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Stability Analysis for Seed Yield and Related Component Traits of Ethiopian Mustard Genotypes (*Brasica Carinata A.Braun*) in Central Highlands of Ethiopia

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ABSTRACT

The experiment was executed to analyses seed yield and related traits stability parameters for nine genotypes of Ethiopian mustard at Holeta, wajitu and woliso representative areas of central highlands of Ethiopia The experiment was carried out in a Randomized complete block design. Stability parameters for nine genotypes of Ethiopian mustard were evaluated and assessed using three different stability methods. The investigation included six characters (date of flowering, date of maturity, plant height, stand percent, seed yield and thousand seed weight). 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. Three genotypes PGRC/E20068/5/1, Open pollinated bulk Yellow Dodolla and Open pollinated Yellow Dodolla were most stable for studied characters in the three central highlands of Ethiopian environments.

Keywords: *Stability Analysis, stability parameters, Ethiopian mustard,*

INTRODUCTION

Ethiopian mustard (*Brassica carinata A.Braun*) is believed to be originated in the highlands of the Ethiopian plateau and the adjoining portion of East Africa and the Mediterranean coast (Gomez-Campo and Prakash, 1999). In Ethiopia, among the highland oilseeds, Ethiopian mustard stands third next to niger seed and linseed in total production and areas coverage. It is often grown on well-drained and organic matter rich soils. The crop is well adapted to cool, long growing season and high rainfall areas at elevation between 2200 and 2800 meters. It is because of its wider adaptability and comparative tolerance to biotic and abiotic stresses as compared to other *Brassica* species grown as oilseeds. However, production of Ethiopian mustard is far below the national average. Under such a situation, it becomes very important to identify genotypes which can show a stable performance over different environments or locations. The genotype x environment interaction as described by the Allard and Bradshaw in 1964 is very important in the development and evaluation of genotypes, since diverse environments can reduce the stability of genotypes (Eberhart and Russell, 1966). The stability is the consistency in performance of genotypes over wide range of environment (Singh and Chaudhary, 1985). Only stable genotypes can guarantee a good yield with decreased risk of losing production and allow the plant breeders to make general recommendations for a range of environments. Keeping these facts in to consideration, the present investigation was carried out by considering nine Ethiopian mustard genotypes comprising one standard and local check to test stability over the three environments of central highlands of Ethiopia.

MATERIALS AND METHODS

Experimental Sites

The experiment was conducted in the representative areas of Central highlands of Ethiopia at Holetta , wajitu and woliso in 2003/2004 cropping season from June to December

Description of Test Materials

A total of nine mustard genotypes that include one standard check and one local check were used in this study. The details of the accessions used in the experiment are given in Table1.

Table1. *List of 9 Ethiopian mustard genotypes used in the study and their description of features*

No.	Genotype	Unique feature
1	Light stem Yellow Dodolla	Light stem
2	PGRC/E20068/3/1	Earliness
3	Open pollinated Yellow Dodolla	Late maturing
4	PGRC/E20068/5/1	Earliness
5	Open pollinated bulk Yellow Dodolla	Late maturing
6	PGRC/E20068/3/1	Earliness
7	Yellow dodolla	Standard check
8	(Zem1X Yellow dodolla)X Zem-1	Low erucic acid
9	Local check	

Experimental Design, Management and Season

The experiment was executed from June 2003 to December 2003. The experiment was laid out in simple Randomized complete design with two replications. A plot of four central rows each five -meter long and 30cm spacing between rows were used for data collection. Each replication was represented by nine plots. The path between replication was 2 m and the spacing between plots within was also 0.6 m. Each plots was manually drilled, a rate of 10 kg/ha and urea and phosphorous fertilizers were applied at the rates of 46/69 kg/ha N/P_2O_5 respectively following the national recommendations. All other recommended agronomic and cultural practices were carried out following practices described by Adefris (2005).

Data Collected

Data Collected on Plot Basis

- Days to flowering (Df): The numbers of days from date of sowing to a stage at which 50% of the plants in a plot open flowers.
- Days to maturity (Dm): The number of days from date of sowing to a stage at which 50% of the plants have reached physiological maturity. It is the time when 50% of the capsules change their color into brown.
- Seed yield per plot (SYPP): Seed yield per plot measured in grams after moisture of the seed was adjusted to 7 percent.
- Thousand seed weight (Tsw): The weight (g) of 1000 seeds from randomly sampled grains.
- Stand percent (SP): The proportion of plants at vegetative stage and at harvest as visually assessed in percentage.

