GENETIC DIVERSITY ANALYSIS FOR QUANTITATIVE TRAITS IN LENTIL (*LENS CULINARIS* MEDIK.) GERMPLASM

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ABSTRACT

The genetic parameters, character association, path coefficient analysis and clustering pattern were studied on a large number of lentil germplasm accessions (one thousand eighty six) during 2009 and 2010 at New Delhi. Significant variation was noticed for all the traits. High heritability estimates were observed for all the traits except number of primary branches/plant followed by seeds/pod. In general phenotypic coefficients of variability were greater than their corresponding genotypic coefficients of variability, High estimates of heritability coupled with high genetic advance and moderate to high GCV were observed for days to 50% flowering (67%) maturity (57%) and pods/plant (24%) and seed yield (80%) indicating that these characters are mainly governed by additive genes and selection of such traits might be effective for the improvement of seed yield. Inclusion of diverse parents in hybridization programme serves the purpose of combining desirable genes in new recombinations. Non-Heirarchial euclidean cluster analysis distributed the genotypes into three broad clusters. Crosses if attempted between cluster 1 and either of cluster II or III would produce desirable recombinants for grain yield. Based on the results of the means of the two years considering together for various traits the following accessions were found superior for early flowering (IC-560333, IC-559639, IC-560111, IC-311161, IC-345491) for extra tall (IC-559744, IC-559608, IC-560040, IC-560291, IC-559763) and for higher number of pods/plant (IC-398094, L-7740, L-169, JBT-3164, L-322) Diversified germplasm possessing different desirable traits may prove useful for incorporation of these traits in the lentil improvement programme.

Key words: Germplasm, Heritability, Lentil, Variability.

INTRODUCTION

Improvement in a crop depends on the type and extent of variability in the desired character in the base material. Information on the nature and magnitude of genetic divergence in the population helps in choosing the diverse parents for meaningful hybridization (Gautam *et. al.* 2013, Arunachalam, 1981; Samsuddin, 1985). The importance of cluster analysis to determine the extent of variability has been reported before (Mahalanobis, 1936). D² statistics has been used for estimating genetic divergence in a number of crops with diverse breeding systems (Murty and Arunachalam, 1966; Bhatt, 1970). D² statistics is a quantitative measure of genetic divergence, where the clustering pattern of the genotypes is arbitrary. The classification using generalized distance is functional where the number of entries is not very large. Vairavan *et al.,* (1973) used canonical analysis for initial grouping of a large number of rice germplasm collections. But simple two-dimensional representation of multidimensional disposition of genotypes cannot be as precise as the Tocher's method of grouping takes into account the full multidimensional space, even when the two canonical vectors justify high proportion of variation (Arunachalam, 1981). Metroglyph analysis has been used in many crops as a method for initial grouping of the genotypes (Anderson, 1957). In the numerical classificatory analysis, the general similarity coefficient has been used for clustering at appropriate phenon level (Gower 1971; Sneath and Sokal, 1973). In the present study, therefore,

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variability for yield and related attributes was estimated in a large collection of one thousand eighty six germplasm accessions over the two years and an attempt was made to group them in different clusters for determining the genetic closeness or divergence among the lentil germplasm accessions. The study of relationship among quantitative traits is important for assessing the possibility of selection of two or more traits and hence for evaluating the effect of selection for secondary traits on genetic gain for the primary trait under consideration. Published reports are either a few or none with regard to the genetic diversity and grouping of the genotypes into different clusters in large number of lentil germplasm accessions.

MATERIALS AND METHODS

One thousand eighty six lentil germplasm collections were grown in augmented block design for two *rabi* seasons 2009 and 2010 in Delhi. In both seasons these accessions were divided in 22 blocks and each block consisted of 50 accessions with five check varieties. The experimental unit was 3 rows plot of 3m. length with spacing of 30 x 10 cm. The recommended agronomical practices were followed to raise a good crop in both the seasons. Observations were recorded on five randomly selected plants for seven characters *viz.* for days to 50% flowering, days to 80% maturity, plant height, pods per plant, seeds/pod & primary branches per plant and seed yield. Statistical analysis was done according to the standard statistical procedures (Federer, 1996; Burton, 1952; Johnson *et al.,* 1955; Al-Jibouri *et al.,* 1958; Dewey and Lu, 1959). Non Heirarchial Euchidean cluster analysis was performed on the pooled data which resulted in the grouping of all the genotypes into three clusters.

