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Multivariate Analysis of Some Economic Characters in Flax

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Abstract: Twenty one parent flax genotypes and twenty F₁ hybrids using principal components analysis based on 16 quantitative characters were used to study the genetic relationship. Analysis of variance exposed high significant differences for all studied characters among genotypes. High Genotypic Coefficient of Variation (GCV) values were observed with high Phenotypic Coefficient of Variation (PCV) for seed yield/plant, number of capsules/plant, fruiting zone length, main stem diameter and seed index which designated that variation for these characters substantially donates to the total variability moderate to low PCV and GCV were perceived for fiber characters, earliness and growth characters, respectively. Most characters, showed high heritability estimated in broad sense (>70%) indicated that selection based on these characters would be effective as they are likely to be controlled by additive genes. The first five principal components were significant and accounted 78.2% of a total variance of all characters. The maximal amount of difference is shown in the first PC axis were 25.3%. Stem diameter, seed yield/plant, number of capsules/plant, straw yield/plant, fruiting zone length, number of apical branches and number of seed/capsules were a primary source of variation of the first PC axes and give high coefficients, respectively. While, the biggest coefficient in PC2 were earliness characters, plant height and fiber length. The other rest PC axes deals with seed index, fiber fineness and oil contented. The flax genotypes were plotted according to the first two PC axis. The most earlier parents Gowhar and L6 were separated according to PC2 since this axis deals with earliness characters.

Key words: Flax genotypes, genotypic coefficient of variation, phenotypic coefficient of variation, PC axis

INTRODUCTION

Most commercial characters are metric in nature and being poly genetically controlled, thus multivariate performance which using principal apparatuses analysis has analogues efficacy to regulate the most suitable combinations of characters. In such analysis, all dependent variables are considered simultaneously in the different cultivars (Singh, 1981). It is necessary for breeders to have much evidence as possible on the genetic control of the prominence agronomic and morphological characters of flax. Many detectives studied genetic variability in flax such as Saeidi *et al.* (2003), Ewes (2006), Savita (2006) and Mohammadi *et al.* (2010). Genotypic and phenotypic coefficients of variability displayed high genotypic coefficient of variation for seed yield/plant and number of primary branches/plant. High PCV was experiential for seed yield/plant and number of capsules/plant (Tadesse *et al.*, 2010). Multivariate analysis of quantitative characters has been rummage-sale to measure genetic relationships within flax genotypes. Categorizing genotypes concurrence into morphological similar groups is most useful for analysis of cultivar variability (Cox *et al.*, 1985). Prasad *et al.* (2001) A

significant negative correlation was obtained between grain yield and plant height. Path coefficient analysis revealed maximum contribution of fertile grains/panicle to grain yield. Rahman *et al.* (2002) stated that highest direct positive effect were recorded for number of fruits per plant. For selecting high yielding genotypes emphasis should be given on number of fruits per plant, stem length, fruit length and average fruit weight. Tariq *et al.* (2003) studied a number of statistics such as genotype mean performance, genotypic variance, genotypic coefficient of variation, ecovalence and regression coefficients were estimated to evaluate the environments effect on the grain yield. Copur *et al.* (2006) reported that breeding for high yielding oil flax varieties, number of capsule should be considered firstly followed by number of primary branch, 1000 seed weight and plant height. Secondhand principal components analysis to generate variability in 51 Kenaf accessions, the first three principal components explained a bout of 66.23% of the total variability (Balogun *et al.*, 2008). Three principal components with eigenvalues of 0.89, 0.77 and 0.66, respectively which together accounted for 27.3% of the total genetic variation (Rajwade *et al.*, 2010).

