



Classification of diverse progeny of Linseed using multivariate analysis techniques

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ABSTRACT

Multivariate technique is used to access the economic importance of linseeds by evaluating eleven agronomic traits. Among the studied traits, high coefficient of variation were observed for seed yield per plant (36.83%) followed by capsule per plant (34.83%) and biological yield (31.37%). Agglomerative hierarchical clustering method classified the 28 crosses into four clusters. A large number of crosses were placed in cluster I (13 crosses) followed by cluster III (10). The cross TL-11 x TL-27 and NDL 2004-05 x GS-234 had early maturing, high seeds per capsule and highest test weight. The first two principal components showed 59.88% of the total variation. The crosses namely R-552 x TL-11, R-552 x A.95.BR-552 x GS-234, R-552 x Shekhar, TL-11 x EC-1392, EC-1392 x GS-234 and EC-1392 x Shekhar were found positive value for both main components. This means that crosses can be used in future exploitations and can represent parent genotypes for some desirable trait. These results can now be used by breeders to develop high yielding linseeds hybrids.

Key words: Agronomic Variables, Cluster Analysis, PCA and Linseeds.

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INTRODUCTION

Flax (*Linum usitatissimum* L.; n = 15), also called linseed, an important oilseed crop belonging to *Linaceae* family, with 14 genera and over 200 species, is the only species in this family with economic and agronomic values [4]. Possibly, this crop species has originated from *Linum angustifolium* Huds. (n = 15), native to the Mediterranean region [4]. The cultivated *Linum* species have more economic values. This crop is grown for fibre (fibre flax), seed oil (linseed) or both seed oil as well as fibre, but recently it has gained a new interest in the emerging market of functional food due to its high content of fatty acids, alpha linolenic acid (ALA), an essential Omega-3 fatty acid and lignin oligomers which constitute about 57 % of total fatty acids in linseed [5]. Improvement in seed yield and related traits for different end uses is essential for the development of linseed hybrids. Multivariate data analysis facilitates a graphic display of the underlying latent factors and an interface between individual samples and variables [3]. Principal component analysis (PCA) has been widely used in plant sciences for a reduction of variables and grouping of genotypes. The main objective of the study was to characterize and classify diverse progeny of linseed based on their overall similarity in agronomic data.

MATERIALS AND METHODS

The experimental material for present investigation comprised of 28 F₁^s developed by crossing eight parental lines (viz., NDL 2004-05, R-552, TL-11, TL-27, EC-1392, A.95.B, GS-234 and Shekhar) in half diallel fashion design during *rabi* 2011-12 and evaluated in *rabi* 2012-13 at research farm of Department of Genetics and Plant Breeding, NDUAT, Faizabad, U.P. (India). The experiment was laid out in randomized complete block design (RCBD) with three replications. The entries were sown in a single row of 3 meter length with inter and intra row spacing of 30 cm and 15 cm, respectively. All recommended agronomic practices were adopted in order to raise normal crop. The observations were recorded from five randomly selected competitive plants from each row on eleven distinct morphological characters.

Descriptive statistics such as mean, Standard Deviation (SD) and Coefficient of Variation (CV) for each one of 11 studied traits were calculated. Cluster analysis (CA) and Principal Component Analysis (PCA) were performed with statistical package programs XLSTAT-18.02 (2016). Grouping of progenies into similarity groups based on their agronomic traits and seed yield was performed using agglomerative hierarchical clustering algorithm. In order to identify the patterns of morphological variation, Principal Component Analysis (PCA) was conducted.

RESULTS AND DISCUSSION

The mean values for 11 agronomic traits for the period of study are given in Table 1. The ranges of variation were maximum for capsule per plant followed by harvest index, secondary branches per plant, days to 50% flowering and biological yield. The highest coefficient of variation were observed for seed yield per plant (36.83%) followed by capsule per plant (34.38%), biological yield (31.37%) and secondary branches per plant (21.47%), while least coefficient of variation was observed for the days to maturity.

