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ASSESSMENT OF GENETIC DIVERSITY IN GERMPLASM OF LINSEED (*LINUM USITATISSIMUM* L.)

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ABSTRACT:- A set of 55 linseed accessions including a check variety (Chandni) were evaluated under rainfed conditions during three crop seasons i.e. 2008-09, 2009-10 and 2010-11. Data were recorded for days to flower initiation, flower completion, maturity, reproductive period, plant height, branches per plant, bolls per plant, plot biomass, harvest index and seed yield. Wide ranges between the mean values with high CV values were exhibited by plant height, bolls per plant, biomass and seed yield accompanied with maximum values of variances and standard deviation, revealed the existence of greater genetic diversity in the accessions for these traits. Dendrogram based on Euclidean distance coefficient using 10 quantitative traits, grouped all the linseed accessions into 13 clusters. Cluster II was the biggest and had 33 accessions followed by Cluster I having 11 accessions. For the development of high yielding varieties, best performing accessions of Clusters I and II could be used in hybridization programme by crossing with accessions of Clusters VII, VIII, IX and X followed by selection in segregating populations.

Key Words: Linum usitatissimum; Genetic Diversity; Cluster Analysis; Agronomic Characters; Pakistan.

INTRODUCTION

Linseed (*Linum usitatissimum* L.) belongs to family Linaceae. It is the only economically important species in the family and is one of the major agro-industrial oilseed crops. Linseed contains 33 - 45% oil and 24% crude protein. The oil produced from it, is of drying type and is used to manufacture paints, varnish, linoleum, oil cloth, patent leather, printer ink, enamels, stickers, tarpaulins, soaps etc. The fiber extracted from straw is used to produce strong yarns such as sewing threads, linen fabrics and linen threads. The coarser grades are used for making twines, canvas bags, quality papers (Savita, 2006).

Linseed is a long day plant and cultivated in 34 countries of the world. Linseed is most neglected crop in Pakistan as well as in developing countries. In Pakistan, it is grown on marginal and sub-marginal lands under irrigated as well as rainfed conditions of Punjab and Sindh provinces on 1018 and 3000 ha, respectively during 2010-11. Its national average yield during 2010-11 was 692 kg ha^{-1} (GoP, 2012). Low yield of this crop is attributed to non-availability of improved varieties to suit the diverse agro-climatic conditions. To overcome the poor yield levels, development of high

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yielding varieties becomes the top priority.

Improvement in any crop depends on the availability of wide genetic diversity. Development of a new variety mainly depends on selection from diverse populations with broad genetic base. Identification of promising genotypes is very useful during breeding from initial parent lines to the final variety release. Therefore, it is essential not only to conserve the genotypes but also to explore the gene-pool of linseed for breeding purposes of well adapted, better quality and high yielding varieties.

Cluster analysis had traditionally been used to distinguish the accessions from each other, their relationships and to get useful information on estimates of genetic diversity. The cluster analysis grouped 60 linseed genotypes into 18 clusters based on morphological traits, identified 4 clusters showing greatest genetic diversity and cross hybridizing between them may increase genetic variation in the breeding population (Adugna et al., 2006).The 144 linseed lines / germplasm were accessed for genetic variability with 14 characters and grouped into 6 clusters (Savita, 2006). Cluster II was the biggest with 124 genotypes followed by cluster III with 12 and cluster I with five genotypes and suggested that the best genotypes in cluster V, II and IV could be used in future breeding programme.

The grouping of the 98 linseed genotypes into 10 clusters indicated presence of a wide range of genetic diversity and by crossing of superior genotypes of distant clusters may result in identifying superior accessions. Bolls per plant, plant height, days to flowering and days to maturity contributed towards the genetic diversity (Fulkar et al., 2007). Genetic diversity in 81 linseed genotypes at two locations revealed considerable diversity among accessions and grouped them into 10 distinctive clusters (Tadesse et al., 2009). The 26 linseed genotypes were grouped into 3 clusters and intercrossing of genotypes from different clusters may help in obtaining new lines with higher yield (Sinha and Wagh, 2013).

The present studies were thus planned to estimate genetic diversity in linseed germplasm using cluster analysis on the basis of morphological traits and to identify the best parent lines for using in future breeding programme.

