

**GENETIC VARIABILITY AND CHARACTER ASSOCIATION AMONG  
THE YIELD AND YIELD ATTRIBUTING COMPONENTS  
IN LENTIL (*LENS CULINARIS* MEDIK.)**

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**Abstract**

Twenty one advanced lines of lentil including three checks were selected. The observations were recorded on five randomly selected plants of each genotype under each replication and per plant. Data were obtained by averaging the values. (i) Pre-harvest observations - days to flowering, days to maturity, (ii) post-harvest observations - plant height (cm), pods per plant, no. of branches per plant, yield per plot (kg/ha), 100-seed weight and plant stand (%) considered. The study revealed that characters *viz.*, 100-seed weight (177.5), plant height (66.1) and seed yield (20.7) showed high GCV appraises. In the present investigation out of eight, only seven components (PCs) exhibited more than 5 Eigen value, and showed about 91.289% total variability among the studied traits. Among the others characters days to maturity was positively and significantly correlated by days to 50% flowering and number of pods per plant suggesting early maturity or late maturity depends on flowering which are directly correlated with seed yield and selection of more number of pods plant gives maximum yield.

**Introduction**

Lentil is important Rabi pulse crop next to chickpea with production of 1.13 million tonnes for 1.43 m/ha area in India (Anon. 2018). In north-eastern parts of the country, lentil is also cultivated as paira crop with rice. It is cultivated for its seed and mostly eaten as Dhal. The seed is decorticated and split. The primary product is the seed which has relatively higher contents of protein, carbohydrate and calories compared to other legumes and is the most desired crop because of its high average protein content and fast cooking characteristic in many lentil producing regions. Lentil residues contain about 10.2% moisture, 1.8% fat, 4.4% protein, 50% carbohydrate, 21.4% fiber and 12.2% ash (Muehlbauer *et al.* 1985). Lentil is a diploid ( $2n = 14$  chromosomes) self-pollinated annual cool season legume crop. Many biotic and abiotic stresses influence lentil yield all over the world i.e. diseases, insect and along with drought, heat salt susceptibility and iron deficiency. Plant breeders must have a mean of choosing the accessions most likely to possess the trait of interest. Until recently, most of characterization and evaluation has been based on the recording of either qualitative and or quantitative morphological characters using standard descriptions. Present investigation was undertaken to estimate the variability parameters and correlation coefficients between grain yield and its components characters in lentil genotypes.

**Materials and Methods**

The present investigation was carried out in the experimental fields of the Regional Agricultural Research Station, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Sagar, (M.P.) during Rabi season of 2014 with 21 lentil improved lines.

The experiment was carried out under RCBD. Each genotype was accommodated in 6 row plot of 4 m length with row to row and plant to plant spacing of 30 and 5 cm, respectively. The experiment was conducted under semi irrigated and medium fertility conditions. Twenty one

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advanced lines including three checks were used for this experiment. All genotypes collected from project co-coordinator, All India Coordinated Research Project on MULLaRP, IIPR, Kanpur.

**Table 1. List of genotypes, source and pedigree.**

Sl. No.	Genotypes	Source	Pedigree
1.	JL-3	JNKVV, Jabalpur	Local selection from Sagar M.P.
2.	IPL-81	IIPR, Kanpur	K75 × PL 639
3.	DPL-62	IIPR, Kanpur	JLS1 × LGI 71
4.	IPL-316	IIPR, Kanpur	Sehore 74-3 × DPL 58
5.	IPL-330	IIPR, Kanpur	KL 178 × DPL62
6.	RKL-603-1	ARS, Kota	L 4682 × DPL 62
7.	IPL-331	IIPR, Kanpur	(94/1570 × DPL 98) DPL 62
8.	VL-523	Almora	VL 120 × DPL 15
9.	DKL-37	Dhaulakaun	DPL-6 × PL-5)
10.	LL-1242	PAU, Ludhiana	LL 148 × L 4603
11.	L-4714	IARI, New Delhi	Precoz × DPL 15
12.	IPL-329	IIPR, Kanpur	KL 178 × DPL 62
13.	PL-164	Pantnagar	DPL 15 × L 4188
14.	KLB -13-6	CSA Kanpur	KLB 08-4 × KLB 303
15.	L-4715	IARI, New Delhi	Sehore 74-3 × Precoz
16.	PL-157	Pantnagar	PL 02 × DPL 58
17.	RKL-1003-21C	ARS, Kota	Mutant of DPL 62
18.	IPL-332	IIPR, Kanpur	(IPL 517 × DPL 62) DPL 62
19.	LL-1318	PAU, Ludhiana	DPL 15 × LL 992
20.	PL- 160	Pantnagar	PL 02 × DPL 15
21.	RVL-12-5	Sehore	JL 3 × DPL 62

