



## GENETIC DIVERSITY ANALYSIS IN LENTIL (*Lens culinaris* MEDIKUS)

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### ABSTRACT

Lentil is one of the most important pulse crop of India, grown in winter season It has versatile uses as food, feed, fuel and fodder. The Field experiment under present investigation was conducted during *rabi* season 2017-18 at Agricultural Research Farm of B.R.D.P.G. College, Deoria (U.P.) The experiment was conducted to evaluate 10 varieties / strains of lentil including four check under irrigated, normal soil condition in Augmented Block Design. The entire experimental field was divided into 10 blocks of equal size and each block had 11 plots. Out of 11 plots in a block, 7 plots was used for accommodating the test genotype. Which were not replicated while remaining 4 checks. The highest number of genotypes appeared in cluster III, which contained 13 entries followed by cluster IX having 12 genotypes, Cluster IX having 12 genotypes, Cluster IV with 10 genotypes and Cluster V, VIII with 9 genotypes in each. Minimum numbers of genotypes were presented in cluster II having 2 genotypes. The highest intra-cluster values were found for cluster IX (17.60) followed by cluster VII (10.33) while the lowest value was recorded in case of cluster VI (4.69). The maximum inter- cluster distance was found between cluster V and VIII (36.77). Between remaining cluster distance showed moderate to low inter- Cluster distance.

**Key words :** Genetic diversity, lentil, morphological marker, protein profiling, UPGMA

Lentils are one of the oldest and an important seed legume crops, cultivated worldwide as human food. It is a self pollinated diploid ( $2n=14$ ) [1] crop with a relatively large genome of 41063 Mbp [2]. It is cultivated mainly for its seed and only red cotyledon type is used as food in Bangladesh. Lentil seeds are valued as a food of both high quality plant proteins (26%) and fiber, in addition, the remaining plant residues can be used as animal feed and fodder for livestock and play an important role in crop rotations because their nitrogen fixing capability. Besides that sprouted lentils now have a reputation as “human food”. Epidemiological studies suggested that lentils have antioxidant, anticancer and probiotic activity which confer protection against some important chronic diseases [3, 4]. In Bangladesh, production of major food crops such as rice wheat does not meet the present requirements of countries population of about 134 million. Agricultural scientists are faced with the complex and urgent task of bringing the “population-food supply” equation into rational balance. Rice and wheat have been the focus of concerned government effort in research and development. Similar attention was long overdue for the pulse crops, commonly known as poor man’s meat. Pulses mainly lentils are vital components in diversification of Bangladesh are predominantly rice-based cropping system. Genetic variation between and within populations of crop species is a major interest of plant breeders and geneticists [5] because it facilitates the efficient sampling and utilization of germplasm resource [6]. The breeders must have the idea of choosing the accession that most likely possesses the trait of

interest. The knowledge of genetic variation and relationships between populations is important to understand the available genetic variability and its potential use in breeding programs. There are several methods to study genetic diversity such morphological, biochemical and molecular markers. Morphological characterization is the first step in the classification and description of any crop germplasm [7, 8] which is a traditional and one of easiest method for traditional plant breeders in selecting the desirable traits. Considerable variations among the characters for use in breeding and selection programmes have been reported for various morphological characters [9, 10 and 11]. Many workers have been reported on genetic variation in lentil through morphological characters [12, 13] and seed storage protein profile [14, 15, 16 and 17]. Among biochemical techniques SDS-PAGE is widely used due to its simplicity and effectiveness for describing the genetic structures of crop gerplasm [18, 19 and 20]. Seed storage proteins profiling provides aid for identification and characterization of diversity in crop varieties and their wild varieties and phylogenetic relationship of the varieties, generating pertinent information to complement evaluation and passport data [21].

### MATERIALS AND METHODS

The present investigation was carried out during *Rabi*, 2017-18 at Agriculture Research Farm of B.R.D.P.G. College Campus, Deoria (UP). Geographical, Baba Raghav Das Post Graduate College Deoria is located in the east part of U.P. India, the site of experiment is located

**Table-1** : Clustering pattern of 74 lentil genotypes (including checks) on the basis of non-hierarchical Euclidean cluster analysis of eleven characters.

