  or responding to  $\alpha_i=0$  can be shown to be:

 $\pm t_a$  ( $\lambda$  (m-1)MSE\*MSL)/(MSL-MSB)[(N-2)MSL-( $t_a^2+n-2$ )MSB]  $\}^{1/2}$  which is a function of  $\lambda$ .

A theoretical confidence interval for the hypothetical  $\lambda_0$  value can be constructed by means of an F-distribution with  $n_1$ =n-2 and  $n_2$ = n(m-1)(p-1) degrees of freedom. For  $\lambda_0$ =1, i.e.,  $\sigma^2_{\delta}$ =0, the interval at the probability level P is

$$F_a(n_1,n_1) \le \lambda_0 \le F_a(n_1,n_2)$$
, where  $F_a(n_2,n_1)=1/F_a(n_1,n_2)$  and  $2a=1-p$ .

The upper limit for a hapothetical  $\lambda_0$  value is  $F'_a(n_1,n_2)$ , which is greater than unity, the rather proximately  $F'_a(n_1,n_2)=[(n_1+\lambda_{ne})/n_1]F_a(n^*,n_2)$  in which  $F_a(n^*,n_2)$  is a central F-value with degrees of freedom  $n^*=(n_1+\lambda_{ne})^2/(n_1+2\lambda_{ne})$ ,  $n_2$  and  $\lambda_{ne}$ 

is anon-central parameter which is equal to  $n_1(\lambda_0-1)$ . After simplification, we have:

$$F'_a(n_1,n_2) = \lambda_0 F_a(n_1 \lambda_0 / 2\lambda_0 - 1, n_2).$$

The prediction interval for  $\alpha=0$  and the upper limits of the confidence interval for  $\lambda_0 \ge 1$  help to evaluate the relative stability of a set of varieties in regional trials.

#### Eberhart and Russell model for estimating phenotypic stability.

This technique was used to compute the phenotypic stability as outlined by Eberhart and Russell (1966) according to this model.

$$Y_{ij} = m + B_i I_j + \partial_{ij}$$

Where:

 $Y_{ij}$ : The genotype mean of the i<sup>th</sup> genotype at the j<sup>th</sup> environment (i=1, 2..., v, i=1, 2...n).

m: The mean of all the genotypes over all environments.

 $B_i$ : The regression coefficient of the i<sup>th</sup> genotype on the environmental index which measures the response of this genotype to varying environments,

 $I_j$ : The environmental index which is defined as the deviation of the mean of all the variation at a given location from the overall mean.

$$[I_j = (\sum_i Y_{ij} / v) - (\sum_i \sum_j Y_{ij} / vn), \sum_j I_j = 0]$$

 $\partial_{ij}$ : The deviation from regression of the i<sup>th</sup> genotype at the j<sup>th</sup> environment.

Eberhart and Russell (1966) proposed that the ideal variety is one that has three characteristics as follows:

a- Regression coefficient significantly different from zero  $(b_i \neq 0)$  and not

significantly different from unity 
$$(b_i = 1)$$
,  $b_i = \sum_{j=1}^{n} y_{ij} I_j / \sum_{j=1}^{n} I_j^2$ .

b- Minimum value of the deviation about regression, i.e.,  $(s_d^2 = 0)$ ,

 $s_{d_i}^2 = \left[\sum_{j=1}^{\infty} \delta_{ij}^2 / (n-2)\right] - s_e^2 / r$ , where  $s_e^2 / r$  is the estimate of the pooled error (or the variance of a variety mean at the j<sup>th</sup> location) and:

$$\sum_{j=1}^{n} \delta_{ij}^{2} = \left[\sum_{j=1}^{n} y_{ij}^{2} - \frac{y_{i}^{2}}{n}\right] - \left(\sum_{j=1}^{n} y_{ij} I_{j}\right)^{2} / \sum_{j=1}^{n} I_{j}^{2}.$$

c- High performance with a reasonable range of environmental variation.

