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Genetic Variability, Heritability and Genetic Advance in Lentil [*Lens culinaris* Medik] Genotypes for Seed Yield and Attributing Traits

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ABSTRACT

Background: The present study was conducted to investigate the morphological characterization for quantitative traits in Lentil by assessing variance, genotypic and phenotypic coefficients of variations, genetic variability, heritability and genetic advance.

Methods: The study was carried out during the Rabi season of 2021-22 using 29 cultivated genotypes of lentil with three replications. The goal of the current study was to ascertain genetic variability for direct selection parameters of parents for further crossing programs. Five plants were chosen at random subjected to morphological observations. The different parameters were analyzed and accordingly the result was compiled.

Result: Analysis of variance showed a significant difference for ten characters studied. The evaluated characters showed varying degrees of mean, variability parameters, heritability and genetic advance among the genotypes investigated. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) recorded ranged from low to high. The high GCV and PCV values were found for number of branches per plant number of pods per plant, biological yield and seed yield. Low GCV and PCV were recorded for days to 50% flowering, days to maturity, plant height and number of seed per pod. Heritability estimates ranged from 44.26% (number of seeds per pod) to 98.37% (number of pods per plant). Genetic advance as percent of mean was found high for number of branches per plant, number of pods per plant, 100 seed weight, biological yield per plant, harvest index and seed yield per plant and low for days to 50% flowering, days to maturity, plant height and number of seeds per pod. Therefore, the result of this study suggests the existence of variability in seed yield and other agronomic traits in genotypes of lentil, which should be exploited in future breeding.

Key words: Genetic advance, Genotype, Heritability, Phenotype, Variability.

INTRODUCTION

Lentils (*Lens culinaris*) are an edible legume crop with diploid chromosomes (2n=14). It is a self-pollinating annual plant distinguished by its lens-shaped seeds. Global cultivation is underway for the cool-season diploid pulse lentil (Kumar and Gupta, 2020). With two seeds typically growing in each pod, the plant grows to approximately 40 cm (16 inch). While they can be grown in a various soil type, including sand and clay loam, lentils prefer deep sandy loam soils with moderate fertility. Flooding or conditions with high water content are intolerable to lentils. Culinary applications of lentils are widespread worldwide. Split lentils, known as dal (sometimes with their hulls removed), are frequently cooked into a thick curry that is typically eaten with rice or rotis in the Indian subcontinent, where lentils are a staple food. Soups and stews frequently contain lentils.

Canada and India are the two countries where lentils are growing the largest as a food crop. Lentils make up 9% of the total area and are produced in 9% of Rabi pulses. Seven states contribute more than 98% of the India's lentil production: Madhya Pradesh (35%), Uttar Pradesh (33%), Bihar (11%), West Bengal (10%), Jharkhand (4%), Rajasthan (4%) and Assam (2%). According to the fourth advanced estimate, India produced 1.28 million tonnes of lentils from 1.42 million hectares of acreage area with productivity of 904 kg/ha (Anonymous, 2022).

Comprehending the genetic variability of lentils is crucial for the crop's ongoing development and growth within the agricultural system. Characterizing the

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germplasm serves as a crucial link between the preservation and application of plant genetic resources (Mulusew *et al.,* 2014; Nag *et al.,* 2015; Bhandari *et al.,* 2017). The tendency of individual genotypes within a population to differ from one another is measured by genetic variability. Genetic variation and the mode of inheritance of both quantitative and qualitative traits are crucial factors to consider when planning a breeding program. Without variability, populations find it more difficult to adapt to changes in their environment, which increases their risk of extinction (Shah *et al.,* 2015; Kumar *et al.,* 2016). Genotypic and phenotypic coefficients of variation (GCV, PCV), Heritability and genetic advance are helpful in determining the degree of variability found in the various lentil genotypes (Upadhyay *et al.,* 2019).

