World Journal of Agricultural Sciences 2 (1): 47-55, 2006
ISSN 1817-3047

Stability Parameters in Yield of White Mustard (*Brassica Alba* L.) in Different Environments

T.H.S. Abou El-Nasr, M.M. Ibrahim and K.A. Aboud

Department of Genetics and Cytology, National Research Center (NRC), Dokki, Cairo, Egypt

Abstract: Stability parameters of 20 genotypes of white mustard were evaluated under four environments in two locations and assessed using three different stability methods. The investigation included five characters (plant height, number of primary branches, number of secondary branches, number of pods on main branch and seed yield). Results revealed significant genotype × environment interactions for all studied traits and the response to environmental changes of each genotype differed as indicated by M.S. pooled deviation and heterogeneity items. Wider ranges of regression coefficient values were observed from the studied stability methods suggesting possibility of selection for specific genotypes patterns. Four genotypes (No. 6, 10, 12 and 13) were most stable for studied characters in four environments. Genetic characterization of white mustard genotypes by SDS-PAGE analysis of protein fractions revealed differences in the banding profile pattern in the altered environment (clay vs. sandy soils). Moreover, some other protein bands were also found in the sandy soil more than in the clay soil.

Key words: Selection · white mustard · genotype-environment interaction · stability measurements

INTRODUCTION

Stability of production under different environments is an important consideration in medicinal plants breeding programs. Some genotypes may fair well in some environments but no so well in others [1]. The development of varieties, which adapted to a wide range of diversified environments, is ultimate goal of plant breeders in crop improvement programs. The adaptability of a variety over diverse environments is usually tested by the degree of its interaction with different environments under which it is planted. A variety or genotype is considered to be the most adaptive or stable one if it has a high mean yield but a low degree of fluctuation in yielding ability when grown over diverse environments [2]. Many investigators among them [3-7], described the importance of genotypes x environmental interaction in stability analysis. White mustard (*Brassica alba*, L.) is an erect annual crop, cultivated as oilseed crops and adapted to wide variety of climatic conditions and suited to many types of soils [8]. It was also used in herbal medicine as antibacterial, antifungal carminative, diuretic, Emetic, Expectorant, Stimulant and ruberfacient [8-11].

Some methods have been proposed to evaluate stability [12-14]. They divided the variance due to environment into combined regression and environmental residual. They also divided the variance due to a genotype x environment interaction into heterogeneity of regression and residual.

The present investigation was an attempt to study the stability of some white mustard genotypes yield and yield components characters under different environmental conditions (clay and sandy soils). In addition, the pattern of proteins electrophoresis of different environments were characterized by gel filtration and SDS-Polyacralymide gel electrophoresis.

MATERIALS AND METHODS

Seed material used in this study was 20 genotypes of white mustard (*Brassica alba,* L.) which were sown at the Experimental Farm Station of National Research Center (NRC) at Shalakan, Kalubia Governorate (clay soil) and at Farm of South El-Tahrir Agricultural Company, El-Behira Governorate (sandy soil), during two successive growing seasons (2002/ 2003) and (2003/ 2004).

Sowing was done in a randomized complete blocks design with three replications in each above mentioned environments. Planting dates were at 22nd October 2002 and 28th October 2003, respectively. At full ripen,

Corresponding Author: Dr. T.H.S. Abou El-Nasr, Department of Genetics and Cytology, National Research Center (NRC), Dokki, Cairo, Egypt

five plants of each replicate per each entry of different generations were harvested and the plant records were considered as already mentioned. Data recorded on:

- Plant height (cm)
- Number of primary branches
- Number of secondary branches
- Number of pods on main branch
- Seed yield per plant (g)

Statistical analysis: A combined analysis of variance was used to evaluate the responses of each character within the experiment and to determine the genotype-environment interaction. Whenever, the variance due to genotype-environment interaction was significant, the analysis was continued in order to estimate the stability parameters. Stability analysis was computed according to Eberhart and Russell [12]. To detect the phenotypic stability under different environments:

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$$

Where; Y_{ij} = Genotype mean of i^{th} genotypes at j^{th} environments, μ_i = Mean of all genotypes over all environments, β_i = the regression coefficient of the i^{th} genotypes on the environmental index, which measure the response of this genotype to varying environments, I_j = Environmental index, which is defined as the deviation of the mean of all genotypes at a given environment from the grand mean, and δ_{ij} = the deviation from regression of i^{th} genotypes at j^{h} environments.