#### Perkins and Jinks' model for estimating phenotypic stability

This technique was used to compute the phenotypic stability as outlined by Perkins and Jinks' (1968) according to this model.

$$Y_{ij} = m + d_i + e_j + g_{ij} + \partial_{ij}$$

Where:

 $Y_{ij}$ : The genotype mean of the i<sup>th</sup> genotype at the j<sup>th</sup> environment (i=1, 2..., v, i=1, 2...n).

m: The general mean,

di: The additive genetic effect,

ei: The additive environmental effect,

gij: The genotype X environmental interaction effect, and

 $\partial_{ii}$ : The error associated with each observation.

Perkins and Jinks' (1968) proposed that the ideal variety is one that has three characteristics as follows:

a- Regression coefficient significantly different from zero  $(b \neq 0)$  and not significantly different from unity (b=1).

b- Minimum value of the deviation about regression, i.e.,  $(s_d^2 = 0)$ .

c- In Perkins and Jinks' model this S.S. is further divided into two parts, i.e., S.S. due to heterogeneity between regression and S.S. due to pooled deviation.

#### Freeman and Perkins' model for estimating phenotypic stability

This technique was used to compute the phenotypic stability as outlined by Freeman and Perkins' (1971) according this model.

$$Y_{ijk} = m + d_i + e_j + g_{ij} + \partial_{ijk}$$

Where:

 $Y_{ijk}$ : The observation of the i<sup>th</sup> genotype at the j<sup>th</sup> environment and k<sup>th</sup> replicate (i=1, 2, ..., v, j=1, 2, ..., k=1, 2, ..., r).

m : The general mean,

d<sub>i</sub>: The additive genetic effect of i<sup>th</sup> genotype,

e<sub>i</sub>: The additive environmental effect,

.g<sub>ij</sub>: The genotype environment interaction effect, and

 $\partial_{ij}$ : The error associated with  $k^{th}$  observation.

This being an objectional point, independent estimate of environmental index in the following three ways:

- (i): Divide the replications into groups, so that the one group may be used for measuring the average performance of varieties in various environments and the other group, averaging over the varieties is used for estimating the environmental index.
- (ii): Use one or more varieties as check and assess the environmental index on the basis of their performance.
- (iii) "F" test: if environment residual (1) S.S. is significant, environmental index is adequately the index of additive environmental effect. If β is not significantly different from unity, then independent environmental values adequately estimate additive environment component and Freeman and Perkins' reduces to Perkins and Jinks' model.

Following tests of significance are performed:

- (a): Heterogeneity of regression is tested against residual S.S.(2).
- (b): Residual interaction (GXE) S.S. against error S.S.
- ©: Environment (residual) S.S. against error S.S.
- (d): Environment (combined) S.S. against environmental (residual) S.S.(1).

The calculation of  $S_{d}^2$ :

1-calculte 
$$\sigma_{v_i}^2$$
 which is S.S. due to variety  $\sigma_{v_i}^2 = \sum_{j=1} y_{ij}^2 - (1/n)y_{ij}^2$ .

2-calculate 
$$S_{d_i}^2 = \left[\sum_{i=1}^n \delta_{ij}^2 / (I-2)\right] - \left(S_e^2 / r\right)$$

where 
$$\sum_{i=1}^{n} \delta_{y}^{2} = \sigma_{v_{i}}^{2} - b \sum_{i=1}^{n} Y_{ij} Z_{j}$$

and  $S_e^2$  = Error mean square.

From the above we can make comparison between the phenotypic stability models as in Table (1).

Table 1. Comparison of phenotypic stability models

No.	Model 1	Model 2	Model 3
	Eberhart and Russell	Perkins and Jinks	Freeman and Perkins
A	Involves three parameters i.e., $\overline{X}$ , $b_i$ , $S_{d_i}^2$	The same as the first model.	The same as the first model.
В	Variation is divided into two fractions, G and E+GXE	Variation is divided into three fractions, G, E and GXE	Variation is divided into three fractions, G, E and GXE
C	(E+GXE) is subdivided into 3 parts, i.e. Env.(linear), GXE (linear) and pooled deviations.	(GXE) is subdivided into heterogeneity due to regression and S.S. due to remainder.	The Env. Is divided into combined regression and residual 1. The GXE is subdivided into heterogeneity of regression & residual 2.
Ď	Does not provide independent estimation for mean performance and environmental index	The same as the first model.	It provides independent estimation of mean performance and environmental index.
E	The degrees of freedom for environment is 1	The degrees of freedom for environment is e-1	The degrees of freedom for environment is e-1
F	Calculation is simple	Calculation is difficult	Calculation is very difficult
G	Less expensive	The same as the first model	More expensive than first and second model