On plant basis

These data was collected from five plants randomly selected from the central rows of each plot and averaged for statistical analysis. Plant height (PHT): The average height of five randomly selected plants was measured in centimeters from the ground surface to the top of the main stem at maturity.

DATA 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 to detect the phenotypic stability under different environments:

$$y_{ijk} = \mu + b_i + \delta ij$$

where y_{ijk} is the phenotypic value of the i^{th} genotype at the j^{th} environment in the k^{th} replicate ($i = 1,2,...,v$; $j = 1,2,...,b$; $k = 1,2,...,n$), μ is the mean of the i^{th} genotype over all the environments, b_i is the regression coefficient that measures the response of i^{th} genotype to the varying environments, I= environmental index obtained as - such that = 0, δij is the deviation from regression of the i^{th} genotype in the j^{th} environment, and is the random component. Perkins and Jinks proposed a different model for stability analysis. In this model, the total variance is first divided into three components, i.e., (1) genotypes (G), first divided into three components, i.e. (1) genotypes (G), The G x E variance is subdivided into 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 feature of this model includes three parameters of stability like, with one exception; the degree of freedom for environment is e-2. Another objection of, to other models was about the partitioning of the degree of freedom. Though, S.S. due to environment (linear) of , 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 δ as the parameter of stability. As far as the ranking of genotypes with respect to their stability is considered, it remains the same under all the three models described above. Eberhart and Russell's model being relatively simple, may, therefore, be preferred for studying stability analysis

The model of Perkins and Jinks

$$Y_{ijk} = \mu + a_i + \varepsilon_i + r_{ik} + \beta_i \varepsilon_j + \delta_{ij} + e_{ij}$$

Where; Y_{ijk}: is the mean performance of the line i in replicate k of environment j, μ is the overall mean, a is the contribution of line i, is the contribution of environment j, r is the contribution of replicate k in environment j, is the linear regression coefficient for line i, is the deviation from regression, and e is the residual variation of line i in replicate k in of environment j. Freeman and Perkins, 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 environmental index on the basis of their performance. The hypothesis that any regression coefficient does not differ from unity was tested by the T-test, using its own standard error for regression. Also the mean square of deviation from regression of each genotype (S), pooled errors in the regression analysis of variance were used to test whether each deviation mean square was significantly different from zero.

Results and Discussion

The combined analysis of variance for all studied traits of nine genotypes presented in Table 2 indicated that significant differences among genotypes, environments and genotype × environment interaction were detected for date of flowering, date of maturity, seed yield and thousand seed weight traits. These results showed 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., 2009.

Table2. *The combined analysis of variance of all studied traits for nine mustard genotypes over three environments tested*

S.O.V	Df	DFL	DM	PH	SP	SY	TSW
Genotypes (G)	8	118.6019**	52.7083**	0.0573**	26.7083ns	38.01518*	0.5396**
Environments (E)	2	719.1852**	1692.0556**	0.6828**	17.0556ns	1608.4259**	0.2948**
Rep./ Env	3	5.3889ns	71.2778**	0.0230*	138.5370*	28.6483ns	0.2222**
G x E	16	65.8935**	25.2222**	0.0165ns	34.3472ns	44.3749**	0.1193**
Error	24	3.3056	6.6528	0.0086	35.8287	14.9953	0.0199

Df; degree of freedom, DFl: date of flowering, date of maturity, PH; plant height, Sp: stand percent, SY; seed yield, TSW: 1000 seed weight,, ** Denote significant at 0.05 and 0.01 probability levels, respectively*

The differences between grand mean(over all environments) and each of the location mean performances for the six studied traits recorded covered a wide range and displayed a good distribution within the range as shown in Table 3. Consequently, the required assumptions for stability analysis are full-filled. Date of flowering differences ranged from 75 days in the first site to 87 in the third site. On the other hand date of maturity differences ranged from 152 days in the site two to 170 days in site third and on other side stand percent shown almost similar performance in all locations tested. Besides these traits studied seed yield in q/ha ranged from 14.08 in the first site to 30.99 in the third site... At last but not least thousand seed weight ranged 3.6gm in site two to 3.9 gm in site one.