Perkins and Jinks [13], proposed a different model for stability analysis. In this model, the total variance is first divided into three components, viz. (1) genotypes (G), (2) environments (E) and (3) genotypes x environment. The G x E variance is subdivided into (a) heterogeneity due to regression and (b) sum of square (SS) due to remainder. The S.S remainder is further divided into S.S due to individual genotype. The main features of this model includes three parameters of stability like [12], with one exception; the degree of freedom for environment is e-2. Another objection of [14], to other models was about the partitioning of the degree of freedom. Though, S.S. due to environment (linear) of [12], being the same as S.S. due to environment (joint regression) of Perkins and Jinks model, yet the degree of freedom is one in the former and s-1 in the latter. In Eberhart and Russell model, b (regression coefficient) is considered as parameter of response and S^2_d as the parameter of stability. As far as the ranking of genotypes with respect to there stability is considered, it remains the same under all the three models described above. Eberhart and Russell's model bing relatively simple, may, therefore, be preferred for studying stability analysis.

The model of Perkins and Jinks [13].

$$Y_{ijk} = \mu + a_i + \varepsilon_j + r_{jk} + \beta_{-i}\varepsilon_j + \delta_{ij} + e_{ijk}$$

Where; Yijk: is the mean performance of the line i in replicate k of environment j, μ is the overall mean, a_i is the contribution of line i, ε_j is the contribution of environment j, r_{jk} is the contribution of replicate k in environment j, β_{-i} is the linear regression coeffecient for line i, δ_{ij} is the deviation from regression, and e_{ijk} is the residual variation of line i in replicate k in of environment j.

Freeman and Perkins [14], proposed independent estimate of environmental index in the following two ways:

1) Divide the replications into groups, so that the one group may be used for measuring the average performance of genotypes in various environment and the other group, averaging over the genotypes is used for estimating the environmental index.
2) Use one or more genotypes as check and assess the evironmental index on the basis of there performance.

The hypothesis that any regression coefficient does not differ from unity was tested by the T-test [15], using its own standard error for regression. Also the mean square of deviation from regression of each genotype (S^2_d), pooled errors in the regression analysis of variance were used to test whether each deviation mean square was significantly different from zero.

Wricke and Weber [16], proposed ecovalence model to evaluate the balanced response of G x E interaction as follows:

$$W_i = \sum_j (Y_{ij} - Y_{i.} - Y_{.j} + Y..)^2$$

Where: W_i is the ecovalence of the i^{th} genotypes, Y_{ij} is the mean performances of genotype (i) in the j^{th} environment, $Y_{i.}$ and $Y_{.j}$ are the genotype and environment mean deviations, respectively and Y.. is the over all mean.

Oil content (%): The oil was extracted on basis of air-dried seed from a random sample of each types of entries. Soxhelt extraction method was used to determine oil content by hexane solvent which described by AOAC [17].

Gel electrophoresis: Total proteins electrophoresis analysis were carried out according to Laemmli [18]. Seeds of four entries of genotypes were defatted with hexane for one week and ground in liquid nitrogen. One milliliter of water soluble extraction buffer was added. After centrifugation for 10 min, a 12,000 rpm under 4°C, the supernatant was collected [19]. Electrophoresis was carried out at 4°C until the bromophenol blue front passed completely through the gel. The gel was stained for 12 h in 0.1% coomassie brilliant blue and distained until the bands were clearly observed.

RESULTS AND DISCUSSION

Data presented in Table 1 indicated that significant differences among genotypes, environments and genotype × environment interaction were detected for all studied traits. These results revealed that mustard genotypes responded differently to the different environmental conditions. This finding suggested the importance of assessment of genotypes under different environments to identify the best genetic makeup for a particular environment. These findings were agreement line with those previously obtained by Ali *et al*., [6], Wani [20] and Ali *et al*., [21].

The differences between grand mean (over all environments) and each of the four environmental mean performances for the five studied traits recorded covered a wide range and displayed a good distribution within the range as shown in Table 2. Consequently, the required assumptions for stability analysis is full-filled [22]. Number of secondary branches differences ranged from 2.90 in the second environment to 2.67 in the first environment.

Eberhart and Russell [12], model provides a mean of partitioning the genotype-environment interaction for each genotype into two parts.

- The variation due to the response of genotype to varying environmental index (sum of squares due to regression).
- The unexplainable deviation from the regression on the environmental index. They added that a stable genotype could have high mean performance.

Significant genotypes × environments (Linear) interaction were detected for all studied traits Table 3. This result indicated that the differences among genotypes for their regression on the environmental index proceeded further to estimate the (bi) values. Pooled deviations mean squares were insignificant suggesting linear regression also assume partial importance considering each individual genotype

The joint regression analysis was conducted for all studied traits according to the procedure described by Perkins and Jinks [13]. All sources of variation mean squares were tested against average error Table 4.

Highly significant differences among genotypes and environments were found for all studied traits. Also, there were high significant differences among genotype x environment interaction for all studied traits. On the other side, heterogeneity between regression mean squares were highly significant when tested against the remainder mean squares for plant height, number of primary branches, number of pods/ main branch and seed yield/ plant. However, the remainder mean squares were highly significant for all traits except number of secondary branches when tested against average error.