Recently, Wani *et al.* (2011) suggested there is a great need to give emphasis on physiological breeding approach to integrate with conventional breeding methods as compliment factor to break present yield ceiling and develop photosynthetically efficient and stress tolerant wheat varieties. El-Ayadi *et al.* (2011) concluded that tow clusters were obtained with highest number of provenances falling under cluster I. The first cluster is composed of the provenances: Agdz, N'koub, Tazarine, Mceissi, Tata and Tissint, the second cluster presented by the provenances: Foum Zguid, Gluemim, Mseid and Assa. Among the clusters formed cluster 1 presents the best means for the majority of traits studied. Ayalneh *et al.* (2012) showed that there are variation in extent of variability, heritability and genetic advance in traits under study which can facilitate selection for further improvement of important traits in tef.

This investigation was directed to assessments the genetic variability for sixteen studied characters and to conclude the relative reputation of the assessed characters which will be cooperative the breeder for selecting applicable combination or parents.

MATERIALS AND METHODS

The experiment was directed at Gemmeiza Agricultural Research Station during the two growing seasons of 2007/2008 and 2008/2009. Twenty one parental genotypes fitting to (*Linum usitatissimum* L.) were castoff. These genotypes were diverged in these origin and purpose. Origin and resolution of these genotypes are shown in Table 1. Seeds of 20 parents were sown and crossed as male with the indigenous cultivars Sakha 3 as female parent to produce 20 F₁ in 2007/2008 growing season. The twenty one genotypes with twenty F₁ hybrids were mounting and assessed in a randomized complete blocks design with three replicates. Each entry was planted in a single row. The row to row reserve was 20 cm and five cm within row with three meters row long for each intentional genotypes.

Data were recorded on ten individual guarded plants from each genotypes on days to flowering, days to 50% flowering, days to maturity, plant high, technological stem length, fruiting zone length, main stem diameter, number of apical branches/plant, number of capsules/plant, number of seeds/capsule, seed index, seed yield/fed, fiber yield/plant, fiber length, fiber fineness and oil content %. The data were endangered to two approaches of statistical analysis. Initially, the analysis of variance (F test) for all sixteen characters was complete to detect the significance of the experiential differences as designated by Sokal and Rohlf (1995). Phenotypic and

Table 1: Genotypes and pedigree of parents

Genotypes	Performance	Pedigree or origin	Purpose
Giza 4	Local cultivar	Pink Giza x Oil Giza	Dual purpose cultivar
Giza 6	Local cultivar	Hindi x Giza 4	Dual purpose cultivar
Giza 8	Local cultivar	Giza 6 x Santa Catalina	Dual purpose cultivar
Sakha 2	Local cultivar	L.2348 x Hera	Dual purpose cultivar
Romania 20	Introduced variety	Romania	Fiber production
Gowhar	Introduced cultivar	India	Oil production
Bombay	Introduced cultivar	India	Oil production
Hermes	Introduced cultivar	Netherlands	Fiber production
LI	Local elite line	Fiber crops Res. Sec.	Oil production
L3	Local elite line	Fiber crops Res. Sec.	Oil production
L4	Local elite line	Fiber crops Res. Sec.	Oil production
L5	Local elite line	Fiber crops Res. Sec.	Oil production
L6	Local elite line	Fiber crops Res. Sec.	Oil production
L15	Local elite line	Fiber crops Res. Sec.	Oil production
L16	Local elite line	Fiber crops Res. Sec.	Oil production
402	Local elite line	Fiber crops Res. Sec.	Oil production
435	Local elite line	Fiber crops Res. Sec.	Oil production
533	Local elite line	Fiber crops Res. Sec.	Oil production
2419	Local elite line	Fiber crops Res. Sec.	Oil production
2467	Local elite line	Fiber crops Res. Sec.	Oil production
Sakha 3	Local cultivar	L.2096x telinka2E	Elite fiber flax line

genotypic coefficient of variability was approximations rendering to Singh and Chaudhary (1997), also heritability in brood sense was dogged according to (Burton and de Vane, 1953) as follow:

Phenotypic coefficient of variation:

$$PCV = \sqrt{\frac{\sigma^2_{ph}}{\bar{x}}} \times 100$$

Genotypic coefficient of variability:

$$GCV = \sqrt{\frac{\sigma^2_g}{\bar{x}}} \times 100$$

where, X is grand mean of the character:

$$\text{Heritability in broad sense} = \frac{\sigma^2_g}{\sigma^2_{ph}} \times 100$$