The observations were recorded on five randomly selected plants of each genotype under each replication and per plant, data were obtained by averaging the values. (A) Pre-harvest observations - days to flowering, days to maturity, (B) post-harvest observations - plant height (cm), pods/plant, No. of branches/plant, yield kg/ha, 100-seed weight in g and plant stand (%).

The mean values of from randomly selected plants while the difference between the lowest and highest values for each character were taken as the range. Estimate of genetic advance (GA) was done by Robinson *et al.* (1949). To test the significance of correlation coefficients, the estimated values were compared with the tabler values (Fisher and Yates 1957) at  $n - 2$  degrees of freedom at 5 and 1% level of significance, where  $n$  being the sample size on which correlation is based. Path analysis was made as described by Dewey and Lu (1959) and Ramanujam and Rai (1963) to assess direct and indirect influences of various components on grain yield. Statistical analysis done with the help of SPSS statistical software. Based on the theoretical arguments of the PCA described by Hair *et al.* (2005) the significant factor loading values higher than or equal to 0.7 were used to identify the most important variables and attributes in each dimension, or principal components (PCs). The purpose of principal component analysis is to derive a small number of linear combinations (principal components) of a set of variables that retain as much information in the original variables as possible. PCA is a well-known method of dimension reduction that can be used to reduce a large set of variables to a small set that still contains most of

the information in the large set (Massay 1965). It is a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components. The first principal component accounts for as much of the variability in the data as possible and each succeeding component accounts for as much of the remaining variability as possible.

### Results and Discussion

Variability indicates a way to describe variance between characters and a scope for selection to plant. Variability is the base of plant breeding because to improve any character of plant variability is a prerequisite. Analysis of variance suggested that differences among the genotypes were highly significant for all the characters (Table 2). Assessment of variability, heritability and genetic advance in a set of 21 lentil genotypes for all the 8 traits was done to determine the extent of variability present in the material. Genotypic and phenotypic co-efficient of variation also indicated the same. In general, it was observed that the phenotypic co-efficient of variation was higher in magnitude for all the traits, than its corresponding genotypic co-efficient indicating the masking influence of environment in the expression of the traits studied.

The study revealed that characters showed high GCV *viz.*, 100-seed weight (177.5), plant height (66.1) and seed yield (20.7) showed high GCV appraises. This is an indicative of less manageable fluctuations; hence it is given to great emphasis should be given on these characters, while formulating breeding programme with this material. High GCV for the characters 100-seed weight, plant height and seed yield earlier also were reported by Hissan *et al.* (2018), However, the estimates of heritability in broad sense was high for most of the traits *viz.*, day to maturity (0.95), 100-seed weight (0.85), days to flowering (0.78) and seed yield (0.70). The results are quite in agreement with the findings obtained by earlier workers Al-Aysh (2014) for seed yield and Tyagi and Khan (2010) for 100-seed weight and grain yield. The magnitude of PCV ranged 0.62 for No. of pods/plant to 192.6 for 100-seed weight and GCV ranged from 0.47 to 177.5 for the same character.