Table 1: The combined analysis of variance of all studied traits for 20 white mustard genotypes over four environments tested

S.O.V.	d.f.	Plant height	No. of primary branches	No. of secondary branches	No. of pods/ main branch	Seed yield/ plant
Environments (E)	3	7301.75**	751.84**	7.14**	2137.61**	1606.82**
Rep./ Env.	8	53.63	3.67	0.78	15.04	19.91
Genotypes (G)	19	1379.65**	33.07*	4.38**	1280.54**	641.28**
G x E	57	567.64**	15.29**	0.91**	45.54**	44.87**
Error	152	27.02	2.47	0.38	9.80	8.98

*, ** Denote significant at 0.05 and 0.01 probability levels, respectively

Table 2: Mean performance of all traits studied under each of the four environments tested

Environments		Plant hieght	No. of primary branches	No. of secondary branches	No. of pods/ main branch	Seed yield/ plant
1		121.67	20.32	3.67	32.47	27.62
2		106.78	9.42	2.90	24.05	25.83
3		133.48	15.92	3.25	37.27	37.55
4		123.72	9.17	2.98	26.45	29.42
Average		121.41	13.70	3.20	30.06	30.11
LSD	0.05	3.09	0.81	0.37	1.64	1.88
	0.01	4.49	1.18	0.54	2.38	2.74

Table 3: Pooled analysis of variance for all studied traits for the 20 white mustard genotypes under two locations over two years, Eberhart & Russell [12]

S.O.V.	d.f.	Plant height	No. of primary branches	No. of secondary branches	No. of pods/ main branch	Seed yield/ plant
Genotypes (G)	19	459.89**	11.03**	1.46**	42.85**	213.76**
Environments (E)+G x E	60	339.56	28.50**	0.66**	48.32**	82.54**
G x E (linear)	19	226.61*	9.93**	0.65**	22.69*	22.34*
Pooled deviation	40	161.99	2.54	0.12	10.85	10.70
1	2	197.64**	0.54	0.41**	22.16**	30.61**
2	2	139.23**	6.28**	0.14	11.65**	51.64**
3	2	1017.64**	7.77**	0.03	11.44**	7.46*
4	2	165.11**	1.41	0.03	11.51**	2.47
5	2	267.07**	2.18**	0.27*	24.09**	26.00**
6	2	20.94*	1.05	0.33**	3.11	3.40
7	2	72.74**	6.96**	0.05	0.60	0.28
8	2	154.28**	1.22	0.02	4.85	4.16
9	2	210.08**	1.41	0.10	20.74**	16.35**
10	2	26.92**	2.32**	0.18	5.62	17.62**
11	2	60.68**	0.76	0.38**	3.84	8.53**
12	2	46.54**	4.36**	0.13	4.32	4.81
13	2	53.27**	0.69	0.01	5.11	0.37
14	2	115.50**	0.51	0.01	2.89	4.32
15	2	11.16	0.76	0.05	31.15**	5.77
16	2	108.94**	3.29**	0.02	7.25*	8.31**
17	2	320.44**	1.98*	0.03	14.39**	9.49**
18	2	172.32**	1.96*	0.12	13.95**	6.47*
19	2	8.18	0.85	0.09	11.03**	0.02
20	2	71.21**	4.58**	0.05	7.38*	5.97*
Pooled error	160	9.005	0.82	0.13	3.27	2.99

*, ** Denote significant at 0.05 and 0.01 probability levels, respectively

Table 4: The joint regression analysis of variance for all studied traits over two locations and two growing seasons (Pirking and Jinks model [13])

S.O.V.	d.f.	Plant height	No. of primary branches	No. of secondary branches	No. of pods/ main branch	Seed yield/ plant
Genotypes (G)	19	459.89**	11.03**	1.46**	42.85**	213.76**
Environments (E) (joint regression)	3	2433.98**	583.95**	2.38**	712.53**	535.61**
G x E	57	189.22**	5.10**	0.30**	15.18**	14.96**
Heterogeneity between regression	19	226.6**	9.93**	0.65**	22.69**	22.34**
Remainder	38	170.52**	2.68**	0.13	11.43**	11.27**
Pooled error	160	8.55	0.78	0.12	3.10	2.84

** Denote significant at 0.01 probability level

Table 5: Partitioning of analysis of variance for all studied traits over two locations and two growing seasons, according to freeman and Perkins [14]

S.O.V.	d.f.	Plant height	No. of primary branches	No. of secondary branches	No. of pods/ main branch	Seed yield/ plant
Genotypes (G)	19	954.84	22.97*	3.30	93.17	412.17*
Environments (E)	3	4911.58*	1132.66**	7.00	1374.85*	977.95*
Combined regression	1	14364.92	3397.06	17.79	3988.05	2889.52
Residual regression	2	184.92	0.46	1.61	68.25	22.16
G x E	57	384.78	11.53	0.74	29.65	32.40
Heterogeneity of rgression	19	478.84	24.77**	1.21**	41.40*	47.38*
Residual	38	337.74	4.91	0.51	23.78	24.91
Error between replicates	80	703.38	58.29	1.97	104.47	166.33

*, ** Denote significant at 0.05 and 0.01 probability levels, respectively

The partitioning analysis of variance model of Freeman and Perkins [14], was also conducted for characters under study and illustrated at Table 5. It could be noticed that the mean squares due to genotypes showed significance for number of primary branches and seed yield/ plant, while insignificance for plant height, number of secondary branches and number of pods/ main branch. Therefore, considerable variations among traits expression were detected between white mustard genotypes. Moreover, highly significant variations were obtained detected for number of primary branches, while significant variation for plant height, number of pods/ main branch and seed yield/ plant and insignificant variation for number of secondary branches due to environmental changes.