After this step, multivariate procedure was used to assess the similarities among varied groups and to evaluate morphological parameters donating to the variation in each genotype. For this determination, principal components analysis was achieved, on the correlation matrix of donated characters for all genotypes. The principle components were communicated as eigenvalue, latent root, and manifested in eigenvector for all studied characters in each principal component axis (Hair *et al.*, 1987). The primary components analysis was also plotted in a joint plot diagram demonstrating the component scores of genotypes based on all typescripts. Also, factor analysis was achieved to regulate the most affecting characters on seed yield since it was the largely implementation in total variance according to Seiler and Stafford (1985). The factor loadings of the rotated matrix were indomitable.

RESULTS AND DISCUSSION

Analysis of variance results are presented in Table 2. The date exposed high significant differences for all the studied typescripts among genotypes, indicating the presence of considerable amount of genetic variability. The dissimilarity due to parents was also significant indicating the differences in genetic background. The phenotypic, PCV, genotypic, GCV, Coefficients of variation as well as heritability approximations are given in Table 3. Consequences showed high phenotypic coefficient of variability for seed yield/plant, number of capsules/plant, seed index, main stem diameter, fruiting zone length and apical branches/plant. The approximation of PCV were squat for earliness and growth characters as well as oil content, which were maintained by Sataphathia *et al.* (1987) who had described high estimates of PCV than GCV for most of the characters. High GCV tenets were experimental with high PCV values for seed yield/plant, number of capsules/plant, fruiting zone length and main stem diameter as well seed index, which designated that the difference for these characters substantially donates to the total variability. The wide range experiential in this investigation is in accordance with the intelligences made by Mirza *et al.* (1996) for number of capsules/plant and seed yield/plant, Mahto and Verma (1998) for number of capsules/plant and 1000 seed weight, Savita (2006) for number of capsules/plant, number of total branches/plant, number of seeds/capsules and seed index and Tadesse *et al.* (2010) for seed yield/plant and number of primary branches/plant. Moderate to low PCV and GCV were noticed for fiber typescripts, earliness and growth characters, respectively settlement with, Ewes (2006), for

growth and earliness characters, and Savita (2006) for oil content, in contrast Singh (2001) described high variability for days to 50% flowering and days to maturity. Some typescripts showed relatively distant difference between PCV and GCV, indicating that environmental possessions had their important on such characters.

Regarding to heritability values in broad sense, high approximations (>70%) were experimental for most characters such as days to maturity, plant height, technical stem length, number of capsules/plant, seed yield/plant, straw yield, oil content and fiber characters. These result designated that the selection based on these characters would be effective as they are likely to be controlled by additive genes. If typescripts has higher heritability estimate, in self pollinated crop, is more likely to be controlled by additive genetic variation, thus selection could be more suitable through phenotypic means. However, the remaining typescripts presented moderate to low values, this due to highly effect by varied environmental factors. High influence of environmental factors on phenotypic variation in these typescripts leads to reduced efficiency of the selection program. Similar conclusions were found by Saeidi *et al.* (2003) and Bhatia *et al.* (2006) and Mohammadi *et al.* (2010).

Heritability estimates along with GCV are usually more useful in predicting the resultant effect of selection than heritability values alone. On the other hand, heritability is not always associated with high GCV but to make effective selection, high heritability should be associated with high GCV. Data from previous results indicated large discrepancy between PCV and GCV for most characters. This was reflected in high heritability estimated for such characters. These results are in harmony with these findings by Tadesse *et al.* (2010). Generally, the genetic Coefficient of variability coupled with the heritability estimates would seem to give the best indication of the amount of genetic variance to be expected from selection.