RESULTS AND DISCUSSION

In an augmented block design the evaluation of the checks is done first to get an estimate of error which is used for deriving adjusted values of the entries. Evaluation of 1086 accessions showed significant differences for the traits viz. flowering, maturity, height, pods/plant and branches/plant. The genetic constants for the characters revealed that magnitude of phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the traits except yield showing environmental factors influencing their

expression to some degree or the other. Wide differences between PCV and GCV implied their susceptibility to environmental fluctuation, whereas narrow difference between PCV and GCV suggested their relative resistance to environmental alterations. The estimate of GCV and PCV are not helpful enough in determining the heritable portion. The amount of advance to be expected from selection can be achieved by estimating heritability along with coefficient of variability. High heritability coupled with high genetic advance was observed in days to flowering, days to maturity, plant height, pods per plant and seed yield. Tyagi and Khan (2011) on the basis of their studies on lentil informed that pods/plant, days to 50% flowering, 100 seed weight showed high variability coupled with high genetic advance (percent mean) signifying the influence of additive gene effect. According to Chakrabaorty and Haque (2000) high estimates of heritability in conjuction with high genetic advance was observed for grain yield, 100 grain weight and no. of pods/plant. Tyagi and Khan (2011) observed high heritability accompanied by moderate to high GCV and genetic gain for number of pods/plant, number of branches, 100 seed weight and seed yield. Studies on heritability and genetic advance indicate that simple selection among germplasm accessions can bring about significant improvement in these traits as the heritability and genetic advance were high. The expected genetic advance could have been biased towards higher side as it is based on the estimates of heritability in broad sense. Moreover in the augmented design the estimation of mean square due to the error is based on the check variety only and hence it might have given the high estimates of genetic variances in it. Material under investigation flowered in 85.6$\pm$ 33.69 days and matured in 132.87$\pm$ 16.28 days. High environmental coefficient of variation was observed in pods per plant. This trait has also high genotypic coefficient of variation. It reflects its genetic potential also. Heritability (bs) was more prominent for flowering and maturity. Environment played role for variation in pods per plant followed by branches per plant, plant height and seeds per plant. Although, pods per plant had high genetic advance as % of mean but high heritability along with high GA as % means was observed in days to flowering. (Table 1) While studying the correlation it was observed that pods

TABLE 1: Estimation of genetic parameters of different characters.

Characters	Mean	MSE	RMSE	CV	R_sq	GCV	PCV	ECV	Heritability	GA as % means 10%
DF	85.66	33.69	5.80	6.78	0.98	9.66	11.80	6.78	0.67	120.48
DM	132.87	16.28	4.04	3.04	0.97	3.52	4.65	3.04	0.57	38.47
PH	40.01	40.04	6.33	15.82	0.96	9.47	18.43	15.82	0.26	25.26
PPP	59.87	243.02	15.59	26.04	0.95	14.43	29.77	26.04	0.24	131.44
SPP	1.79	0.05	0.21	12.01	0.94	4.92	12.98	12.01	0.14	0.01
BPP	3.25	0.33	0.57	17.63	0.95	6.39	18.75	17.63	0.12	0.08
Yield	2.92	0.21	0.45	8.36	0.96	18.52	16.21	8.63	0.18	5.64