It was evident that all used models of analysis of variance cleared that there were significant genetic background variations among white mustered genotypes

Table 6a: Estimates of phenotypic stability parameters for plant height of 20 mustard genotypes grown under four diverse environments

Genotypes	x	b_i-ER	S^2d_i-ER	β_{-i} -PJ	b_i-FP	S^2d_i-FP	W_i
1	120.575	2.3**	197.64**	1.3	2.41	-579.61	1017.06
2	125.325	1.13	139.23**	0.13	1.19	-598.51	284.91
3	128.325	1.73**	1017.64**	0.73	1.61	-133.93	2229.45
4	115.825	1.14	165.11**	0.14	1.08	-594.76	336.06
5	125.475	1.4*	267.07**	0.40	1.45	-558.04	593.38
6	114.825	1.31*	20.94*	0.31	1.25	-658.28	76.69
7	109.325	2.61**	72.74**	1.61	2.62	-640.59	1090.10
8	115.675	1.88**	154.28**	0.88	2.07	-640.40	595.76
9	104.350	2.19**	210.08**	1.19	2.11	-469.60	941.09
10	119.975	0.98	26.92**	-0.02	0.91	-677.4	53.65
11	123.675	0.36**	60.68**	-0.64	0.20	-643.02	270.98
12	147.500	0.38**	46.54**	-0.62	0.46	-699.46	233.56
13	119.575	0.25**	53.27**	-0.75	0.25	-660.07	310.52
14	132.500	0.26**	115.5**	-0.74	0.46	-636.33	432.85
15	134.225	0.39**	11.16	-0.61	0.25	-692.72	160.55
16	111.925	0.39**	108.94**	-0.61	0.44	-639.37	355.25
17	109.350	0.39**	320.44**	-0.61	0.14	-414.9	787.21
18	138.150	0.29**	172.32**	-0.71	0.33	-575.35	528.93
19	115.575	0.33**	8.18	-0.67	0.29	-703.06	180.66
20	116.000	0.32**	71.21**	-0.68	0.32	-651.54	310.55
LSD 0.05	4.16						
0.01	5.48						

Table 6b: Estimates of phenotypic stability parameters for number of primary branches of 20 mustard genotypes grown under four diverse environments

Genotypes	x	b_i-ER	S^2d_i-ER	β_{-i} -PJ	b_i-FP	S^2d_i-FP	W_i
1	15.415	1.38*	0.54	0.38	1.32	-58.12	13.549
2	13.665	1.30	6.28**	0.30	1.24	-55.03	20.427
3	13.165	1.33	7.77**	0.33	1.34	-54.14	24.977
4	13.085	1.53**	1.41	0.53	1.56	-56.92	27.547
5	14.000	0.89	2.18**	-0.11	0.92	-57.58	5.475
6	12.998	1.17	1.05	0.17	1.17	-57.83	4.715
7	11.000	1.22	6.96**	0.22	1.26	-52.91	18.343
8	11.083	1.40*	1.22	0.40	0.97	-57.31	4.143
9	11.583	1.54**	1.41	0.54	1.48	-57.62	28.731
10	12.083	1.15	2.32**	0.15	1.11	-57.24	6.588
11	15.333	0.92	0.76	-0.08	0.97	-57.49	2.154
12	15.748	0.92	4.36**	-0.08	1.07	-53.27	9.235
13	15.920	0.65*	0.69	-0.35	0.56	-57.99	11.913
14	16.000	0.31**	0.51	-0.69	0.28	-57.64	42.450
15	14.665	0.76	0.76	-0.24	0.67	-57.13	6.406
16	15.333	0.73	3.29**	-0.27	0.65	-57.03	12.839
17	15.253	1.08	1.98*	0.08	0.98	-58.09	4.508
18	12.835	0.64*	1.96*	-0.36	0.49	-57.68	15.482
19	12.335	0.61*	0.85	-0.39	0.51	-57.64	15.258
20	12.585	0.72	4.58**	-0.28	0.57	-55.86	15.792
LSD 0.05	1.26						
0.01	1.66						

b_i and S^2d_i: tested against 1.0 and 0.0, respectively, *, ** Denote significant at 0.05 and 0.01 probability levels, respectively
Wi = stability rank of Wricke and Weber [16]

and the response of tested quantitative characters. Also, significant different changes were displayed due to environments. However, all used statistical models confirmed significant genotypes x environmental interaction for most studied traits. These results were in good agreement with those reported by Hasan [23] and Sardana & Borthakur [24].