Multivariate analysis: Multivariate analysis of quantitative typescripts has been used beforehand to measure genetic associations within flax genotypes. This procedure could determination phenotypic measurement into fewer and easily visualized dimensions. The analysis which used principal component analysis and factor analysis seemed to elucidate pattern of variation in agronomic attributes which are of economic standards importance and to obtain the initial factor solution using eigenvalue. These principles could measure the explained variance associated with each factor (Hair *et al.*, 1987). Based on 16 agronomic typescripts principal component

Table 2: Analysis of variance for the studied characters of flax genotypes

SOV	df	Main															
		First flower	50% flower	Maturity	Plant height	T. stem length	M. stem length	Stem diameter	Fructing zone	N. apical branches	Capsules / plant	Seeds/ Capsule	Seed index	Seed yield	Straw yield	Fiber length	Fiber fineness
Reps	2	7.54	12.54**	2.740	0.25	7.83	0.0249	8.61	1.309**	10.49	0.285	0.024	333.00	0.0036	1.24	216.00**	1.489*
Genotypes	40	43.08**	19.42**	15.030**	58.57**	53.53**	0.2384**	40.20**	0.331**	40.82**	0.476**	1.269**	23241.00**	0.0580**	49.19**	470.70**	4.850**
Parents	20	59.56**	34.26**	28.120**	68.32**	67.45**	0.3517**	56.15**	0.333*	33.31**	0.354**	1.720**	13852.00**	0.0870**	62.57**	352.00**	2.434*
Crosses	19	27.82**	4.65	1.990	13.79**	19.10**	0.0695**	23.63**	0.312*	24.27**	0.146	0.776**	21743**	0.0260**	18.51**	617.45**	7.581**
P vs. C	1	3.45	3.11	1.150	714.40**	429.26**	1.1850**	36.11**	0.669*	505.50**	9.206**	1.585*	239481**	0.0730**	364.52**	56.04	1.281
Error	80	5.36	4.06	0.915	5.71	4.05	0.0281	7.52	0.159	3.79	0.134	0.254	387	0.0020	2.58	36.50	0.454

*, ** Significant and highly significant at 0.05 and 0.01 level of probability, respectively

Table 3: Phenotypic PCV, genotypic GCV, coefficients of variation and heritability estimates in sixteen characters

Char. Para.	Yield characters																Fiber characters			
	First flower	50% flower	Maturity	Plant height	T. stem length	M. stem diameter	Fructing zone	Apical branches	Cpsules /plant	Seeds/ capsules	Seed Index	Seed yield	Straw yield	Fiber length	Fiber fineness	Oil content				
σ ² _g	12.57	5.12	4.705	17.62	16.49	0.0701	10.89	0.057	12.34	0.114	0.338	76/80	0.0/87	15.54	144.73	1.465				
σ ² _e	5.36	4.06	0.915	5.71	4.05	0.0281	7.52	0.159	3.79	0.134	0.254	387.0	0.0020	2.58	36.50	0.454				
σ ² _p	17.93	9.18	5.620	23.33	20.54	0.0982	18.41	0.216	16.13	0.248	0.592	800.5	0.0207	18.12	181.23	1.918				
H ² _b	70.11	55.77	38.720	75.53	80.28	71.3800	59.15	26.390	76.50	45.970	57.090	95.16	90.3400	85.76	79.85	76.380				
PCV	3.89	2.54	1.770	5.20	6.74	13.5600	16.73	10.120	20.21	5.990	10.980	27.33	7.9500	7.28	5.84	4.080				
GCV	3.26	1.89	1.620	4.52	6.04	11.4600	12.87	5.200	17.96	4.060	8.290	26.61	7.5600	6.74	5.22	3.570				

Table 4: Principal components analysis associated with 41 flax genotypes showing eigenvalues and eigenvectors of characters in the first five PC axes