DF = days to 50% flowering; DM = days to 80% maturity; PI
BPP = branches (primary) per plant

per plant had high significant and positive correlation with maturity, plant height, seeds per pod, branches per plant, yield. Plant height, pods per plant and branches per plant played role in seeds per pod as these traits had significant and positive correlation with seeds per pod, but it had significant and negative correlation with flowering. Similarly, branches per plant had significant and positive correlation with pods per plant and seeds per pod. Maturity had significant positive relationship with flowering and plant height (Table 2). All the Genotypes were grouped into three clusters on the basis of non-heirarchial eucledean cluster analysis. The genetic differences between the clusters are reflected in cluster means. Genotypes grouped under cluster I were of medium flowering and maturing type having better seeds/pod, branches/plant, pods/plant and plant height. Cluster II and III were having early and late maturing genotypes respectively, with moderate to high yielding contributing traits. Crosses made between cluster I and either of cluster II or III could produce desirable recombinants for grain yield. (Table 3 & figure 1) It was also concluded from the results that very few germplasm accessions belonged to superior or highly desirable category like very early flowering in < 65 days, extra tall (> 60 cm) for high
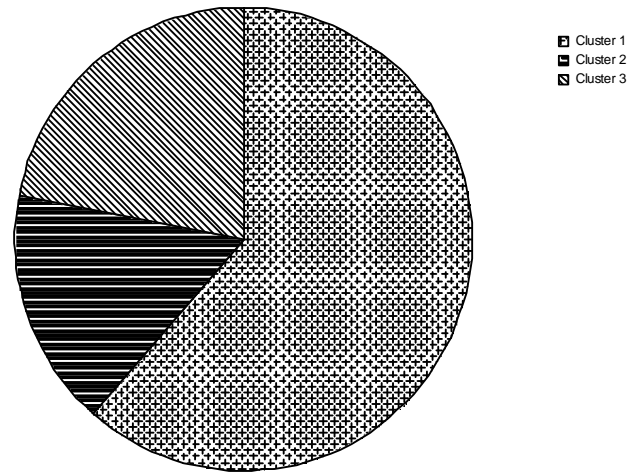

Cluster 1
Cluster 2
Cluster 3

FIG. 1: Clustering pattern.

TABLE 3: Distribution of genotypes in different clusters.

		Number of genotype	% of Total
Cluster	1	633	58.2%
	2	198	18.2%
	3	256	23.6%
	Combined	1087	100.0%
Total	1087	100.0%	

TABLE 2. Genotypic (Above diagonal) and phenotypic (Lower diagonal) correlation of different characters.

Phenotypic				Genotypic			Yield
	DF	DM	PH	PPP	SPP	BPP	
DF	1.000	0.662(**)	-0.094(**)	0.002	-0.140(**)	-0.043	0.298(*)
DM	0.675(**)	1.000	0.123(**)	0.155(**)	0.020	-0.021	0.312(*)
PH	-0.064(*)	0.107(**)	1.000	0.310(**)	0.278(**)	-0.030	0.319(*)
PPP	-0.071(*)	0.055	0.321(**)	1.000	0.324(**)	0.172(**)	0.789(**)
SPP	-0.099(*)	-0.030	0.218(**)	0.337(**)	1.000	0.239(**)	0.205(*)
BPP	0.028	-0.015	-0.086(*)	0.202(*)	0.201(**)	1.000	0.114
Yield	0.351(*)	0.367(*)	0.397(*)	0.881(**)	0.308(*)	0.218(*)	1.000

**Correlation is significant at the 0.01 level (2-tailed)
*Correlation is significant at the 0.05 level (2-tailed)

TABLE 4: Cluster means of different traits.

	DF		DM		PH		PPP		SPP		BPP		Yield	
	Mean	Std. Deviation	Mean	Std. Deviation	Mean	Std. Deviation	Mean	Std. Deviation	Mean	Std. Deviation	Mean	Std. Deviation	Mean	Std. Deviation
Cluster 1	84.43	8.61	133.86	4.55	43.05	6.97	69.01	18.04	1.89	0.18	3.42	0.63	2.94	1.29
2	72.63	5.64	122.86	3.99	35.47	6.54	41.99	16.28	1.65	0.30	2.98	0.53	2.21	0.98
3	99.95	7.41	138.33	4.36	34.39	7.68	46.16	16.05	1.59	0.25	2.95	0.62	3.62	2.12
Combined	85.66	11.70	132.87	6.58	40.01	8.12	59.87	21.11	1.79	0.26	3.25	0.65	2.92	0.54

