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Stability Analysis for Seed Yield and Related Component Traits of Linseed Genotypes (*L/NUMUSITATISSIMUM L*) in Central Highlands of Ethiopia

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Abstract: *The experiment was executed to analyses seed yield and related traits stability parameters for ten genotypes of linseed at Holeta, Kulumsa, Bekoji and Asassa representative areas of central highlands of Ethiopia. The experiment was carried out in a Randomized complete block design. Stability parameters for ten genotypes of linseeds were evaluated and assessed using three different stability methods. The investigation included six characters (seed yield per plot, oil content, oil yield, date of flowering, date of maturity and plant height). Results revealed significant genotype × environment interactions were detected for seed yield, oil content, date of flowering and plant height 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. Two genotypes PGRC/E10306 X Chilalo Y/3 and Omega X CI-1525/Y/44 were most stable for studied characters in the four central highlands of Ethiopian environments.*

Keywords: *Stability Analysis, stability parameters, linseed genotypes,*

1. INTRODUCTION

In Ethiopia Linseed (Linum usitatissimum L.) is one of the most important oldest plant species cultivated for seed yield and oil traits. In Ethiopia, among the highland oilseeds, linseed stands second next to niger seed in total production and areas coverage (Adugna, 2000).. 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 1600 and 2800 meters. Production of linseed 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 ten linseed genotypes comprising one standard check to test stability over the four environments of central highlands of Ethiopia.

2. MATERIALS AND METHODS

2.1. Experimental Sites

The experiment was conducted in the representative areas of Central highlands of Ethiopia at Holetta , Kulumsa ,Bekoji and Asasa in 2008/2009 cropping season from June to December

2.2. Description of Test Materials

A total of ten Linseed genotypes that include one standard check (Tolle) were used in this study. The name of the genotypes used in the experiment are given in Table1

Table1. *List of Ten Linseed genotypes used in the study area in 2008 cropping season*

No.	Name of genotypes
1	PGRC/E 10306 X Chilalo Y/3
2	PGRC/E 10306 X CI 1525/3/B
3	Omega X CI 1525/Y/44
4	PGRC/E 10306X CI-1525/1/A
5	CI -1652 X Omega /B/53
6	Omega X CI -1525/14/A
7	Omega X CI -1525/Y/43
8	CI-1652 X Omega/B//58
9	Omega X CI 1525/B/44
10	Tolle

2.3. Experimental Design, Management and Season

The experiment was executed from June 2009 to December 2009. The experiment was laid out in Randomized Complete Block Design with three 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 ten plots. The path between replication was 1.5 m and the spacing between plots within was also 0.4 m. Each plots was manually drilled, a rate of 25 kg/ha and urea and phosphorous fertilizers were applied at the rates of 23/23 kg/ha N/P2O5, respectively following the national recommendations.

2.4. Data Collected

I. data collected on plot basis

1. 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.

2. 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.

3. Seed yield per plot (SYPP): Seed yield per plot measured in grams after moisture of the seed was adjusted to 7 percent..

4. Oil content (Oc): The proportion of oil in the seed to total oven dried seed weight

measured by nuclear magnetic resonance.

5. Oil yield (Oy): The amount of oil in grams obtained by multiplying seed yield per plot

by corresponding oil percent.

II. 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.

2.5. Data Analysis

A combined analysis of variance was used to evaluate the responses of each trait 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 ith genotype in the jth 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.

3. RESULTS AND DISCUSSION

The combined analysis of variance for all studied traits of ten genotypes presented in Table 2 indicated that highly significant differences among genotypes, environments and genotype × environment interaction were detected for seed yield, oil content, date of flowering and plant height traits. These results showed that linseed 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 Yadv RK, *et al.*, 2017.