Data in Table 6 showed that, with the exception of genotypes No. 2, 4 and 10, significant (b_i) values were detected for all other genotypes in plant height. Also, the slope of the regression genotype did not deviate significantly from unity in genotypes No. 11, 12 and 17 for number of primary branches as shown in Table 6a and b.

The deviation from regression mean squares (S^2d_i) were highly significant suggesting that these genotypes were sensitive.

The highest yielding genotypes were No. 1, 2, 3 and 4. The b_i and S^2d_i values were significantly different from unity and zero, respectively for seed yield. Whereas, genotype No. 7 was moderate for seed yield and the (b_i)

Table 6c: Estimates of phenotypic stability parameters for number of secondary branches of 20 mustard genotypes grown under four diverse environments

Genotypes	x	b_i-ER	S^2d_i-ER	β_{-i} -PJ	b_i-FP	S^2d_i-FP	W_i
1	4.083	-2.04	0.41**	-3.04	-2.41	-1.73	4.116
2	3.165	0.40	0.14	-0.60	1.11	-1.80	0.399
3	3.248	0.20	0.03	-0.80	0.37	-1.90	0.297
4	3.418	1.4	0.03	0.40	1.30	-1.55	0.109
5	4.668	-2.57**	0.27*	-3.57	-3.89	-1.59	5.074
6	3.665	-0.17	0.33*	-1.17	0.74	-1.77	1.140
7	3.083	0.76	0.05	-0.24	1.85	-1.79	0.118
8	3.333	0.71	0.02	-0.29	0.74	-1.94	0.066
9	3.083	1.48	0.10	0.48	2.59	-1.88	0.276
10	4.085	1.73	0.18	0.73	2.41	-1.73	0.547
11	3.833	2.95**	0.38**	1.95	5.19	-1.43	2.138
12	2.915	1.17	0.13	0.17	2.04	-1.60	0.275
13	2.833	1.84	0.01	0.84	4.07	-1.80	0.273
14	2.915	2.27*	0.01	1.27	4.07	-1.80	0.599
15	2.833	1.12	0.05	0.12	2.04	-1.93	0.116
16	2.750	2.12	0.02	1.12	3.89	-1.93	0.488
17	2.415	1.97	0.03	0.79	2.22	-1.95	0.271
18	2.665	1.74	0.12	0.74	2.41	-1.84	0.452
19	2.498	1.51	0.09	0.51	2.41	-1.84	0.277
20	2.498	1.59	0.05	0.59	3.15	-1.92	0.222
LSD 0.05	0.49						
0.01	0.65						

Table 6d: Estimates of phenotypic stability parameters for number of pods / main branch of 20 mustard genotypes grown under four diverse environments

Genotypes	x	b_i-ER	S^2d_i-ER	β_{-i} -PJ	b_i-FP	S^2d_i-FP	W_i
1	33.000	1.47	22.16**	0.47	1.35	-80.96	68.367
2	31.575	1.02	11.65**	0.02	1.16	-91.99	23.311
3	30.525	1.32	11.44**	0.32	1.14	-94.08	34.011
4	29.500	1.30	11.51**	0.30	0.82	-96.69	32.323
5	28.675	0.70*	24.09**	-0.30	0.48	-91.83	57.870
6	30.075	1.32	3.11	0.32	1.23	-96.58	16.736
7	25.600	1.65*	0.60	0.65	1.68	-104.12	46.498
8	26.650	1.55	4.85	0.55	1.46	-100.30	42.286
9	26.650	1.79*	20.74**	0.79	1.66	-81.42	107.750
10	25.825	1.56	5.62	0.56	1.30	-90.26	43.553
11	37.425	1.18	3.84	0.18	1.11	-101.62	11.287
12	31.525	0.66*	4.33	-0.34	0.54	-99.09	20.614
13	29.925	0.61	5.11	-0.39	0.55	-96.54	26.242
14	30.000	0.51	2.89	-0.49	0.63	-104.39	31.014
15	32.075	0.57	31.15**	-0.43	0.60	-92.01	81.198
16	34.475	0.68*	7.25*	-0.32	0.67	-102.21	25.275
17	33.250	0.55	14.39**	-0.45	0.43	-99.87	50.589
18	31.925	0.62	13.95**	-0.38	0.60	-93.61	43.603
19	28.150	0.38	11.03**	-0.62	0.46	-94.34	63.119
20	24.400	0.55	7.38*	-0.45	0.60	-104.07	36.109
LSD 0.05	2.51						
0.01	3.30						

b_i and S^2d_i: tested against 1.0 and 0.0, respectively, *, ** Denote significant at 0.05 and 0.01 probability levels, respectively
Wi = stability rank of Wricke and Weber [16]

value was not significantly different from unity. The minimum deviation from regression mean squares (S^2d_i) pooled over the four environments was obtained by genotypes 7, 13 and 19.