Table 1: Descriptive statistics for different agronomical traits

Variable	Observations	Minimum	Maximum	Mean	Std. deviation	C.V. (%)
DF	28	70.67	84.00	77.30	4.26	5.51
DM	28	131.33	141.00	135.36	3.11	2.30
PH	28	37.00	50.00	42.35	3.21	7.57
PB/P	28	3.53	6.80	5.11	0.61	11.99
SB/P	28	13.93	34.20	22.03	4.73	21.47
C/P	28	29.13	115.13	64.36	22.13	34.38
S/C	28	6.70	8.70	7.81	0.48	6.08
TW	28	4.67	8.23	6.19	0.82	13.18
BY	28	3.69	14.65	8.55	2.68	31.37
HI	28	22.67	47.42	33.59	5.11	15.20
SY/P	28	1.04	5.28	2.89	1.07	36.83

Table 2: Principal component analysis of linseed progenies

Main components	Eigenvalue	Percent of variance (%)	Cumulative percentage (%)
PC1	4.41	40.04	40.04
PC2	2.18	19.84	59.88
PC3	1.18	10.76	70.04

Table 3: Mean Values of Different clusters for 11 agronomic traits

Cluster	No. of Crosses	DF	DM	PH	PB/P	SB/P	C/P	S/C	TW	BY	HI	SY/P
I	13	77.00	134.97	42.05	5.43	22.93	67.34	7.97	6.11	8.73	33.11	2.88
II	2	73.83	133.00	42.93	5.17	26.00	83.90	8.07	6.70	9.24	36.63	3.37
III	10	78.03	136.13	41.68	4.65	17.68	42.57	7.51	6.37	6.73	32.34	2.19
IV	3	78.44	136.00	45.49	5.29	29.98	110.98	7.92	5.62	13.39	37.86	4.98

Where; DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, PB/P: Primary branches per plant, SB/P: Secondary branches per plant, C/P: Capsules per plant, S/C: Seeds per capsule, TW: Test weight, BY: Biological yield, HI: Harvest index and SY/P: Seed yield per plant

In this study, according to principal component analysis, three principal components (PC1, PC2 and PC3) had eigenvalues greater than one and accounted for 70.04% of the total variance in the data (Table 2 & Figure 1). In this respect El-Mansy [2] reported that first three PC's were significant and accounted for 81.1 and 81.4% of the variation among F_3 families in two population of cotton. Similarly, Balogun *et al.* [1] founded that the first three PC's explained about 66.23% of total variance on Kenaf. The proportions of the total variance attributable to the first three PC were 40.04%, 19.84% and 10.76%. In Figure 2 (biplot) it is possible to see the dispersion of characteristics according to score and the correlation between them. First main component (PC1) was positively correlated with all the characters studied except test weight. The second main component (PC2) was positively correlated with the days to flowering, days to maturity, plant height, seeds per capsule and harvest index, whereas, negatively correlated with the primary branches per plant, secondary branches per plant, capsules per plant, test weight, biological yield and seed yield. This means that selecting the hybrid for higher seed yield with higher test weight is difficult because in both main components negative correlation with test weight were obtained. The biplot

indicates that the 28 crosses in this experiment could be categorized at three groups (*i.e.* A, B and C). So that, crosses found in groups “A” had late in flowering and maturity, the third group (C) had higher values for the test weight. The group “B” had higher values for the rest of characters. All examined hybrids only seven have positive values for both main components. Those hybrids were: R-552 x TL-11, R-552 x A.95.B, R-552 x GS-234, R-552 x Shekhar, TL-11 x EC-1392, EC-1392 x GS-234 and EC-1392 x Shekhar. This means that those hybrids can be used in future exploitations and can represent parents’ genotypes for some desirable trait.