Table3. *Mean performance of all traits studied under each of the three environments tested*

Environment/loc	DFL	DM	PH	SP	SY	TSW
1	75	155	1.71	82	14.08	3.9
2	78	152	1.97	81	29.87	3.6
3	87	170	2.21	80	30.99	3.8
Average	80	158	1.96	81	24.98	3.8

Eberhart and Russell, model provides a mean of partitioning the genotype-environment interaction for each genotype into two parts. Variation due to the response of genotype to

different environmental index (sum of squares due to regression) and the un explainable deviation from the regression on the environmental index. They added that a stable genotype could have high mean performance. For each environment, analysis of variance on 6 characters was carried out individually as well as pooled over the environments. The pooled analysis of variance showed significant differences amongst genotypes for all the observed traits except stand percent in each of the three locations (Table 4). Pooled analysis of variance for genotype x environment interaction indicated highly significant difference for genotype, Environment plus (genotype environment interaction) and environment linear for all the traits studied except plant height and stand percent. This revealed significant variation among genotypes and among environments. Pooled deviations mean squares were insignificant for date of flowering, date of maturity, plant height and stand percent suggesting linear regression also assume partial importance considering each individual genotype.

Table4. *Pooled analysis of variance for all studied traits for the nine mustard genotypes under three locations, Eberhart and Russell*

S.o.v	Df	DFL	DM	PH	SP	SY	TSW
Genotypes (G)	8	59.3009**	26.3542**	0.0286**	13.3542ns	19.0076*	0.2698**
Env.+(G X Env.)	18	69.2407**	105.2129**	0.0452**	16.2129ns	1963.4250**	0.069**
Environment(linear)	1	719.1852**	1692.0556**	0.6828**	17.0556ns	1608.4259**	0.2948**
G X Env,(linear)	8	62.3325**	22.2026**	0.0078ns	4.4451ns	13.1732*	0.0650*
Pooled Deviation	9	3.1653ns	2.6841ns	0.0078ns	26.5797ns	27.7348**	0.0482*
Pooled error	27	1.7685	6.9167	0.0051	23.6204	8.2561	0.0212

The joint regression analysis was conducted for all studied traits according to the procedure described by Perkins and Jinks. All sources of variation mean squares were tested against mean square error Table 5. Highly significant differences among genotypes and environments were found for date of flowering, seed yield and thousand seed weight studied traits. Also, there were high significant differences among genotype x environment interaction for date of flowering, seed yield and thousand seed weight studied traits. On the other side, heterogeneity between regression mean squares were highly significant when tested against the remainder mean squares for date of flowering and significant for date of maturity and thousand seed weight. However, the remainder mean squares were highly significant for seed yield and significant for date of flowering and thousand seed weight when tested against average error.

Table5. *The joint regression analysis of variance for all studied traits over three locations in main growing seasons (Perkins and Jinks Model)*

S.o.v	Df	DFL	DM	PH	SP	SY	TSW
Genotype(d/f b/n genotypes (G)	8	59.3009**	26.3542**	0.0286**	13.3542ns	19.0076*	0.2698**
Environment(joint regression)	2	359.5926**	846.0278**	0.3414**	8.5278ns	804.2130**	0.1474**
.Genotype X Environment	16	32.9468**	12.6111ns	0.0082ns	17.1736ns	22.1874**	0.0596**
Heterogeneity regression	8	62.3325**	22.2026*	0.0078ns	4.4451ns	13.1732ns	0.0650*
Reminder	8	3.5610*	3.0196ns	0.0087ns	29.9021ns	31.2017**	0.0542*
Error	27	1.7685	6.9167	0.0051	23.6204	8.2561	0.0212

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

The partitioning analysis of variance model of Freeman and Perkins was also conducted for traits under study and indicated at Table 6. It could be noticed that the mean squares due to genotypes showed significance for date of flowering and seed yield per quintal, while insignificance for date of maturity and stand percent were observed between Ethiopian mustard genotypes. Moreover, highly significant variations were obtained for plant height and thousand seed weight. It was evident that all used models of analysis of variance indicated that there were significant genetic background variations among Ethiopian mustered genotypes and the response of tested quantitative traits. Also, significant different changes were observed for plant height due to environments. However, all used statistical models confirmed significant genotypes x environmental interaction for plant height studied trait. These results were in good agreement with those reported by Ibrahim *et al*, 2006.