It was concluded that, genotype No. 17 was stable for number of primary branches on the basis of (b_i) which did not differed significantly from unity and ranked second for the mean performance compared with the other genotypes.

The results[5, 26, 27], were more or less in line with these findings.

In addition to high yield, consistency over several environments is much desired for commercial exploitation of the genotype. Wricke's ecovalence model was employed as a stability measurement. This statistic, termed ecovalence (W_i), was simpler to compute and more directly related to genotype-environment interactions. Genotypes with $W_i = 0$ were regarded as perfectly stable.

Table 6e: Estimates of phenotypic stability parameters for seed yield / plant of 20 mustard genotypes grown under four diverse environments

Genotypes	x	b_i-ER	S^2d_i-ER	β_{-i} -PJ	b_i-FP	S^2d_i-FP	W_i
1	46.175	1.98**	30.61**	0.98	1.65	-138.11	138.47
2	41.525	1.92*	51.64**	0.29	2.04	-134.56	171.48
3	39.400	1.63	7.46*	0.63	1.46	-165.19	46.69
4	38.675	1.72*	2.47	0.72	1.47	-165.79	46.51
5	35.825	1.65	26.00**	0.65	1.25	-149.65	85.74
6	34.000	1.34	3.40	0.34	1.12	-163.33	15.67
7	30.350	1.26	0.28	0.26	1.13	-164.07	6.22
8	33.350	0.37	4.16	-0.63	0.28	-156.20	40.00
9	28.025	0.81	16.35**	-0.19	0.52	-157.69	35.69
10	31.250	0.40	17.62**	-0.60	0.37	-142.77	63.57
11	28.750	0.50	8.53**	-0.50	0.41	-162.63	37.59
12	26.325	0.50	4.81	-0.50	0.42	-165.32	29.67
13	24.575	0.84	0.37	-0.16	0.77	-163.33	2.71
14	25.675	0.62	4.32	-0.38	0.65	-163.54	20.33
15	24.075	0.74	5.77	-0.26	0.60	-159.46	16.97
16	26.925	0.58	8.31**	-0.42	0.44	-160.20	30.97
17	24.675	0.72	9.49**	-0.28	0.53	-157.64	24.88
18	22.175	0.71	6.47*	-0.29	0.64	-159.08	20.24
19	19.175	1.00	0.02	0.00	1.01	-164.19	0.05
20	21.275	0.71	5.97*	-0.29	0.58	-159.48	18.79
LSD 0.05	2.40						
0.01	3.16						

b_i and S^2d_i: tested against 1.0 and 0.0, respectively, *, ** Denote significant at 0.05 and 0.01 probability levels, respectively
Wi = stability rank of Wricke and Weber [16]

Table 7: SDS-PAGE analysis of water soluble and non-soluble proteins of white mustard under variable environments

		Water soluble proteins					Water non-soluble proteins			
		Resources with band density (%)					Resources with band density (%)			
Band no.	MW (kD)	Sandy soil	Sandy soil	Clay soil	Clay soil	MW (kD)	Sandy soil	Sandy soil	Clay soil	Clay soil
1	200	+	+	+	+	112	+++15	+++14	++9	++9
2	138	+	+	+	+	96	+4	+4	++6	++7
3	100	+	+	+	+	90	+	+	+	+
4	99.5	+	+			76	+	+	+	+
5	87	+	+	+	+	66	+	+	+	+
6	81	+	+	+	+	62	+3	+4	++10	++8
7	75	+	+	+	+	48	+3	+3	++7	++6
8	60	+	+	+	+	44	+3	+4	++10	++7
9	58	+	+	+	+	36	++4	++4	+2	+2
10	50	+	+	+	+	35	++4	++5	+3	+3
11	46	+	+	+	+	24	+4	+4	++8	++8
12	42	+	+	+	+	21	+3	+5	++9	++10
13	30	+++19	+++19	++8	++8	15	+++10	+++13	+2	+2
14	20	+++19	+++18	++8	++8	14	++5	++5	+2	+2
15	13	+++11	+++10	++8	++6	9	+++12	++5	+2	+3
16	12	+	+			8			+	+
17						7			++9	++8
18						5	+++21	+++21	+++14	+++12

Such genotypes would not change its performances from one environment to another and probably not exist. According to the meaning of the word "ecovalence" the average stable genotype possesses high ecovalence (low values of W_i = high ecovalence). W_i parameters clearly showed that genotypes No. 19, 13 and 7 considered to be a stable genotypes for seed yield and one or more of the yield attributes recorded (Table 6). Earlier results of Eberhart and Ruseell [12], Perkins and Jinks [13] and Freeman and Perkins [14], are in accordance with these findings.