Cluster No.	Number of genotypes	Genotypes
I	7	GM-223199A, DPL-15, PL-7, NDL-96-12, NDL-96-15, NDL-96-4, NDL-96-10
II	2	L-4594, LL-699
III	13	EC-78389, GM-223199A, GM-78532, EC-267604, EC-223199A, 78536, L-4603, GM-223233, GM-267687, EC-262572, 78471, 255401, NDL-1
IV	10	EC-267672, EC-223397, EC-1, GM-223209, EC-78409, GM-78474, 78417, EC-223229, LL-1122, LL-631
V	9	LL-1161, PL-117, IPL-321, EC-78405, EC-223789, GM-27190, GM-78521, EC-75483, NDL-98
VI	8	GM-2675630, GM-78505, PL-02, ILWL-118, EC-78536, LL-1203, GM-267638, ILL-766
VII	4	78474, NDL-21, NDL-96-3, NDL-96-1
VIII	9	LL-1114, GM-223150, EC-223188, NDL-96-21, NDL-96-11, NDL-96-31, NDL-96-36, NDL-96-21, DPL-15
IX	12	DPL-62, NDL-97-1, EC-78425, IPL-81, NDL-36, L-4147, DPL-58, NDL-24, L-4076, L-639, DPL-62, IPL-81

**Table-2** : Estimates of average intra and inter-cluster distances for the 9 clusters in lentil.

	I	II	III	IV	V	VI	VII	VIII	IX
I	<b>4.892</b>	12.550	12.584	17.672	25.168	11.034	14.745	26.277	37.986
II		<b>10.013</b>	18.917	25.407	38.004	14.265	20.391	18.467	33.575
III			<b>10.967</b>	20.921	31.669	17.937	24.967	39.459	46.898
IV				<b>13.213</b>	24.171	24.676	20.295	31.508	34.614
V					<b>5.913</b>	46.297	33.316	36.776	51.617
VI						<b>4.695</b>	12.525	28.098	28.793
VII							<b>10.339</b>	22.054	24.546
VIII								<b>8.667</b>	24.109
IX									<b>17.600</b>

Bold figure represents intra-cluster distance

at 26.5 °N latitude, 83.79 °E longitudes and 68 meters (223 feet) above the mean sea level. The climate of district Deoria is semi-arid with hot summer and cold winter. Nearly 80% of total rainfall is received during the monsoon (only up to September) with a few showers in the winter. A germplasm collection of 70 varieties/strains of lentil comprising exotic as well as indigenous (appendix-I) and four check varieties viz., (NDL-1, DPL-15, IPL-81, DPL-62) constituted the experimental materials for this study. These genotypes exhibited wide spectrum of variation for various agronomical and morphological characters which were obtained from Pulse Section Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad. The used checks in experiment are well adopted varieties of the region.

## RESULTS AND DISCUSSION

The genetic divergence existing in 74 (70 germplasm and 4 check varieties) lentil genotypes studied by employing non-hierarchical Euclidean cluster analysis for eleven quantitative characters. The 74 genotypes grouped into

nine different non-overlapping clusters. The distribution of 74 lentil accessions into ten clusters is given in Table-1.

The highest number of genotypes appeared in cluster III, which contained 13 entries followed by cluster IX having 12 genotypes, cluster IV with 10 genotypes and cluster V, VIII with 9 genotypes in each. Minimum numbers of genotypes were presented in cluster II having 2 genotypes followed by cluster VII with 4 genotypes and cluster VI with 8 genotypes and cluster I with 7 genotypes.

The estimates of intra and inter-cluster distance for thirteen clusters are presented in Table-2. The highest intra-cluster value was found for cluster IX (17.600) followed by cluster VII (10.339), cluster I (4.892), cluster III (10.967), cluster IV (13.213) and cluster II (10.013) while the lowest value was recorded in case of cluster VI (4.695). The maximum inter-cluster distance was found between cluster V and VIII (36.776). Between remaining cluster distance showed moderate to low inter cluster distance. The same result reported in lentil [22, 23 and 24].