Table6. *Partitioning of analysis of variance for all studied traits over three locations in main crop growing seasons, according to Freeman and Perkins Model*

S.o.v	Df	DFL	DM	PH	SP	SY	TSW
Genotpes (G)	8	55.453*	29.1481ns	0.0199**	21.7032ns	17.8301ns	0.2748**
Environment(E)	2	420.2593**	1190.7037**	0.4531**	87.8148ns	262.0567**	0.2925*
Combined regression	1	823.9518**	2247.3140**	0.8947**	132.7452ns	2073.4128**	0.0012ns
Residual (1)	1	16.5667	139.0934	0.0015	42.8844	23.0409	0.0573
Interaction(GXE)	16	32.8004**	11.1620ns	0.0116ns	16.9814ns	32.4203ns	0.0642ns
Heterogeneityb/w regression	8	61.1208**	16..6397ns	0.0159ns	12.5312ns	18.1877ns	0.0954ns
Residual(2)	8	4.4810	5.6843	0.0116	21.4316	46.653	0.0331

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

Stability Parameters

In the present study, genotypes were tested for 3 parameters of stability for all the observed characters. In order to classify the genotypes into various categories with respect to stability and suitability for particular environments, all nine genotypes were tested for 3 stability parameters, i.e. mean, bi and S2di. The genotypes showing superiority and stability for different traits have been summarized in Table 7. The genotype, PGRC/E20068/5/1 besides having stable and high performance for seed yield q/ha, was also having stable performance for thousand seed weight. Likewise, Open pollinated bulk Yellow Dodolla has stable and high performance for date of flowering, plant height and thousand seed weight. In addition to superiority and stability for seed yield per q/ha Open pollinated Yellow Dodolla also showed stability for date of flowering date of maturity plant height and 1000-seed weight. Similarly, Open pollinated Yellow Dodolla was having superior performance for thousand seed weight, plant height high mean performance for date of flowering and date of maturity. This genotype also showed stable and superior performance for date of flowering, date of maturity and plant height. A total of four genotypes showed maturity earlier than the average days of maturity and stability over the environments. These results are in agreement with those of Badwal and Labana (1989) and Mahto and Haider (2012),

Table7. *Estimates of phenotypic stability parameters for all tested nine mustard genotypes grown under three environments*

Tested traits	Stability Parameters	Genotypes									Over all mean
		1	2	3	4	5	6	7	8	9	
Date of flowering	Mean	84	75	85	75	84	75	83	78	83	80
	Bi	0.6725	1.1054	0.4473	0.7940	0.4633	0.8834	0.2843	1.1263	3.2236	
	SD	-1.7436	-1.4137	-1.0874	-0.6405	-1.7509	-0.9639	-1.7296	9.3668	12.5341	
Date of maturity	Mean	161	156	160	156	160	155	161	157	163	159
	Bi	0.8451	1.3794	0.7757	1.1066	0.6737	0.9997	0.9039	0.6337	1.6821	
	Sd	-5.0311	-3.1378	-3.3705	-2.6597	-6.7567	-2.1327	-5.3679	-6.9146	-2.7222	
Plant height	Mean	1.99	1.86	2.12	1.78	2.00	1.88	1.96	1.86	1.89	17.32
	Bi	1.2345	1.2244	1.1202	1.0410	1.2817	0.4283	1.1510	0.4835	1.0353	
	Sd	-0.0027	-0.0011	0.0025	-0.0030	0.0006	-0.0044	-0.0050	0.0012	0.0358	
Stand percent	Mean	80	84	79	82	76	79	82	83	83	81
	Bi	3.9577	-0.1466	-1.0993	2.4186	0.2199	-0.1466	1.4511	1.3925	0.9528	24.98
	Sd	-15.8028	-6.9944	3.2560	-5.5388	13.7880	-6.9944	-2.4443	-14.7950	62.1594	
Seed yield	Mean	22.03	24.12	25.58	29.36	28.39	23.07	22.56	25.44	24.23	
	Bi	0.5442	1.1666	0.6641	1.3739	1.1617	1.2078	0.8637	0.9270	1.0911	
	Sd	5.0621	59.4168	40.9898	-5.9692	9.9964	-0.8692	-7.4707	-0.8093	74.9619	
1000 seed weight	Mean	3.90	3.43	4.05	3.45	4.17	3.58	3.92	3.95	3.37	3.76
	Bi	2.0072	-1.0439	1.8774	-0.3779	0.4460	-0.3163	2.5117	0.9743	-0.0173	
	Sd	-0.0182	0.0648	0.0183	-0.0204	-0.0211	0.0372	-0.0212	2.9213	0.2209	

**bi: Regression Coeff, ,sd, Mean Square Deviation from Linear Regression*

CONCLUSION

The genotypes; PGRC/E20068/5/1, Open pollinated bulk Yellow Dodolla and Open pollinated Yellow Dodolla, exhibited higher mean and showed stable performance over environments for most of the yield components

traits. Thus, these genotypes can be utilized to develop stable strains having wider adaptability for different location of central highlands of Ethiopia

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