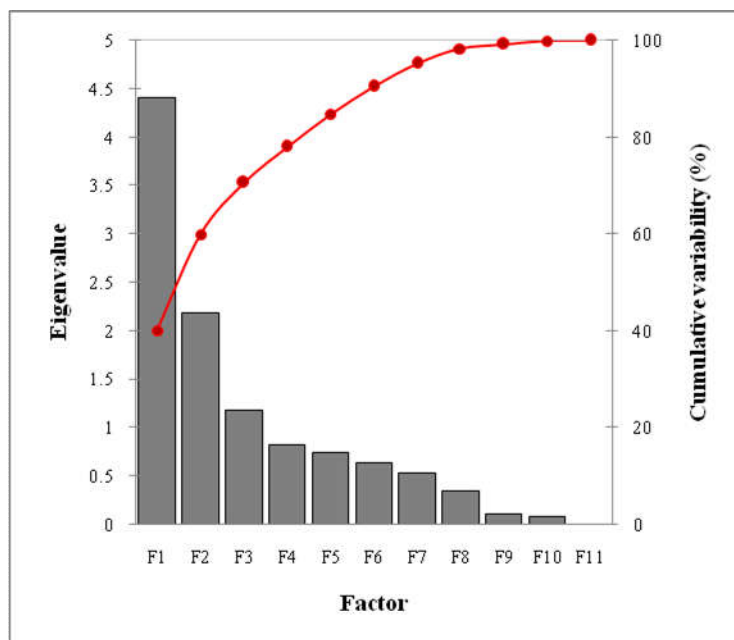
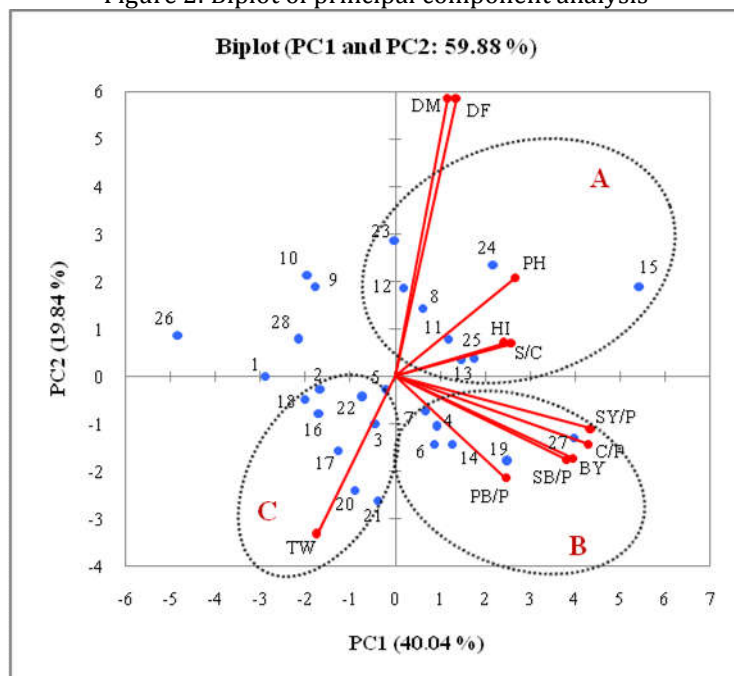


Figure 1: Scree plot showing variation for different PC values

Figure 2: Biplot of principal component analysis



Where; DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, PB/P: Primary branches per plant, SB/P: Secondary branches per plant, C/P: Capsules per plant, S/C: Seeds per capsule, TW: Test weight, BY: Biological yield, HI: Harvest index and SY/P: Seed yield per plant

Based on cluster analysis, the 28 crosses were separated into four major groups which each have two or more subgroups (Figure 3). The most of the crosses were included in cluster I and III (13 and 10 crosses) followed by cluster IV. From the table 3, cluster I and cluster III had poor mean value for seed yield. The

cross TL-11 x TL-27 and NDL-2004-05 x GS-234, which has the early flowering, early maturing, high seeds per capsule and highest test weight, was separated. Crosses from cluster IV (TL-11 x EC-1392, TL-27 x EC-1392 and A.95.B x Shekhar) were actually the cross with the high mean values for seed yield, harvest index, biological yield, capsule per plant and secondary branches per plant. Based on the present results it was recommended that crosses are made in breeding programmes between the genotypes in cluster II and cluster IV.