Two field experiments were carried out at Mazora (West Elfashn, Beni-Swef Governorate) during 2002 and 2003 growing seasons to estimate two stability models. Twelve maize three-way crosses of hybrids (310, 320, 321, 322, 323, 324, 325, 326, 327, 352, Wataneia 1 and Nefertety) were used for the output example. These hybrids were evaluated under five dates of sowing (10<sup>th</sup> March, 30<sup>Th</sup> March, 20<sup>Th</sup> April, 10<sup>th</sup> May and 30<sup>Th</sup> May) for the two seasons (2002 and 2003). Randomized complete block design with four replications was used. Plots consisted of four redges, 6 m long and 80 cm apart. Planting was done in hills spaced 25 cm along the redge. Two kernels were planted per hill and thinned later to one plant per hill to provide a population of approximately 22,000 plants/feddan (Feddan 4200 m²). All cultural practices were applied as recommended. Data were recorded on the two central redges for number of days to 50% tasseling, ear height, ear length and grain yield adjusted to 15.5% grain moisture and converted to ardab/feddan (ardab=140 kg.)

#### **OUTPUT EXAMPLE**

Table 2. Mean data averaged over replications

Var.	Loc.1	Loc.2	Loc.3	Loc.4	Loc.5	Loc.6	Loc.7	Loc.8	Loc.9	Loc. 10	Mean
T.W.C.3	27.6	28.4	33.4	32.7	28.4	28.5	28.1	30.2	24.7	15.1	27.7
T.W.C.3	20.8	31.4	34.0	30.9	21.4	28.3	27.3	30.9	13.2	19.3	25.8
T.W.C.3	22.6	27.8	30.0	31.7	26.2	25.3	29.5	29.6	21.7	20.9	26.5
T.W.C.3	23.0	29.6	34.6	30.0	28.3	25,4	24.8	27.5	23.0	21.0	26.7
T.W.C.3	24.9	29,6	38.2	34.6	28.5	27.8	28.5	24.5	22.3	20.4	27.9
Γ.W.C.3	19.6	32.8	34.9	38.2	30.8	31.8	29.7	29.4	18.6	22.8	28.9
T.W.C.3	25.4	34.4	39.5	33.6	36.7	28.9	25.9	31.8	17.1	21.7	29.5
T.W.C.3	22.5	28.9	34.5	29.9	27.9	31.3	26.3	25.4	18.5	24.4	26.9
T.W.C.3	19.3	25.5	31.7	34.6	25.0	25.5	24.3	27.6	17.2	17.4	24.8
T.W.C.3	22.4	26.9	29.1	25.6	23.7	26.1	24.5	25.2	20.4	16.7	24.1
Watanei	19.2	29.5	31.4	31.9	29.8	24.3	26.6	24.1	22.3	20.3	25.9
Nefertety	22.6	25.9	26.1	32.0	21.5	27.1	23.0	25.8	8.5	12.4	22.5
Mean	22.5	29.2	33.1	32.1	27.4	27.5	26.5	27.7	27,7	18.9	19.4

# Genotypic stability

Tai model for estimating genotypic stability. Table 3. The values of alfa and lambada

Var.	α	λ
1-T.W.C.310	-0.129	2.031
2-T.W.C.320	0.284	2.023
3-T.W.C.321	-0.306	0.637
4-T.W.C.322	-0.243	0.645
5-T.W.C.323	0.021	1.243
6-T.W.C.324	0.291	1,180
7-T.W.C.325	0.338	2.201
8-T.W.C.326	-0.181	1.251
9-T.W.C.327	0.155	0.646
10-T.W.C.352	-0.363	0.493
11-Wataneia 1	-0.185	1.332
12-Nefertety	0.318	2.688

Table 4. The probability values for hyperbola of 90, 95 and 99% confidence interval for  $\lambda_0=1$ .