Oil content %: The oil content of white mustard genotypes increased in sandy soil than clay soil in both

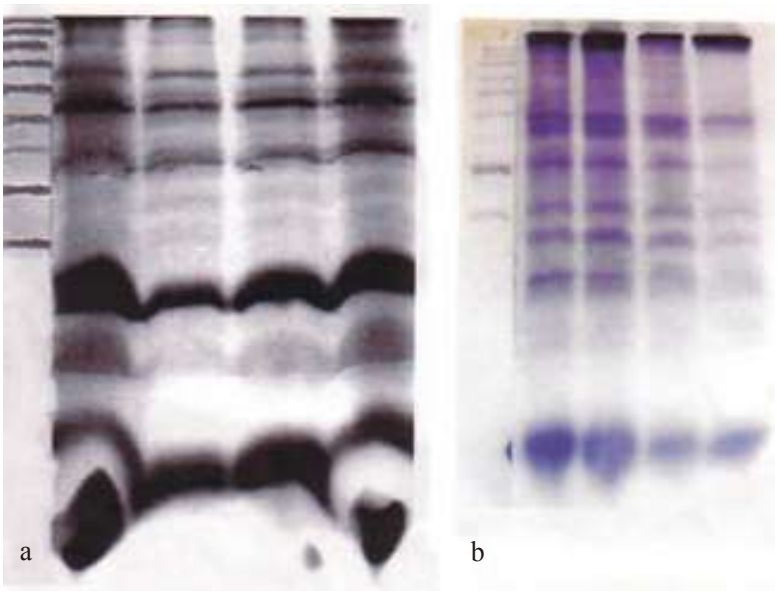

Fig. 1: SDS-PAGE for total soluble proteins of white mustard (a) non-soluble proteins (b)

two growing seasons. These values are (39.26, 42.05%) and (45.01, 49.09%) clay and sandy soil in first and second seasons, respectively.

These data revealed that over all mean values of oil content gave highest values in the second season in sandy soil only.

Genetic characterization of some genotypes of white mustard (*Brassica alba*) by SDS-PAGE analysis: SDS-PAGE of water soluble proteins extracted from four white mustard genotypes revealed that a total of 16 bands with different molecular weights ranged from 200 to 12 kDa in Table 7. Among such protein bands, two bands with molecular weight 99.5 and 12 kDa were presented in the sandy soil, while they were absent in the clay soils in two growing seasons at 2002/ 2003 and 2003/ 2004.

The other protein bands showed that no significant differences upon the presence and the absence of the detected bands. On the other hand, three bands with molecular weights 30, 20 and 13 kDa clearly revealed high density in the sandy soil than in the clay soil with percentages presented in Table 7, which reached more than two fold in most bands.

Among a total of 18 protein bands detected by SDS-PAGE from the water non-soluble fraction, two bands were clearly observed in the clay soils and disappeared in the sandy soil in the two seasons (Fig. 1). Meanwhile, it is interest to note that 13 bands showed outstanding differences based upon the band density in two soils and evidently showed that some minor genes specifically work under a biotic stress (sandy soil) and simultaneously other genes switched off in the same environmental stress. Whereas, seven bands with different molecular weights 112, 36, 35, 15, 14, 9 and 5 showed two fold band density in the sandy soil than in the clay soil. However, other seven bands showed the opposite direction, wherever their band density were much abundant in the clay soil than in the sandy soil Table 7.

In conclusion, the results of SDS-PAGE analysis of proteins of white mustard showed that some new proteins, which were synthesized in response to an altered environment (clay vs. sandy soils) have been obtained as stress proteins, these results are in agreement with many reports Luis *et al.*, [27], Fareida and Afiah [28]. Moreover, some other protein bands represented by their high density percentages were also found much more abundant in the sandy soil than in clay soil.

This finding agreed with Dell' Aquila and Spada [29], El-Enany [30] and Teutonica *et al.*, [31]. They reported that the tolerance to biotic stresses like drought, and salt display a continuous genetic variations because the variation is influenced by simultaneous segregation of several genes.

REFERENCES

1. Dhillon, S.S., K. Sing and K.S. Bar, 1999. Stability analysis of elite strain in Indian mustard. Proc. 10th Intl. Rapeseed Congress held at Canberra, Aust.