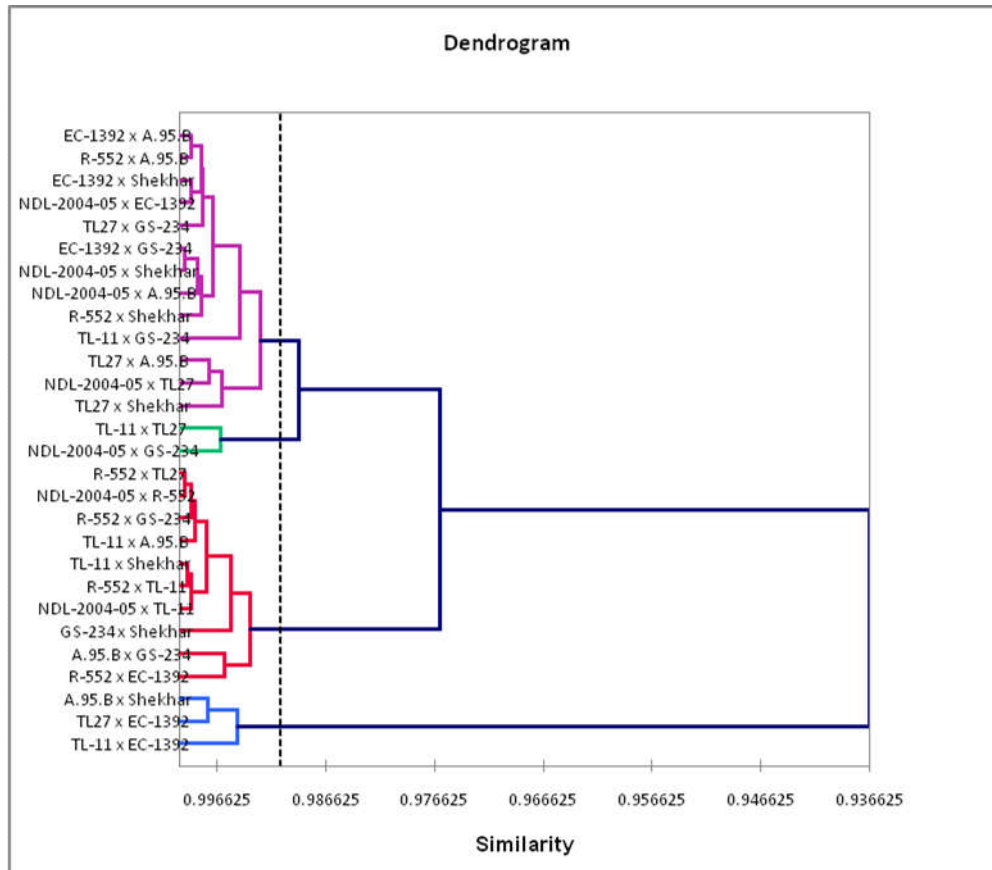


Figure 3: A cluster diagram generated after hierarchical cluster analysis of the means for eleven agronomical traits

CONCLUSION

A high genetic variability was observed in the studied linseed crosses. It is suggested that, the crosses can be used in future exploitations by breeders to develop high yielding linseeds hybrids. From the all examined crosses only seven have positive values for both main components. The crosses TL-11 x TL-27 and NDL-2004-05 x GS-234 had highest mean value for seeds per capsule and test weight. Those crosses can be used in future as hybrid for higher seed yield.

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