MATERIALS AND METHOD

A set of 55 linseed accessions including a check variety (Chandni) were evaluated under rainfed conditions during three crop seasons i.e. 2008-09, 2009-10 and 2010-11 at National Agricultural Research Center (NARC), Islamabad, Pakistan. Data were recorded for days to flower initiation, flower completion, maturity and reproductive period, and plant height (cm), branches per plant, bolls per plant, plot biomass (g), harvest index (%) and seed yield ($kgha^{-1}$). Data of each character was subjected to analysis to calculate means, minimum and maximum values, variances, standard deviations (SD), standard errors (SE) and coefficient of variations (CV%) through MS Excel Software. Cluster analysis (Sneath and Sokal, 1973) was performed to construct Dendro-

gram by using Statistica, Version 6 Software.

RESULTS AND DISCUSSION

Descriptive statistics for 10 traits of 55 accessions of linseed germplasm revealed that days to flower initiation ranged from 115 to 128 with mean value of 119 (Table 1). Five genotypes viz., LS-14, LS-19, LS-20, LS-27 and LS-55 initiated early flowering (115 - 116 days) than check (Chandni) taking 117 days. Days to flower completion ranged from 147 (LS-46 and LS-48) to 159 (LS-53) having mean value of 151. Forty-one accessions completed flowering earlier than check (152 days) by taking 147 to 151 days in this regard. Days to maturity ranged from 177 (LS-44 and LS-45) to 185 (LS-14 and LS-33) with mean of 181 days. Forty entries matured in 177 - 182 days hence, earlier than check (183 days). Mean value for reproductive period was 63 days (57 - 70 days). Only one genotype (LS-14) had longer reproductive period (70 days) as compared to check (66 days).

Plant height ranged from 67 to 105 cm with mean value of 89 cm (Table 1). The check genotype Chandni had an average plant height of 85 cm and 15 accessions were dwarf than check ranged from 67cm (LS-47) to 84cm (LS-29). Branches per plant ranged from 3.9 to 7.8 with mean value of 5.2 branches plant^{-1}. Eight genotypes viz., LS-1, LS-2, LS-3, LS-7, LS-9, LS-25, LS-44 and LS-54 were found with maximum branches per plant than check (5.9 branches) ranging from 6.1 to 7.8. Average bolls per plant were 88 with a range of 58 (LS-27)-137 (LS-54). Forty accessions were better than check (76 bolls) with a range of 77 - 137 bolls per plant. Biomass per plot ranged from 400 g (LS-53) to 1654 g (LS-13)

Table 1. Descriptive statistics for 10 traits of 55 accessions of linseed germplasm

Traits	Mean	Range	Variance	SD	SE	CV%	Entries better than check		
							Chandni (Check)	Better	Entries Range
DFI	119	115-128	4.92	2.22	0.30	1.87	117	5	115 -116
DFC	151	147-159	4.63	2.15	0.29	1.43	152	41	147 -151
DM	181	177-185	3.10	1.76	0.24	0.97	183	40	177 -182
RP	63	57-70	6.05	2.46	0.33	3.93	66	1	70
PH	89	67-105	94.77	9.74	1.31	10.92	85	15	67 - 84
BR	5.2	3.9-7.8	0.73	0.86	0.12	16.70	5.9	8	6.1 - 7.8
BOLLS	88	58-137	257.91	16.06	2.17	18.34	76	40	77 -137
BM	1024	400-1654	81355.81	285.23	38.46	27.86	1059	23	1075 -1654
HI	18.40	7.19-26.67	14.90	3.86	0.52	20.98	17.00	37	17.08 -26.67
SY	801	422-1178	24734.71	157.24	21.21	19.64	800	24	822 -1178

DFI = Days to flower initiation; DFC=Days to flower completion; DM=Days to maturity; RP = Reproductive period; PH = Plant height (cm); BR = Number of branches per plant; BOLLS = Number of bolls per plant; BM=Plot biomass (g); HI = harvest index (%) and SY = Seed yield (kg ha^{-1}).

with an average of 1024 g. The check genotype Chandni possessed biomass of 1059 g and 23 genotypes excelled it with a range of 1075-1654 g. Harvest index ranged from 7.19% in LS-41 to 26.67% in LS-25 with a mean value of 18.40%. However, the check genotype had the value of 17.00% and 36 accessions surpassed it ranging from 17.08% to 26.67%. Seed yield ranged from 422 kg ha^{-1} (LS-41) to 1178 kg ha^{-1} (LS-37) with mean value of 801 $kgha^{-1}$. The Chandni had the seed yield value of 800 kg ha^{-1} and 24 accessions were better than it with a range of 822 - 1178 kg ha^{-1}.