Case	90%	95%	99%
· ·	±	±	±
1	0.208	0.357	0.523
2	0.407	0.505	0.739
3	0.498	0.618	0.905
4	0.575	0.714	1.045
5	0.643	0.798	1.169
6	0.704	0.874	1.280
7	0.761	0.944	1.383
8	0.813	1.010	1.478
9	0.863	1.071	1.568
10	0.909	1.129	1.653
11	0.954	1.184	1.734
12	0.996	1.236	1.811
13	1.037	1.287	1.885
14	1.076	1.335	1.956
15	1.114	1.382	2.024
16	1.150	1.428	2.091
17	1.186	1.472	2.155
18	1.220	1.514	2.218
19	1.254	1.556	2.278
20	1.286	1.596	2.337

Table 5. The combined analysis of grain yield for 12 maize genotypes over ten

Source of variation	d.f	Sum of Squares	Mean Squares	F
Genotypes (G)	11	1765.125	160.465	9.546
Environments	9	10062.41	1118.045	66.509
Rep. in Envi.	30	2614.156	87.138	5.184
G X Env.	99	2867.688	28.966	1.723
Error	330	5547.438	16.810	

Table 6. Analysis of variance for mean data of grain yield for 12 maize genotypes over ten environments.

Source of variation	d.f	Sum of Squares	Mean Squares	F
Genotypes (G)	11	441.227	49.112	5.539
Environments	9	2515.563	279,507	38.594
G X Env.	99	716.977	7.242	
Total	119	3673.766	Ţ	

#### Phenotypic stability:

# Eberhart and Russell model for estimating phenotypic stability.

Table 7. Mean performance of grain yield and phenotypic stability measurements for 12 maize genotypes over ten environments.

	Mean	Phenotypic stability			
Genotypes	performance	b <sub>vi.</sub>	S <sup>2</sup> d <sub>vi</sub>	T <sub>bvi</sub> -1	
1-T.W.C.310	27.735*	0.881	4.629	580	
2-T.W.C.320	25.767	1.262	4.716	1.270	
3-T.W.C.321	26.529	0.718	-1.267	-2.384	
4-T.W.C.322	26.739	0.776	-1.295	-1.900	
5-T.W.C.323	27.953**	1.019	1.186	0.119	
6-T.W.C.324	28.861**	1.268	1.071	1.690	
7-T.W.C.325	29.522**	1.312	5.549	1.446	
8-T.W.C.326	26.960	0.834	1.280	-1.029	
9-T.W.C.327	24.818	1.143	-1.359	1.224	
10-T.W.C.352	24.078	0.665	-1.817	-3.138	
11-Wataneia 1	25.964	0.830	1.632	-1.022	
12-Nefertety	22.497	1.293	7.638	1.234	
G. Mean	26.452	0.99999			

L.S.D. for genotypes = 0.876, 1.043 and 1.371 at 10%, 5% and 1%, respectively.

Table 8. The combined analysis for the studied traits of twelve maize genotypes over ten environments.

Source of variation	d.f	Sum of Squares	Mean Squares	F
Total	119	3673.766		
Genotypes (G)	11	441.227	40.113**	5.539
Env + (G x Env.)	108	3232.53	29.931**	4.961
Environment (Linear)	1	2515.563	2515.589**	208.469
G X Env. (Linear)	11	137.714	12.256	1.038
Poold Deviation	96	579.208	6.033	
1-T.W.C.310	8	70.662	8.832	1.558
2-T.W.C.320	8	71.360	8.919	1.574
3-T.W.C.321	8	23.495	2.936	0.518
4-T.W.C.322	8	23.264	2.907	0.513
5-T.W.C.323	8	43.112	5.389	0.951
6-T.W.C.324	8	42.192	5.274	0.931
7-T.W.C.325	8	78.023	9.752	1.721
8-T.W.C.326	8_	43.862	5.482	0.967
9-T.W.C.327	8	22.748	2.844	0.502
10-T.W.C.352	8	19.088	2.386	0.421
11-Wataneia 1	8	46.683	5.34	1.030
12-Nefertety	8	94.730	11.840*	2.089
Pooled error	360	2040.399	5.668	