Parameters	PC axes					Communality
	1	2	3	4	5	
Eigenvalue	4.054	3.3428	2.452	1.6259	1.0418	
PC % of variation	0.253	0.209	0.153	0.102	0.065	12.5165
Cumulative	25.33	46.23	61.56	71.78	78.23	0.782
Characters	Eigenvector					Communality
	1	2	3	4	5	
Plant height	-0.454	0.648	-0.409	-0.192	0.112	0.844
Technical stem	0.135	0.65	-0.729	0.111	-0.044	0.987
Main stem	-0.813	-0.309	-0.149	0.14	0.078	0.803
Fruiting zone length	-0.704	0.032	0.347	-0.36	0.187	0.782
No. of apical branch	-0.652	-0.043	0.145	0.13	-0.474	0.689
No. of capsules	-0.775	-0.115	-0.155	0.124	-0.275	0.728
No. of seed	-0.602	0.215	-0.373	-0.368	0.067	0.688
Seed index	0.003	-0.07	0.083	0.835	-0.233	0.763
Seed yield	-0.808	-0.034	-0.18	0.158	0.126	0.727
Straw yield	0.747	0.174	-0.095	-0.291	-0.255	0.747
Fiber length	0.14	0.647	-0.718	0.138	-0.056	0.975
Fiber fineness	-0.086	-0.033	0.201	-0.572	-0.204	0.418
Oil content	0.13	-0.436	-0.228	0.222	0.672	0.759
First flower	-0.031	0.742	0.473	0.129	0.117	0.807
50% flower	-0.102	0.799	0.503	0.164	0.054	0.931
Maturity	-0.139	0.712	0.542	0.116	0.185	0.868

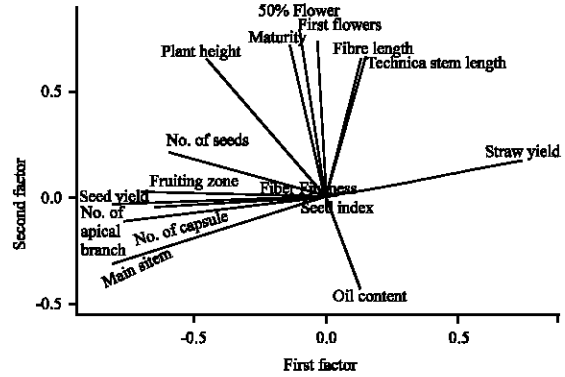


Fig. 1: Loading plot of 16 agronomic characters in principal component analysis of 41 flax genotypes

analysis was conducted for 41 flax genotypes, 21 parents and 20 F1 progenies. In an analysis with sixteen variables, sixteen axes were existed, however, only those which exhibited high multivariate variations were considered. The first five principal components PC, axes accounted for about 78.2 of total variance of all characters. The joint values and their contribution toward the total variation associated with the first five axes as well as their 16 vectors of each character for 41 genotypes are presented in Table 4. The first five principal components were significant and accounted 78.2% of a total variance of all characters. While the first three PC axes accounted for 61.6% of variation, among genotypes showing the highest joint eigenvalues 4.054 , 3.343 and 2.452, respectively (Table 4). In this respect El-Mansy (2009) reported that the first three canonical functions were significant and accounted for 81.1 and 81.4% of the variation among F3 families in two population of cotton. Likewise, Balogun *et al.* (2008) found that the first three of principal components explained about 66.23% of a total variance on Kenaf. Ayalneh *et al.* (2012) showed that there are variation in extent of variability, heritability and genetic advance in traits under study which can facilitate selection for further improvement of important traits in tef. The relative magnitude of the Eigen coefficient of each character related it to the first five axes from the components analysis might provide an interpretation

for each component axis. Though no clear guidelines existed to determine the significance of a trait coefficient, one rule of thumb is to treat coefficients > 0.5 as having a large enough effect to be considered important (Hair *et al.*, 1987; El-Mansy, 2000). The sign of the coefficient is irrelevant, and in fact arbitrary, though negatively correlated characters will generally have opposite signs on a given axis. Each character was an important source of variation in, at least, one principal component axis. Some characters may have great importance in determining plant phenotypes than others (Brown, 1991). The principal component analysis (Table 4, Fig. 1) showed that main stem diameter, seed yield, number of capsule/plant, straw yield, fruiting zone length, number of apical branches and number of seeds/capsule were a primary source of variation of first PC axis and gave high coefficients. Hence, the higher PC1 score for genotypes, the higher values for above characters would be. As these characters deals with yield and its attributes characters, we have essentially a component, or an axis, dealing with yield characters. All variable an this axis had negative loading except straw yield had positive. Leading the sign of loading indicate the direction of relationship between the variable and axis.