The greater variation was displayed by plant height, branches per plant, bolls per plant, biomass, harvest index and seed yield with coefficient of variation (CV) values of 10.92, 16.70, 18.34, 27.86, 20.98, and 19.64%, respectively accompanied with high values of variance and standard deviation showing existence of diversity in the accessions for these traits (Table 1). Remaining traits showed less amount of variation as had low values of CV (0.97-3.93%). Adugna et al. (2006), Savita (2006), Fulkar et al. (2007), Tadesse et al. (2009) and Sinha and Wagh (2013) reported wide range of

Table 2. Linseed germplasm accessions in different clusters

Lineage	Cluster	Number of accessions	Accessions names
I	Cluster-I	11	LS-1, LS -23, LS -14, LS - 32, LS - 39, LS -15, LS-8, LS-19, LS-11, LS-29, LS-55
	Cluster-II	33	LS-2, LS -48, LS -9, LS-3, LS -46, LS -50, LS - 7, LS-44, LS-54, LS-5, LS-33, LS -18, LS-21, LS-38, LS -47, LS -43, LS -45, LS -16, LS -6, LS-52, LS -35, LS -36, Chandni, LS -24, LS - 31, LS -25, LS -26, LS -49, LS - 4, LS -22, LS - 10, LS-17, LS-34
	Cluster-III	1	LS-12
	Cluster-IV	1	LS-30
	Cluster-V	1	LS-40
	Cluster-VI	1	LS-42
II	Cluster-VII	1	LS-13
	Cluster-VIII	1	LS-27
	Cluster-IX	1	LS-37
	Cluster-X	1	LS-20
III	Cluster-XI	1	LS-51
IV	Cluster-XII	1	LS-53
V	Cluster-XIII	1	LS-41

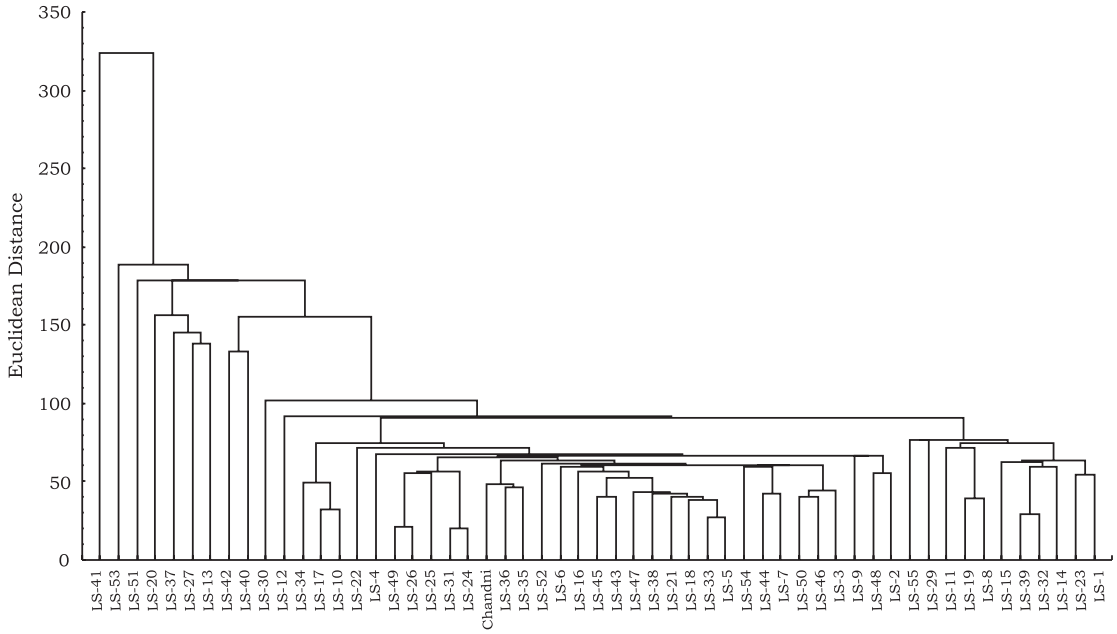

Figure1. Dendrogram based on 10 traits of 55 linseed germplasm accessions

genetic diversity in linseed.