**Table-3** : Cluster mean for different characters for 9 cluster in lentil germplasm

Cluster number	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches /plant	Secondary branches/ plant	Pods/ plant	Seeds /pod	100 Seed weight (g)	Biological yield/ plant (g)	Harvest index (%)	Seed yield/ plant (g)
I	84.89	114.89	21.00	2.26	10.20	26.92	1.96	4.25	8.41	20.31	42.20
II	79.20	108.65	25.19	2.66	10.50	30.43	2.01	4.25	16.19	33.36	48.70
III	71.32	101.02	18.51	2.44	10.79	23.33*	2.06	4.98	6.29*	15.71	41.92
IV	73.23	98.97	23.37	3.10	9.09*	26.93	1.90	4.99**	21.13	36.41	59.65
V	88.58**	116.50**	24.11	2.32	9.22	26.60	1.95*	3.72	11.53	27.57	40.24*
VI	62.53*	95.63*	29.68**	1.77*	9.24	28.96	1.78	3.57*	12.00	25.66	45.66
VII	72.78	100.38	23.09	3.37**	12.74**	35.06	2.33**	4.93	32.70**	56.26	56.41
VIII	85.78	110.38	20.75	2.17	9.54	36.86**	2.13	7.69	30.50	61.66**	47.36
IX	65.78	98.13	16.90*	1.92	10.29	34.66	2.03	4.59	6.80	10.11*	70.58**

Lowest value\*, Highest value\*\*

**Table-4** : Genetic divergence in lentil germplasm

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches / plant	Secondary branches/ plant	Pods/ plant	Seeds /pod	100 seed weight (g)	Biological yield/ plant (g)	Harvest index (%)	Seed yield/ plant (g)
Contribution (%)	19.10	13.25	2.52	0.01	0.33	9.77	0.01	0.01	32.95	22.07	0.01

The cluster means for 11 characters are presented in Table-3. The genotypes of cluster V took maximum days to flowering ( $\bar{X}$  = 88.58). The genotypes with early days to flowering were concentrated in cluster VI ( $\bar{X}$  = 62.53).

The genotypes of cluster V showed highest mean for days to maturity ( $\bar{X}$  = 116.50) followed by cluster I ( $\bar{X}$  = 114.89) and cluster VIII ( $\bar{X}$  = 110.38). The genotypes with early days to maturity appeared in cluster II ( $\bar{X}$  = 108.65) followed by cluster VI ( $\bar{X}$  = 95.63). The highest cluster mean for plant height was observed in cluster VI ( $\bar{X}$  = 29.68 cm) followed by cluster II ( $\bar{X}$  = 25.19 cm). Lowest mean value of plant height was found in cluster IX ( $\bar{X}$  = 16.90 cm). Cluster VII ( $\bar{X}$  = 3.37) showed highest cluster mean for number of primary branches followed by cluster IV ( $\bar{X}$  = 3.10). However, the lowest value was recorded in cluster VI ( $\bar{X}$  = 1.77). The result of morphological evaluation of the characters showed significant genetic variation of different yield and yield contributing characters in the varieties indicating the scope and their warranty to use in the breeding programmes [25, 26, 27]. The genotypes of cluster VII possessed maximum number of secondary branches per plant ( $\bar{X}$  = 12.74). The genotypes with low number of secondary branches per plant was concentrated in cluster IV ( $\bar{X}$  = 9.09). The genotypes occurring in cluster VIII ( $\bar{X}$  = 36.86) produced highest cluster mean for number of pods per plant, while

the genotypes of cluster III ( $\bar{X}$  = 23.33) were recorded for lowest mean for this trait. The highest cluster mean for number of seeds per pod was exhibited by cluster VII ( $\bar{X}$  = 2.33), while lowest cluster mean was noted in cluster V ( $\bar{X}$  = 1.95). Cluster VII ( $\bar{X}$  = 32.70) comprised of entries observed with highest mean for biological yield. The lower value was recorded for cluster III ( $\bar{X}$  = 6.29). Cluster VIII ( $\bar{X}$  = 61.66%) comprised of entries which produced highest mean for harvest index. The lower value was observed for cluster IX ( $\bar{X}$  = 10.11%) followed by cluster III ( $\bar{X}$  = 15.71%). Rest of the clusters showed moderate mean value for this character. The 100-seed weight was the highest in the genotypes of cluster IV ( $\bar{X}$  = 4.99) while it was lowest for entries occurring in cluster VI ( $\bar{X}$  = 3.57) and remaining clusters had moderate cluster means of 100-seed weight. The highest cluster mean for seed yield per plant was observed in case of cluster IX ( $\bar{X}$  = 70.58) which indicate that lines having very high seed yield were concentrated in this cluster. The genotypes with very low seed yield were grouped in cluster V ( $\bar{X}$  = 40.24).

Highest relative contribution toward genetic divergence recorded by the number of pods/plant (9.77%) followed by days to 50% flowering (19.10%), harvest index (22.07%) and days to maturity (13.25%) while, remaining characters contribution were very low. The relative contributions of different characters toward divergence are given in Table-4.

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