MATERIALS AND METHODS

Experimental materials and management

The pre sent study was carried out in the rabi season of 2021-22 at the Crop Research Center of Sardar Vallabhbhai Patel University of Agricultural and Technology Meerut-250110 (U.P.) comprising 29 cultivated genotypes (Table 1), of lentil *viz*; DPL-15, DPL-62, IPL- 81, IPL-406, IPL-316, IPL-526, K-75, Sehor-74-3, ILL-7663, Pant L-7, Pant L-117, B-77, JL-3, P-2016, L-4710, L-4717, L-1114, LL-1122, LL-1203, Pant L-02, LL-931, LL-1161, ILWLS-118, DPL-58, LL-699, IPL-321, ILWL-118, L-4076, L-4603 in RBD with three replications. Each genotype was sown over a three-meter-long area in two rows. The distance between plants was maintained at 10 cm and there was a 30-cm gap between rows. All advised agronomic practices were followed in order to grow a good crop of lentils. The goal of the current study was to ascertain genetic variability for direct selection parameters of parents for further crossing program. Five plants were chosen at random subjected to morphological observations *viz*; days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight, biological yield per plant, harvest index and seed yield per plant.

Statistical analysis

Each replication's genotypes mean values were used for statistical analysis. For ten traits, the significance of genotype variations was assessed by employing a randomized block design to analyze the data. Analysis of variance was calculated using the formulas of Panse and Sukhatme (1969) and Fisher (1918), GCV, PCV and heritability were calculated using the formulas provided by Burton (1952) and Genetic advance was determined using the method recommended by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Analysis of variance

The highly and significantly different genotypes were found by doing an analysis of variance for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, biological yield per plant, harvest index, seed yield per plant and 100 seed weight (Table 2). This suggests that the current material chosen for the study had enough variability, demonstrating the appropriateness of the selection process for crop improvement. Similar results were also observed for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, biological yield per plant, harvest index, seed yield per plant and 100 seed weight by (Hussan *et al.,* 2018; Sakthivel *et al.,* 2019).

Variability parameters

Range of mean performance and coefficient of variation of genotypes, heritability and genetic advance studied are given in (Table 3).

Mean

Grand mean value was found 83.61 for days to 50% flowering while range for this trait was 69.67-89.67 for genotypes (L-4710 and LL-1122) respectively. The results indicated that there is a variation sufficient for this trait and earliness can be created by selecting best genotype that will ultimately lead to early maturity. Days to maturity range from 112.67 days to 119.67 days for genotypes (Pant L-02

Table 1: Details of genotypes with their source.

DPL-15	IIPR, Kanpur
DPL-62	IIPR, Kanpur
IPL- 81	IIPR, Kanpur
IPL-406	IIPR, Kanpur
IPL-316	IIPR, Kanpur
IPL-526	IIPR, Kanpur
K-75	CSAUAT, Kanpur
Sehor-74-3	Local selection in MP
ILL-7663	ICARDA, Syria
Pant L-7	GBPUAT, Pantnagar
Pant L-117	GBPUAT, Pantnagar
B-77	AAU, Jorhat
JL-3	JNKVV, Jabalpur
P-2016	IIPR, Kanpur
L-4710	IARI, New Delhi
L-4717	IARI, New Delhi
L-1114	IARI, New Delhi
LL-1122	PAU, Ludhiana
LL-1203	PAU, Ludhiana
Pant L-02	GBPUAT, Pantnagar
LL-931	PAU, Ludhiana
LL-1161	PAU, Ludhiana
ILWLS-118	Wild accession (Collection)
DPL-58	IIPR, Kanpur
LL-699	PAU, Ludhiana
IPL-321	IIPR, Kanpur
ILWL-118	Wild accession (Collection)
L-4076	IARI, New Delhi
L-4603	IARI, New Delhi