## Perkins and Jinks' model for estimating phenotypic stability.

Table 9. Mean performance of grain yield and phenotypic stability measurements for 12

maize genotypes over ten environments.

g-100,	Mean	Phenotypi	Phenotypic stability			
Genotypes	performance	b <sub>vi.</sub>	Bi	$S_{d_i}^2$		
1-T.W.C.310	27.735	0.881	119	4.629		
2-T.W.C.320	25.767	1.262	0.262	4.716		
3-T.W.C.321	26.529	0.718	282	-1.267		
4-T.W.C.322	26.739	0.776	224	-1.295		
5-T.W.C.323	27.953**	1.019	0.019	1.186		
6-T.W.C.324	28.861**	1.268	0.268	1.071		
7-T.W.C.325	29.522**	1.312	0.312	5.549		
8-T.W.C.326	26.960	0.834	166	1.280		
9-T.W.C.327	24.818	1.143	0.142	-1.359		
10-T.W.C.352	24.078	0.665	335	-1.817		
II-Wataneia I	25.964	0.830	170	1.632		
12-Nefertety	22.497	1.293	0.293	7.638		
G. Mean	26.452	0.99999	Sum=-5.9E-07			

L.S.D. for genotypes = 0.876, 1.043 and 1.371 at 10%, 5% and 1%, respectively.

Table 10. Analysis of variance of grain yield for 12 maize genotypes over ten environments.

Source of variation	d.f	Sum of Squares	Mean Squares	F
Lines(Different Genotypes)	11	441.227	40.112	5.539
Environments (Joint Regression)	9	2515.563	279.507	38.594
G X Env.	99_	716.977	7.242	
Heterogeneity between regression	11	137.777	12.525	
Remainder	88	579.208	6.582	
Error	360	170.033	0.472	

#### Freeman and Perkins' odel for estimating phenotypic stability.

Table 11. Mean performance of grain yield and phenotypic stability measurements for 12

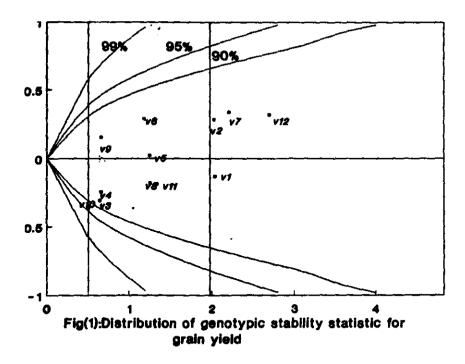
maize genotypes over ten environments.

	maize genotypes over ten environments.								
Var.	Mean	A	b <sub>i</sub>	В	С	A-C	D	E	$S_{d_i}^2$
1	27.73	257.04	1.213	331.70	402.5	-145.4	-36.36	21.85	-58.21
2	25.77	367.96	1.332	364.19	485.2	-117.2	-29.30	21.85	-51.15
3	26.53	140.36	0.684	186.93	127.8	12.5	3.14	21.85	-18.71
4	26.74	181.96	0.920	251.43	231.2	-49.3	-12.32	21.85	-34.17
5	27.95	257.38	1.102	301.28	332.0	-74.7	-18.66	21.85	-40.51
6	28.86	518.03	1.192	325.91	388.5	129.5	32.38	21.85	10.53
7	29.52	469.39	1.184	323.76	383.4	85.9	21.49	21.85	-0.36
8	26.96	180.49	0.785	214.48	168.3	12.2	3.06	21.85	-18.79
9	24.82	291.37	1.024	280.00	286.8	4.57	1.14	21.85	-20.71
10	24.08	126.23	0,777	212.36	164.9	-38.7	-9.68	21.85	-31.53
11	25.96	234.53	0.817	223.40	182.6	51.9	12.99	21.85	-8.86
12	22.49	408.56	1.183	323.38	382.5	26.0	6.51	21.85	-15.34
Sum		3433.3	12.213	3338.8	3535.8	-102.5	-25.63	262.19	-287.8

$$\mathsf{A} = \sigma_{v_i}^2 / 4 \ , \ \mathsf{B} = 1 / 2 \sum_{i=1}^{n} Y_{ij} Z_i \ , \ \ \mathsf{C} = \mathsf{b_l} \ \mathsf{X} \ \mathsf{B}, \ \ \delta_{ij}^2 = A - C \ , \ \mathsf{D} = \delta_{ij}^2 / (L - 2) \ , \ \mathsf{E} = S_e^2$$

Table 12. Analysis of variance of grain yield for 12 maize genotypes over ten environments.