Difference between the PCV and GCV was high for plant height, no. of branches/plant and 100-seed weight. In the present investigation, high to moderate heritability coupled with high to moderate genetic advance as percentage of mean was exhibited for four traits *viz.*, days to flowering, days to maturity, grain yield and 100-seed weight. The trait plant height (0.25) showed medium heritability with high genetic advance (30.7). Plant stand (7.3) exhibited moderate genetic advance and moderate heritability. The presence of high heritability coupled with high-expected genetic advance indicated predominance of additive gene action in the expression of these characters and consequently greater chance of improving these traits through simple selection. These results are in conformity with the findings of Mekonnen *et al.* (2014) for 100-seed weight and seed yield.

Higher magnitude of genotypic correlation helps in selecting genetically controlled characters and gives a better chance for seed yield improvement than that would be expected on the basis of phenotypic association alone (Robinson *et al.* 1951). The correlation matrix depicting trait associations is presented in Table 4. The tables revealed that plant stand, days to maturity and plant height are significantly and positively correlated with seed yield (0.43) at both levels. The degree of association was highest between plant stand and seed yield. It was followed by maturity and plant height. Hissan *et al.* (2018) also suggested that seed yield is positively and significantly correlated with days to maturity and flowering, which means late flowering due to temperate conditions. Among the others characters days to maturity was found to positively and significantly correlated by days to 50% flowering (0.61) and no. of pods per plant (0.45) suggesting early

**Table 2. Mean sum of squares for various characters in lentil.**

Source of variation	Degree of freedom	Mean sum of squares							No. of pods/plant
		Seed yield (kg/ha)	100-seed wt.	Days to flowering	Days to maturity	Plant stand (%)	Plant height (cm)	No. of br./plant	
Replications	2	85520.018	7.349	3.111	1694.71	36.0385	6816.504	0.0235	0.1945
Genotypes	20	336025.011**	91.3778**	40.0873**	327.319**	63.7795**	4433.51**	0.5953**	1.2492**
Error	40	59285.925	7.38255	4.92775	138.1476	18.26497	2656.7296	0.53015	0.3236

\*\* Highly significant at 1% level of significance.

**Table 3. Estimates of parameters of genetic variability for 8 characters in 21 lentil genotypes.**

Character	Mean	Range		PV	GV	PCV (%)	GCV (%)	Heritability (%)	Genetic advance	GA % over mean
		Min.	Max.							
Seed yield (kg/ha)	1793	1186	2354	197655	138369	24.8	20.75	0.70	641.13	35.76
100-seed weight	3.65	2.67	5	49.38	42.00	192.6	177.5	0.85	12.32	337.44
Days to flowering	69	63	86	22.51	17.58	6.87	6.07	0.78	7.63	11.05
Days to maturity	124	117	129	99.51	94.59	8.04	7.84	0.95	19.52	15.74
Plant stand (%)	71.81	43	85	41.02	22.76	8.91	6.64	0.55	7.31	10.19
Plant height	44.4	36.6	54.4	3545.12	888.39	134.10	67.12	0.25	30.74	69.23
No. of branches/plant	2.83	2.2	4	0.56	0.03	26.15	6.01	0.06	0.09	3.12
No. of pods/plant	144.07	87	264	0.79	0.46	0.62	0.47	0.59	1.08	0.75

**Table 4. Phenotypic (below diagonal) and genotypic (above diagonal) correlation coefficient among 8 characters in 21 lentil genotypes.**

Character/ trait	Seed yield (kg/ha)	100-seed wt.	50% flowering	Maturity (Day)	Plant stand (%)	Plant height (cm)	No. of branches/ plant	No. of pods/plant
Seed yield (kg/ha)	<b>1.0000</b>	0.2410	0.2882	0.3625**	0.4325**	0.3408**	-0.1634	-0.1474
100-seed wt.	0.2410	<b>1.0000</b>	0.0064	0.7030**	-0.1221	0.0863	-0.1578	0.1823
50% flowering	0.2882	0.0064	<b>1.0000</b>	0.6122**	0.6578**	0.0901	-0.6242	0.0670
Maturity (day)	0.3625**	0.7030**	0.6122**	<b>1.0000</b>	0.3343**	0.3165**	-0.4596**	0.4574**
Plant stand (%)	0.4325**	-0.1221	0.6578**	0.3343**	<b>1.0000</b>	0.5803**	-0.5206**	-0.3469
Plant height (cm)	0.3408**	0.0863	0.0901	0.3165**	0.5803**	<b>1.0000</b>	-0.5956**	-0.1637
No. of branches/plant	-0.1634	-0.1578	-0.6242	-0.4596	-0.5206	-0.5956	<b>1.0000</b>	0.1468
No. of pods/plant	-0.1474	0.1823	0.0670	0.4574**	-0.3469**	-0.1637	0.1468	<b>1.0000</b>