and Sehore-74-3), respectively with mean of 115.83 so early varieties can be developed by selecting best genotypes. Plant height showed a range from 35.10 to 49.33 (cm) for genotypes (DPL-58 and IPL 406), respectively with general mean of 42.64. Number of branches per plant with mean of 13.31, ranged from 8.47 to 17.77 for genotypes (DPL-15 and DPL-58) respectively with a wide variation of (9.3). The number of pods per plant ranged from 37.40 to 104.90 for genotypes (K-75 and L-4710), respectively with a mean value of 104.90. The number of seeds per pod varied from 1.45 to 1.78 for genotypes (L-4717 and IPL -81), respectively with the general mean value of 1.63. The 100 seed weight varied from 1.65 to 3.47 for genotypes (B-77 and DPL-62), respectively with a mean of 2.55. The biological yield per plant varied from 2.96 to 7.89 for genotypes (K-75 and L-4710), respectively with mean value of 4.69. The values of harvest index varied from 23.42 to 53.74 for genotypes (DPL-58 and ILWL-118), respectively with a mean of 43.82. Seed yield per plant varied from 1.22 to 2.89 for genotypes (PantL-7 and P-2016), respectively with mean of 2.04. Hence, high yielding varieties can be developed by selecting these genotypes. Similar results were also observed for traits viz., Days to 50% flowering, Days to maturity, Plant height (cm) and biological yield per plant by (Sharma *et al.,* 2021; Pawar *et al.,* 2021; Shanti *et al.,* 2021 and Bhartiya *et al.,* 2015).

Table 2: Analysis of variance for different ten morphological traits in Lentil.

Source of variation	df	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	No. of seeds per pod	100 seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
Replication	2	0.56	2.21	0.29	0.37	1.49	0.004	0.070	0.04	6.70	0.014
Treatment	28	75.07**	14.87**	41.83**	23.92**	510.13**	0.018**	0.501**	3.59**	123.30**	0.674**
Error	56	1.13	1.31	1.89	0.57	2.80	0.005	0.021	0.03	3.10	0.009
Total	86	25.19	5.75	14.86	8.17	167.95	0.010	0.178	1.19	42.32	0.225
CV (%)		1.27	0.99	3.22	5.67	2.78	4.51	5.62	3.72	4.02	4.57
C.D. at 5%		1.75	1.88	2.25	1.24	2.75	0.12	0.24	0.29	2.89	0.15

*, ** significant at 5% and 1% level, respectively.

GCV and PCV

Analysis of genotypic coefficient variance (GCV) and phenotypic coefficient variance (PCV) of different traits indicated that phenotypic coefficient variances (PCV) were slightly greater than the genotypic coefficient variances (GCV) for all the traits, exhibited that these traits less influenced by environment factors. Similar findings were also reported by (Chowdhury *et al.,* 2019; Sharma *et al.,* 2022 and Shanti *et al.,* 2021). The high GCV and PCV values were found for number of branches per plant (20.97% and 21.72%), number of pods per plant (21.63% and 21.81%), biological yield per plant (23.20% and 23.49%) and seed yield per plant (23.12% and 23.57%), Chowdhury *et al.,* 2019; Shanti *et al.,* 2021 and Pawar *et al.,* 2021 also reported similar results. Moderate GCV and PCV were observed for 100 seed weight (15.67% and 16.64%) and harvest index (14.44% and 14.99%). Similar results were also recorded by (Singh *et al.,* 2013 and Sakthivel *et al.,* 2019). Low GCV and PCV were exhibited by days to 50% flowering (5.94% and 6.07%), days to maturity (1.84% and 2.09%), plant height (8.56% and 9.14%) and number of seeds per pod (4.02% and 6.04%). Similar results have also been reported for days to maturity, plant height, number of pods per plant, harvest index and seed yield per plant by (Hussan *et al.,* 2018 and Sharma *et al.,* 2021).

Heritability

Heritability is a good indicator of transmission of characters from parents to their progeny. Its estimates help in selection of genotypes from diverse genetic populations. Therefore, high values of heritability considered in suitable selection

Table 3: Estimation of genetic parameters for ten morphological characters related to yield in twenty-nine genotypes of Lentil.