Source of variation	d.f	Sum of Squares	Mean Squares	F
Genotypes (G)	11	2481.125	225.557	
Environments	9	11807.00	1311.889	
Combined Regression	1	6796.283	6796.283	10.851
Residual (1)	8	5010.717	626.340	
Interaction (G*E)	99	3642.75	36.795	1.684
Heterogeneity of Reg.	11	275.311	25.028	1.145
Residual (2)	88	3367.44	38.266	1.751
Error between replicate	240	5243.88	21.849	



#### DISCUSSION OUTPUT

### Genotypic stability

Genotypic stability statistics  $\alpha_i$  and  $\lambda_i$  are presented in Table (3) and graphically illustrated in Fig. (1) draw by using the probability values in Table 4 for studied traits. The values ( $\alpha = -1$  and  $\lambda = 1$ ) will be referred to perfect stability. However, the values ( $\alpha = 0$  and  $\lambda = 1$ ) will be referred to average stability, whereas the values ( $\alpha > 0$  and  $\lambda = 1$ ) will be referred to below average stability, however the values ( $\alpha < 0$  and  $\lambda = 1$ ) will be referred as above average stability.

In respect of genotypic stability for grain yield as estimated by Tai (1971), results in Table (3) and Fig.(1) show that the hybrids T.W.C.323, T.W.C.324, and T.W.C.325 had grain yield above average of stability. On the other hand the hybrids T.W.C.310, T.W.C.320, T.W.C.321, T.W.C.322, T.W.C.326, T.W.C.327, T.W.C.352, Wataneia 1 and Nefertety were not stable.

#### Phenotypic stability

Combined analysis of variance and regression analysis for the studied characters are presented in Tables 5 & 8. Mean squares of maize genotypes were highly significant for all traits. Highly significant mean squares due to environments and genotype x environments interaction for all traits studied indicated that genotypes considerably varied across different environments. Environment + (genotype x environment) interaction was partitioned into environment (linear), genotype x environment (linear) interaction (Sum of squares due to regression,  $b_i$ ) and unexplained deviation from regression (Pooled deviation mean squares,  $S^2$ d). Insignificant genotype x environment (linear) mean squares for all traits studied indicated that genotypes did not differ genetically in their response to different environments when tested with pooled deviation.

Results of stability parameters for grain yield of the twelve maize genotypes are presented in Table 7. Data obtained clearly indicated that yield was significantly affected by genotypes. The highest grain yield (ard/fed) was given by genotype 7 (TWC.325) being 29.52 ard/fed followed by genotypes T.W.C.324, T.W.C.323, T.W.C.310 and T.W.C.326 that produced 28.86, 27.95, 27.74 and 26.96 ard/fed, respectively. On the other hand, the lowest yield was given by genotypes Nefertety and T.W.C.352 which recording 22.50 and 24.08 ard/fed, respectively.

Results of phenotypic stability Tables 7,9 and 11 indicated that the value of regression coefficient did not significantly differ from unity (b = 1) for all genotypes studied except 3 and 10. Also, values of deviation from regression (S<sup>2</sup>d) did not significantly differ from zero (S<sup>2</sup>d = 0) for all genotypes except Nefertety. Actually b measures the reaction of the genotype to the environmental effects, then it is considered as a parameter of response, while S<sup>2</sup>d exhibit the degree of stability. Mean performance of yield for genotypes T.W.C.325, T.W.C.324, T.W.C.323 and T.W.C.310 were significantly greater than those of all other genotypes. It is evident that genotypes T.W.C.325, T.W.C.324, T.W.C.323 and T.W.C.310 had regression coefficient and deviation from regression did not significantly differ from one and ze 3, respectively. Therefore, genotypes T.W.C.325, T.W.C.324, T.W.C.323 and T.W.C.310 met all the stability characteristics of the stable genotypes as described by Eberhart and Russell (1966), Perkins and Jinks'(1968) and

Freeman and Perkins(1971), and could be recommended as a stable maize genotypes for yield.