Table2. *The combined analysis of variance of all studied traits for ten linseed genotypes over four environments tested*

S.O.V	Df	SY	Oc	OY	DF	DM	PH
Genotypes (G)	9	277875.2231**	8.0205**	51847.6630**	26.2602**	20.1528*	136.6306**
Environments (E)	3	5610967.2972**	171.6699**	947221.6111**	4764.3639**	24313.2750**	754.0306**
Rep in Envt	8	310491.0250**	0.0270ns	50803.1417**	6.4250**	8.1083ns	14.1667ns
G x E	27	67090.0997**	0.9153**	9976.6481ns	9.7096**	18.3059**	33.3762**
Error	72	53071.0806	0.0241	7271.4102	2.8417	8.6731	19.7593

*, ** 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 74 days in the fourth site to 105 in the 2nd site. On the other hand date of maturity differences ranged from 122 days in the site fourth to 179 days in site 2nd and on other side plant height shown the differences ranged from 89 cm in 2nd site to 94cm in the first locations tested. Besides these traits studied seed yield in kg/ha ranged from 1027 in the fourth site to 2034 in the 2nd site. On the other hand oil content percent ranged from 34.71% in the fourth site to

40.5%in the first site. Similarly oil yield kg/ha shown the difference ranged 358kg/ha to 632 kg/ha to these sites, respectively.

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

Environment/loc	Seed yield kg/ha	Oil content Percent	Oil yield kg/ha	Date of 50% flowering	Date of 50% maturity	Plant height
Holetta	1558	40.5	632	94	170	94
Bekoji	2034	37.4	762	105	179	89
Kulumsa	1271	36.96	470	82	130	90
Asasa	1027	34.71	358	74	122	90
Average	1473	37.4	556	90	150	93

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 unexplainable 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 six characters was carried out individually as well as pooled over the environments. The pooled analysis of variance showed significant differences amongst genotypes for the majority of the observed traits in each of the four 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 seed yield, oil content, oil yield, date of flowering, date of maturity and plant height traits studied. This revealed significant variation among genotypes and among environments. Pooled deviations mean squares were also significant for oil content, date of flowering and date of maturity. In the other side insignificant pooled deviation was recorded for seed yield, oil yield and plant height a 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 four locations, Eberhart and Russell*

S.o.v	Df	Sy	Oc	Oy	DFL	DM	PH
Genotypes (G)	9	92625.0744**	2.6735**	17282.5543**	8.7534**	6.7176*	45.5435**
Env.+(G X Env.)	30	207159.273**	5.9969**	34567.0481**	161.725**	815.93426**	35.14722**
Environment(linear)	1	5610967.297**	171.669**	947221.611**	4764.363**	24313.275**	754.0306**
G X Env,(linear)	9	21286.8265ns	0.5473**	2659.9546ns	3.8074**	7.0494*	14.1110*
Pooled Deviation	20	21286.8265ns	0.1656**	3292.5121ns	2.6560**	5.0654*	8.6693ns
Pooled error	80	26271.0250	0.0081	3874.8611	1.0667	2.8722	6.4000

Df: degree of freedom, sy : seed yield, Oc ; oil content, DFl ; date flowering, Dm; Date of maturity;Ph; plant height

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 between genotypes were found for seed yield, oil content, oil yield, plant height and significant difference were found fore date of 50% flowering and date of 50% maturity. Also, there were high significant differences among genotype x environment interaction for seed yield, oil yield, for date of flowering, date of maturity and plant height studied traits. On the other side, heterogeneity between regression mean squares was highly significant when tested against the remainder mean squares for seed yield and significant for date of flowering date of maturity and plant height. At the same time, the remainder mean squares were highly significant for seed yield and date of maturity traits when tested against average error.

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

S.o.v	Df	Sy	Oc	Oy	DF	DM	PH
Genotype(d/f b/n genotypes (G)	9	92625.0744**	2.6735**	17282.5543**	8.7534*	6.7176*	45.5435**
Environment(joint regression)	3	1870322.4324**	57.2233**	315740.5370**	1588.1213**	8104.4250**	251.3435**
.Genotype X Environment	27	22363.3666**	0.3051ns	3325.5494**	3.2365**	6.1020**	11.1254**
Heterogeneity regression	9	21286.8265**	0.5473ns	2659.9546ns	3.8074*	7.0494**	14.1110*
Reminder	18	22901.6366**	0.1840ns	3658.3468ns	2.9511ns	5.6282**	9.6326ns
Error	80	26271.0250	0.0081	3874.8611	1.0667	2.8722	6.4000

*, ** 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 highly significance difference for oil content, oil yield and date of maturity, while insignificance for date of flowering were observed between tested genotypes. It was evident that all used models of analysis of variance indicated that there were significant genetic background variations among linseed genotypes and the response of tested quantitative traits. However, all used statistical models confirmed significant genotypes x environmental interaction for date of flowering and plant height studied trait. These results were in good agreement with those reported by Ibrahim *et al*, 2006,Yadv and Gupta,2000.