biomass and high no of pods > 120 pods/plant and such accessions may prove useful donors (Table 5 Figure 2,3,4) Studies on genetic parameters, genetic divergence and diversity analysis are either few or none especially on large number of germplasm accessions of lentil, However, Biswas *et al.,* (1985), Jeena and Singh (2001 & 2002) Rathi *et al.,* (1998) Sharma *et al.,* (1996) Singh *et al.,* (2001), Singh and Gupta (1994) have reported their results on relatively small number of genotypes.
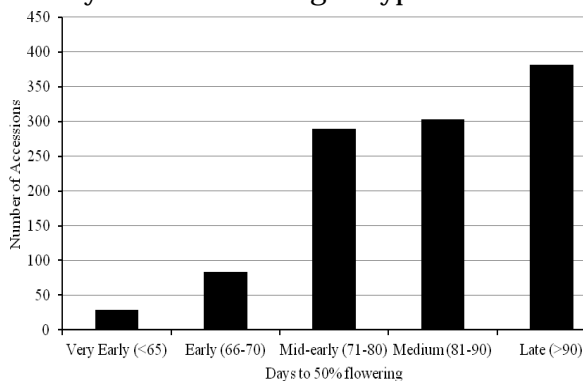

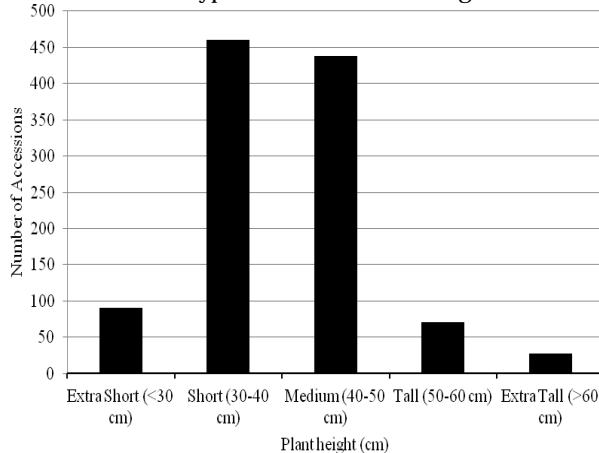**FIG. 2: Genotypes for different flowering durations**

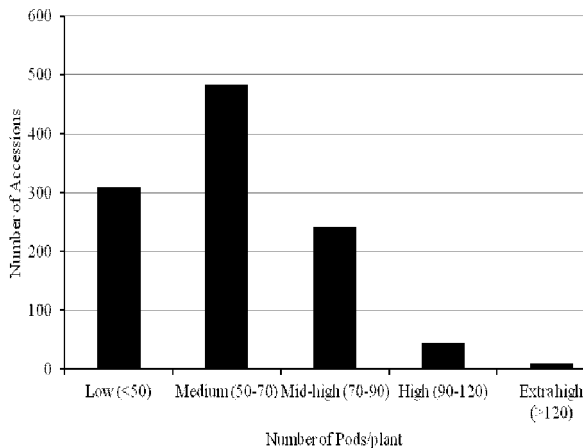**FIG. 3: Genotypes in different plant height categories**

FIG. 4: Genotypes for number of pods

TABLE 5: Listing of desirable genotypes for various traits.

Desirable categories	Accessions
Very early (< 65 days)	RKL-1012, RKL-1015, RKL-1012, IC-560333, L-2171, L-2166, IC-559639, L-1290, L-1289, L-1823, L-1787, L-1754, IC-560111, IC-560148, L-1535, L-1822, L-1755, L-1788, L-1839, L-1365, IC-311161, IC-345491, L-1830, L-1828, L-2141, L-1821, L-1752, L-7707
Extra tall (> 60 cm)	IC-559744, L-218, IC-559608, IC-559767, IC-560040, L-1016, IC-560291, L-1018, IC-559763, L-1644, IC-201675, L-228, IC-418326, L-192, IC-559773, L-1013, IC-560123, L-229, IC-559769, L-360, IC-560236, IC-560045, L-2176, IC-560035, P-18125, L-226, L-7818
No. of pods Extra high (> 120)	L-169, JBT-3164, L-7740, JBT-3164, L-322, L-4594, IC-398094, L-359, L-1729

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