\*, \*\* = Significant p = 0.05% levels, respectively.

maturity or late maturity depend flowering which are directly correlated with seed yield and selection of more no. of pods plant gives maximum yield. Carrasco *et al.* (1985) also suggested that yield could be raised by selecting for earliness, tallness and more pods per plant-1, which is evident in the present study.

**Table 5. Eigen values.**

Number	Eigen value	Per cent	Per cent	Cum per cent	Chi square	df	Prob > chi.sq
1	2.9957	37.446		37.446	59.086	27.453	0.0004*
2	1.6996	21.245		58.691	35.759	24.385	0.0642
3	1.0575	13.219		71.910	23.045	19.481	0.2595
4	0.9074	11.343		83.253	16.447	14.288	0.3055
5	0.6429	8.036		91.289	8.714	9.628	0.5245
6	0.2967	3.708		94.997	2.006	5.536	0.8908
7	0.2582	3.227		98.224	1.187	2.350	0.6333
8	0.1420	1.776		100.000	0.000	.	.

**Table 6. PC values of rotation component matrix for eight variables of 21 genotypes of lentil.**

Traits	Principal components			
	PC1	PC2	PC3	PC4
Seed yield (kg/ha)	0.604	0.023	0.275	0.656
100-seed weight	0.223	0.491	0.745	0.064
50% flowering	0.609	0.284	-0.548	0.266
Maturity	0.728	-0.596	-0.148	-0.041
Plant stand	0.768	-0.429	-0.147	0.051
Plant height	0.712	-0.299	0.263	-0.351
No. of branches/plant	-0.759	0.116	-0.034	0.465
Pods/plant	-0.085	0.857	-0.112	-0.239

Rotation method: Varimax with Kaiser normalization.

Hundred-seed weight showed positive and significant correlation with maturity (0.70) at genotypic level. Days to 50% flowering revealed positive and significant correlation with maturity (0.61) and plant stand (0.65) and negative and significant correlation with number of branches/plant (0.62). Plant height was exhibited positive and significant correlation with plant stand (0.58), seed yield (0.34) and maturity (0.31) and negative and significant correlation with number of branches/plant (0.59) at both phenotypic and genotypic level. Positive correlation of plant height with seed yield has also been reported by Kumar *et al.* (2004). Number pods per plant revealed significantly positive correlation with maturity and negative correlation with plant stand at genotypic level. Similar results were also reported by Tadesse *et al.* (2014).

In present experiment out of eight, only five components (PCs) exhibited more than Eigen value, and showed about 91.289% total variability among the studied traits (Table 5). So these five PCs were given due importance for further explanation. The PCs 1 showed 37.446% while, PC2,

PC3, PC4 and PC5 exhibited 21.245, 13.219, 11.343 and 8.036 variability, respectively among the genotypes for the traits under study.

**Table 7. Interpretation of rotated component matrix for the traits having values  $>\pm 0.05$  in each PC.**

	PC1	PC2	PC3	PC4
Characteristics	Plant stand	Pods/plant	100-seed weight	Seed yield (kg/ha)
	Maturity	Maturity	Seed yield (kg/ha)	-
	Plant height	100-seed weight	-	-
	50% flowering	-	-	-
	Seed yield (kg/ha)	-	-	-

Screen plot explained the percentage of variance associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. PC1 showed 37.446 variability with Eigen value 2.9957, which then declined gradually. Semi curve lines are observed in each PC. From the graph, it is clear that the maximum variation was observed in PC1 in comparison to other four PCs. So, selection of lines from this PC will be useful (Fig. 1).