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	Sy	Oc	Oy	DFL	DM	PH
Genotypes (G)	9	198327.4736*	5.290122**	34806.64**	13.60556ns	8.061111ns	121.3403**
Environment(E)	3	3552402.379**	113.6265**	569065.2**	3346.367**	16248.68**	480.3125**
Combined regression	1	8568672.325*	340.8405**	1415953**	9990.823**	48742.19**	1307.97**
Residual (1)	2	1044267.406**	0.01945**	145621.5ns	24.13875ns	1.93175ns	66.484*
Interaction(GXE)	27	44783.53657ns	0.609793**	6441.893ns	7.098148**	14.47963ns	23.02546*
Heterogeneityb/w regression	9	21007.47104ns	1.0884**	1800.385ns	10.58729ns	9.614878ns	38.54819ns
Residual(2)	18	56671.56934ns	0.370489**	8762.646ns	5.353578ns	16.91201ns	15.2641
ErroB/n Replicates	40	84170.0125	0.027625	12011.98	2.825	9.85	17.5375

*, ** 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 ten genotypes were tested for 3 stability parameters, i.e. mean, bi and S^2di. The genotypes showing superiority and stability for different traits have been summarized in Table 7. The genotype, PGRC/E10306 X Chilalo Y/3 besides having stable and high performance for seed yield q/ha, was also having stable performance for oil yield kg/ha, date of maturity and plant height. Likewise, Omega X CI 1525/Y/44 has stable and high performance for seed yield kg/ha, oil yield kg/ha and date maturity. In addition to superiority and stability for seed yield per kg/ha PGRC/E 10306 X Chilalo Y/3 also showed stability for plant height. None of 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 ten linseed genotypes grown under four environments*

Tested traits	Stability parameter	Genotypes										Over all mean
		1	2	3	4	5	6	7	8	9	10	
Seed yield	Mean	1797	1371	1559	1289	1529	1453	1394	1445	1485	1305	1473
	Bi	1.0282	0.9385	1.3441	1.3180	1.0318	0.8096	0.8133	1.0162	0.8578	0.8427	
	SD	17786.736	-25058.330	-23774.459	32068.242	12334.177	-26142.396	-17174.697	-8344.929	-7171.124	-11118.739	
Oil content	Mean	35.73	38.39	37.84	37.90	36.78	38.22	37.29	37.58	36.69	37.65	4.73.
	Bi	1.0874	0.9089	1.0063	1.1117	1.0143	1.1147	1.0663	0.8362	0.6083	1.2459	
	Sd	0.4626	0.1020	0.1002	0.3135	0.0573	0.0353	0.0149	0.3946	0.0133	0.0806	
Oil yield	Mean	692	522	594	479	590	545	527	534	599	471	555
	Bi	1.0609	0.9391	1.3082	1.2149	1.0991	0.8338	0.8421	0.9904	0.8616	0.8498	
	Sd	1716.69	-3757.92	-3528.58	6069.93	2498.76	-3734.23	-2791.62	-133.69	-1634.23	-528.60	
Date of flowering	Mean	87	91	89	90	91	89	90	90	87	91	90
	Bi	1.0764	0.9151	1.0452	0.8709	0.9623	1.1442	1.0404	0.9268	1.0829	0.9358	
	Sd	1.43	-1.06	0.53	1.72	1.80	1.01	0.36	0.46	2.06	7.58	
	Mean	153	151	151	150	149	150	150	149	151	148	150

Date of Maturity	Bi	0.93	0.94	1.07	1.04	1.006	1.0048	1.012	0.941	1.0755	0.9627	
	Sd	0.6755	0.6884	1.0667	6.7816	0.6316	2.7300	14.0104	-2.6698	-1.9796	-0.0030	
Plant height	Mean	93	95	92	91	97	96	97	94	90	86	93
	Bi	0.8531	1.1087	1.0428	-0.1137	0.9593	1.1467	1.0417	1.5164	1.1276	1.3175	
	Sd	5.5377	30.0785	-3.2453	-3.4015	-0.9388	-3.0879	-3.4195	-0.4789	-4.0627	5.7118	

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

4. CONCLUSION

The genotypes; PGRC/E10306 X Chilalo Y/3, and Omega X CI 1525/Y/44, 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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