Cluster analysis was performed to construct Dendrogram, which revealed the minimum distance of the clusters and the extent of morphological relationships between the pairs of accessions within each cluster group. Dendrogram based on Euclidean distance coefficient using 10 quantitative traits grouped 55 linseed accessions into 5 lineages and 13 clusters (Figure 1). The first lineage is consisted of six clusters (Table 2) accumulating 48 accessions; 11 in Cluster-I, 33 in Cluster-II and one each in Clusters III, IV, V and VI. Accessions were characterized by medium to tall plants, more bolls per plant, medium seed yield, late flowering and maturity (Table 3). Second lineage is consisted of four Clusters (VII, VIII, IX and X) each having single accessions. These clusters have accessions with taller plants, more bolls per plant, high biomass, high harvest index and high seed yield. Third, fourth and fifth lineages consisted of single clusters namely XI, XII and XIII, respectively, and each having single accession with low yield. For the development of high yielding varieties, best performing accessions of Clusters I and II could be used in hybridization programme by crossing with access-ions of Clusters VII, VIII, IX and X followed by selection in segregating populations.

Findings of Adugna et al. (2006) grouped 60 linseed genotypes into 18 clusters and by crossing between genotypes of 4 clusters showing greatest genetic diversity may increase genetic variation in the breeding populations. Savita (2006) grouped linseed lines into 6 clusters and suggested that best genotypes in cluster V, II and IV can be used for

Table 3. Cluster means for 10 traits of linseed germplasm

Traits	DFI	DFC	DM	RP	PH	BR	BOLLS	BM	HI	SY
Cluster-I	118	151	182	64	95	5.2	88	1247	17.02	937
Cluster-II	119	151	181	62	88	5.2	87	877	19.47	744
Cluster-III	120	151	183	63	104	5.1	107	1416	13.42	844
Cluster-IV	117	150	182	65	83	4.4	72	973	22.78	985
Cluster-V	120	150	180	60	86	4.6	98	1479	10.71	704
Cluster-VI	119	151	180	61	83	5.5	94	1597	10.75	763
Cluster- VII	119	151	182	63	97	5.3	110	1654	14.21	1044
Cluster-VIII	116	151	183	66	82	4.4	58	1527	15.50	1052
Cluster-IX	119	151	181	62	86	4.4	90	1462	18.13	1178
Cluster-X	115	149	181	66	96	4.4	103	1311	19.58	1141
Cluster-XI	121	149	181	61	72	4.2	67	520	25.00	578
Cluster-XII	125	159	184	59	92	5.8	119	400	25.00	445
Cluster-XIII	119	152	180	60	90	4.4	78	1321	7.19	422

DFI = Days to flower initiation; DFC=Days to flower completion; DM=Days to maturity; RP = Reproductive period; PH=Plant height (cm); BR=Number of branches per plant; BOLLS = Number of bolls per plant; BM=Plot biomass (g); HI= harvest index (%) and SY = Seed yield (kgha-1)

future breeding programme. Fulkar et al. (2007) grouped linseed genotypes into 10 clusters indicated presence of a wide range of genetic diversity and by crossing of superior genotypes of distant clusters may result in identifying superior accessions. Tadesse et al. (2009) grouped linseed genotypes into 10 distinctive clusters and reported that improvement in genotypes would be brought through by crossing accessions from different clusters followed by selection in segregating populations. Sinha and Wagh (2013) grouped linseed genotypes into 3 clusters and suggested that intercrossing of genotypes from different clusters may help in obtaining new lines with higher yield.

The wide range of genetic diversity was observed in the present germplasm collection. It is also suggested that said diversity could be utilized for improvement in linseed by crossing best performing lines of different clusters, followed by selection in segregating generations.

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