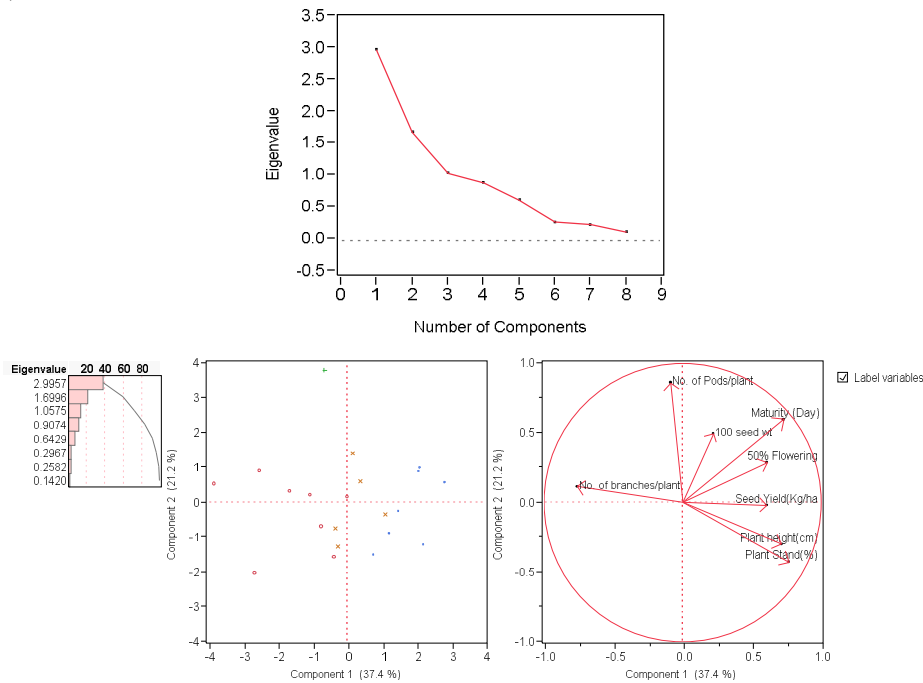


Fig. 1. Label of variables.

The rotated component matrix, sometimes referred to as the loadings, is the key output of principal components analysis. It contains estimates of the correlations between each of the variables and the estimated components. Rotated component matrix revealed that the PC1 which accounted for the highest variability (37.446%) was mostly related to physiological and yield traits

like plant stand, maturity, plant height, days to 50% flowering and seed yield. PC2 was also dominating by yield related traits i.e. Maturity, 100-seed weight and 50% flowering. The PC3 was found to be dominating by yield traits i.e. 100-seed weight and seed yield. While, PC4 was found to be related to 100-seed weight and branches per plant (Tables 6 and 7).

Lentil production in India has always been important as it is the one of the most important Rabi crops in the country. In fact, India is the largest producer of the lentil crop in the world. On the basis of present investigation some important finding comes. High GCV was found for the characters, namely 100-seed weight, plant height and seed yield. Estimates of heritability in broad sense was high for most of the traits *viz.*, days to maturity (0.95), 100-seed weight (0.85), days to flowering (0.78) and seed yield (0.70). High to moderate heritability coupled with high to moderate genetic advance as percentage of mean was exhibited for four traits *viz.*, days to flowering, days to maturity, grain yield and 100-seed weight. Rotated component matrix revealed that the PC1 which accounted for the highest variability (37.446%) was mostly related to physiological and yield traits like plant stand, maturity, plant height, days to 50% flowering and seed yield.

Variability gives a way to describe variance between characters and a scope for selection to plant. Yield in lentil could possibly be improved by increasing in traits *viz.*, days to maturity, 100-seed weight, days to flowering and seed yield. The presence of high heritability coupled with high-expected genetic advance indicated predominance of additive gene action in the expression of these characters and consequently greater chance of improving these traits through simple selection. Higher magnitude of genotypic correlation helps in selection for genetically controlled characters and gives a better chance for seed yield improvement.

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