Characters	Mean	Range		GCV (%)	PCV (%)	Heritability (%)	GA as percentage of mean
		Min	Max				
Days to 50% flowering	83.61	69.67	89.67	5.94	6.07	95.60	11.96
Days to maturity	115.83	112.67	119.67	1.84	2.09	77.47	3.33
Plant height (cm)	42.64	35.10	49.33	8.56	9.14	87.59	16.50
No. Of branches per plant	13.31	8.47	17.77	20.97	21.72	93.20	41.70
No. Of pods per plant	60.12	37.40	104.90	21.63	21.81	98.37	44.20
No. of seeds per pod	1.63	1.45	1.78	4.02	6.04	44.26	5.51
100 seeds weight (g)	2.55	1.65	3.47	15.67	16.64	88.60	30.38
Biological yield (g/plant)	4.69	2.96	7.89	23.20	23.49	97.50	47.18
Harvest index (%)	43.82	23.42	53.74	14.44	14.99	92.82	28.67
Seed yield (g/plant)	2.04	1.22	2.89	23.12	23.57	96.24	46.73

for a particular character in genotypes. Heritability estimates ranged from 44.26% (number of seed per pod) to 98.37% (number of pods per plant). Maximum percentage of heritability was observed for number of pods per plant (98.37%), followed by biological plant per plant (97.50%), seed yield per plant (96.24%), days to 50% flowering (95.60%), number of branches per plant (93.20%), harvest index (92.82%), 100 seed weight (88.60%), plant height (87.59%), days to maturity (77.47%) and number of seeds per pod (44.26). Similar results for days to maturity, number of pods per plant, 100 seed weight and harvest index were also discussed by (Vanave *et al.,* 2019; Bhattacharjee *et al.,* 2023).

Genetic advance

The genetic advance is a useful parameter of the efficient selection progress that can be expected as a result of exercising selection on the base population. High genetic advance as per cent of mean was recorded for number of branches per plant (41.70%), number of pods per plant (44.20%), 100 seed weight (30.38%), biological yield per plant (47.18%), harvest index (28.67%) and seed yield per plant (46.73%). While low genetic advance as a percent of mean was showed by days to 50% flowering (11.96%), days to maturity (3.33%), plant height (16.50%) and number of seeds per pod (5.55%). Similar results for number of pods per plant, plant height and seed yield per plant were also reported by (Ghimire *et al.,* 2019; Akter *et al.,* 2020).

CONCLUSION

In order to find significant variations between genotypes for a variety of parameters, such as days to 50% flowering, days to maturity, plant height and seed yield per plant, among others, the study used an analysis of variance (ANOVA). The outcomes validated the selection procedure and its suitability for crop improvement by confirming the existence of notable heterogeneity among the genotypes. The potential for genetic improvement was further highlighted by variability indicators such as mean performance, coefficient of variation, heritability and genetic progress. The mean performance across traits like days to 50% flowering and plant height showed considerable variation, suggesting that the selection of specific genotypes can lead to early maturity and improved yield. Notably, significant genotypic and phenotypic coefficient variances (GCV and PCV) for variables such as the number of branches per plant and biological yield per plant imply that these traits are less impacted by environmental factors, making them reliable targets for selection. The biological yield per plant and the number of pods per plant were found to have strong heredity, which makes them excellent candidates for selection, according to heritability estimations. great progress can be accomplished by selection, as seen by high heritability and great genetic advancement, especially in variables like the number of branches per plant and seed yield per plant. The study concludes by showing that the genotypes under evaluation have a considerable degree of genetic variability, heritability and genetic advancement, which qualifies them for breeding and selection initiatives targeted at enhancing agricultural performance. The results are in line with other studies, which supports the possibility of using focused breeding techniques to create high-yielding, early-maturing cultivars.

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Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article.

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