Similarly, for PC2 the larger coefficients are on 50% flowering, days to first flower, maturity, plant high, technological stem length and fiber length. This axis deals with earliness characters and two morphological characters with one fiber properties. These results indicated that the relative importance of yield and earliness characters in the total variation among the studied flax genotypes. However, the other rest PC axes deals with seed index and fiber fineness (PC4) as well as oil content (PC5). Chandra (1977) found that the most important characters were plant high 49.7% and seed weight 30.89% which accounted for 84.64% of the total

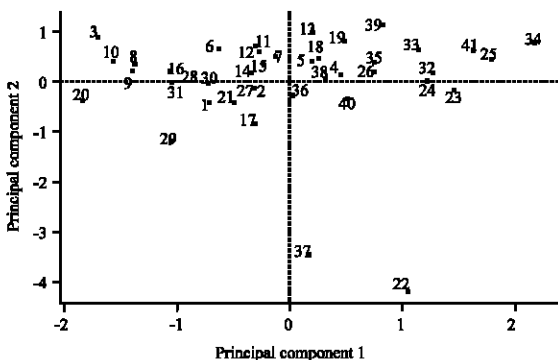


Fig. 2: Plot of first and second principal components form PC analysis between 41 flax genotypes

variation among 57 flax genotypes. However, Balogun *et al.* (2008) stated that the first three of PC axes explained about 66.23% of the total variation among 51 Kenaf genotypes. PC1 gave higher loadings to fiber, best and core yields.

It is great important to note that some typescripts may have great reputation in decisive plant phenotypic than other since each typescripts was an important source of variation in one axis El-Mansy (2009). Furthermore, each genotype could be plotted at the component score on. Each PC axis-each component score is a linear combination of the typescripts, similar to an index, such that the maximal amount of variance is shown in the first PC and second maximal amount on the second component, etc. The two dimensional distance between genotypes might reflect a summary of differences based on all typescripts restrained to the extent that the first two PC axes are affective in capturing the combined variance of all characters (Fig. 2). Therefore, the first two PC axes were used to plotting the studied genotypes, parents and F1 progenies. It is unblemished that most flax genotypes were separated according to PC1 axis. On the other side the earlier parent. Gowhar and L.6 were separated rendering to PC2 since this axis deals with earliness characters. Abd El-Salam *et al.* (2010) studied the relative importance of typescripts affecting genetic divergence in cotton and separated nine parental genotypes into five groups using principal components. While, El-Mansy *et al.* (2010) by using factor analysis to group some cotton genotypes on the factor according to which variable were more effecting. Generally, genotypes with more extreme scores on axes for which character coefficients were high appeared to possess higher score in their mean performance. Rajwade *et al.* (2010) grouped 70 flax genotypes on the basis of PC analysis and Eigne values. The genotypes "Sheetal and Ayogi" were placed away from rest of the genotypes. By viewing these

results, one could obtain a visual non numeric grasp of the amount of genetic variability existing among the flax genotypes. Since, such an analysis over time would be useful in describing any movement in the genetic bases of the crop. El-Ayadi *et al.* (2011) concluded that tow clusters were obtained with highest number of provenances falling under cluster I. The first cluster is composed of the provenances: Agdz, N'koub, Tazarine, Mceissi, Tata and Tissint, the second cluster presented by the provenances: Foun Zguid, Gluemim, Mseid and Assa. Among the clusters formed cluster 1 presents the best means for the majority of traits studied.

CONCLUSION

It possibly will be abridged that high heritability assessed in broad sense (>70%) designated that selection based on these typescripts would be effective as they are likely to be controlled by additive genes. The first five main components were significant and accounted 78.2% of a total variance of all typescripts.

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