2. Arshad, M., B. Ahmed, A.M. Haqqani and M. Bashir, 2003. Genotype-Environment interaction for grain yield in chickpea (*Cicer arietinum* L.).
3. Finaly, K.W. and G.N. Wilkinson, 1963. The analysis of adaptation in plant breeding program. Aust. J. Agric. Res., 14: 742-754.
4. Ahmed, J.M., M.H. Chonldhry, S. Salahuddin and M.A. Ali, 1996. Stability for grain yield in wheat. Pak. J. Bot., 28: 61-65.
5. Khan, A., M. Rahim, N.J. Maik and A. Khan, 1998. Phenotypic stability of pod yield and related characters in bunch type peanut genotypes Sarhad. J. Agric. Res., 14: 441-446.
6. Ali, N., M.S. Nawaz, M.Y. Mirza and G.R. Hazara, 2001. Stability analysis for pod yield in groundnut. Pak. J. Bot., 33: 191-196.
7. Mirza, M.Y., A. Qayyum, A. Naazar, M.S. Nawaz and S.S. Mehdi, 2002. Stability analysis for yield in soybean. Pak. J. Agric. Sci., (In press).
8. Duke, J.A. and E.S. Ayensu, 1985. Medicinal Plants of China Reference Publications, Inc. ISBN 0-917256-20-4. Details of over 1200 medicinal plants of China and brief details of their uses.
9. Holtom, J. and W. Hylton, 1979. Complete Guide to Herbs. Rodale Press 1979 ISBN 0-87857-262-7 A good herbal.
10. Yeung, Him-Che, 1985. Handbook of Chinese Herbs and Formulas. Institute of Chinese Medicine, Loss Angeles, A very good Chinese herbal.
11. Bown, D., 1995. Encyclopedia of Herbs and their uses. Dorling Kindersley, London, ISBN 0-7513-020-31, Eberhart, S.A. and W.A. Russel (1966). Stability parameters for comparing varieties. Crop. Sci., 6: 36-40.
12. Eberhart, S.A. and W.A. Russel, 1966. Stability parameters for comparing varieties. Crop. Sci., 6: 36-40.
13. Perkins, J.M. and J.L. Jinks, 1968. Environmental and genotype environmental components of variability III. Multiple lines and crosses. Heredity, 23: 339-356.
14. Freeman, G.H. and J.M. Perkins, 1971. Environmental and Genotype-environmental components of variability VIII. Relations between genotypes grown in different environments and measures of these environments. Heredity, 27: 15-23.
15. Steel, R.G.D. and J.H. Torrie, 1985. Principles and Procedures of Statistics. McGraw-Hill, New York.
16. Wricke, G. and W.E. Weber, 1986. Quantitative Genetics and Selection in Plant Breeding. W. de Gruyter, Berlin.
17. AOAC., 1980. Official Methods of Analysis, Association Official Agricultural Chemists, P.O. Box 540, Benjamin Franklin Station, Washington D.C.
18. Laemmli, U.K., 1970. Cleavage of structural proteins during assembly of the head of bacteriophage T_4. Nature, 227: 680-685.
19. Bajji, M., S. Lutts and J.M. Kinet, 2000. Physiological changes exposure to and recovery from polyethylene-issued from Durum wheat (*Triticum durum* Desf.) cultivars differing in drought resistance. J. Physiol., 156: 75-83.
20. Wani, S.A., 1992. Genotype x environment interaction for yield and its components in Indian mustard. Adv. Plant Sci., 5: 421-425.
21. Ali, N., J. Fazad and M.Y. Mirza, 2003. Selection of stable rapeseed (*Brasica napus* L.) genotypes through regression analysis. Pak. J. Bot., 35: 175-180.
22. Russell, W.A. and G.L. Prior, 1975. Stability of yield performance of nonprolific and prolific maize hybrids. Iowa State J. Res., 50: 17-27.
23. Hasan, A.M., 1978. Stability analysis of roselle varieties (*Hibiscus sabdariffa*). Indonesian Pemberitaan, 28: 76-83.
24. Sardana, S., A.K. Ghosh and D.N. Borthakur, 1984. Adaptability of promising roselle varieties to the uplands of Tripura. Ind. J. Agric. Sci., 54: 642-645.
25. Yadav, T.P. and P. Kumar, 1978. Stability analysis for pod yield and maturity in bunch group of gram nut. Ind. J. Agric. Res., 12: 1-4.
26. Yadav, I.S. and D. Kumar, 1983. Stability for seed boldness in black gram. Madras Agric. J., 70: 193-194.
27. Luis, M.A., R.I. Mansalva, J.G. Cavilones and R. Rodrignez, 1987. Molecular and spectroscopic characterization of low Molecular weight seed storage protein from yellow mustard (*Sinapis alba* L.). Intl. J. Biochem., 19: 889-907.
28. Fareida, M.E.S. and S.A.N. Afiah, 1998. Changes in polypeptide pattern as indicator of salt tolerance in some *Brassica* species. Proceeding of the 26th Annual meeting of Genetics Alex. 29-30 Sept.
29. Dell'Aquila, A. and P. Spada, 1993. The effect of salinity stress upon protein synthesis of germinated wheat embryos. Ann. Bot., 72: 97-101.
30. El-Enany, E., 1995. Proline effect on shoot organogenesis and protein synthesis in salinity-stressed tomato cultures. J. Islamic Acad. Sci., 8: 131-144.
31. Teutonico, R.A., B. Yandell, J.M. Satagopan and T.C. Osbora, 1995. Genetic analysis and mapping of genes controlling freezing tolerance in Brassica. Molecular Breeding, 1: 329-339.