According to the above and Table 1, the study suggests that used models 1 or 2 for analysis stability parameters, which are less expensive than model 3.

Those three genotypes; 5(TWC.323), 6 (TWC.324) and 7(T.W.C.325) met the assumptions of stable genotype. They had regression coefficient, b, and S<sup>2</sup>d which were not significantly differ from unity and zero, respectively and had mean performance significantly greater than those of all other studied genotypes. In addition they show above average degree of genotypic stability. Hence, these three-way crosses, i.e. 5(TWC.323), 6 (TWC.324) and 7(TWC.325) may be recommended to be released as a commercial stable high yielding hybrid and/or incorporated into a breeding stock in any future breeding program.

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# GESTAB برنامج بيسك لتقدير الثبات في الذرة الشامية لبعض النماذج الإحصائية أحمد عبد العزيز مرسى عطية

المعمل المركزي لبحوث التصميم و التحليل الإحصائيي- مركز البحوث الزراعية- الجيزة.

تهدف هذه الدراسة إلى تقديم برنامج صمم بلغة البيسك لتقدير معالم الثبات الوراثي و المظهري للصفات تحت الدراسة لبعض النماذج الإحصائية، هي نموذج تاي (١٩٧١) للثبسات السوراثي وللثبسات المظهري ثلاث نماذج هي نموذج ابرهارت و راسيل (١٩٦٦)، نموذج بيركنز و جينكز (١٩٦٨) و فريمان و بيركنز (١٩٢٨).

البرناميج يعمل على أجهزة BM-PCs و المتوافقة معها لتطبيقات لغة البيسك المختلفة الميسك المختلفة والبرناميج يعمل على أجهزة QBASIC وجاري اعدادة للعمل تحت بيئة الويندوز، ذلك بهدف تسهيل العمليات الحسابية لنموذج (بيركنز و جينكز) و نموذج (فريمان و بيركنز ) كما جاء في جدول رقم (١) و بالتسالي

استخدام المعلومات المتاحة من هذه التقديرات لمعرفة درجة ثبات التراكيب الوراثية المختلفة فـــ البيئـــات المختلفة. المختلفة

التطبيق، تقييم بعض الهجن الثلاثية من الذرة الشامية ، حيث تم تقييم ١٢ هجين ثلاثي: (٣١٠، ٣٢٠، ٣٢٠، ٣٢٠، ٣٢٠، ٣٢٠ وطنية ١ ، نفرتيتي) وفلك باستخدام ٣٠٠، ٣٢٠، ٣٢٠، ٣٢٠ و مدروت و فلا المساوية في أربع مكررات، و تمت الزراعة في خمس مواعيد هي (١٠ مسارس ، ٣٠ أبريل ، ١٠ مايو و ٣٠ مايو) خلال موسمي ٢٠٠٢ و ٢٠٠٣ للمحصول (أربب/فدان) وذلك بمنطقة مازورا غرب الفشن محافظة بديسويف.

نتائج البرنامج، باستخدام البرنامج لا توجد اي صعوبات في حسابات أي نموذج و لاكن مع عنصر التكاليف ينصح باستخدام النماذج الأقل تكلفة و هي نموذج ابرهارت و راسيل (١٩٦٦)، نموذج بيركنسز و جبيكز (١٩٦٨) و ١٣٤، ٣٢٣ و ٣٣٥ قد أعطت درجة ثبات فوق المتوسط وأن بساقي التراكيب، ٣١٠، ٣٢١، ٣٢١، ٣٢١، ٣٢٠، ٣٥٢، ٣٥٢، وطنية ١ و نفرتيتي لم تعطى أي درجة من الثبات .

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