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ASSESSMENT OF GENETIC VARIABILITY IN INDIGENOUS COLLECTION OF LENTIL (*Lens culinaris* MEDIK.)

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ABSTRACT

The present investigation comprised 53 lentil genotypes including three checks and was laid out in an Augmented Block Design to assess the extent of genetic variability, heritability and genetic advance among yield and its contributing traits. Analysis of variance revealed significant differences among the genotypes for most of the traits studied, indicating the presence of substantial genetic variability. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for seed yield per plant, whereas moderate values were recorded for number of primary branches, number of secondary branches, number of seeds per pod, 1000-seed weight, and biological yield. High heritability coupled with high genetic advance as percent of mean was observed for number of primary branches, number of secondary branches, number of seeds per pod, 1000-seed weight, biological yield, and seed yield per plant, indicating the predominance of additive gene action and effectiveness of direct selection for these traits. The study concluded that substantial genetic variability exists among the lentil genotypes and traits such as number of pods per plant, number of seeds per pod, biological yield, and 1000-seed weight may be considered as important selection criteria for developing high yielding lentil varieties.

Key words : Variability, Heritability, PCV, GCV, Lentil.

Introduction

Lentils, scientifically known as *Lens culinaris* Medik., are a kind of bushy annual herbaceous plant of the “Leguminosae” family and subfamily “Papilionaceae” of legumes. They are frequently referred to as Masur, with a chromosomal number of $2n = 14$. They are known for their flat disc seeds that resemble lenses. Usually eaten dry (whole, split and decorticated), these seeds have a high biological content and are simple to prepare and digest. Lentils are the most traditionally produced crop among the legumes. Plant seeds are mainly consumed as dal and are used extensively as a pulse. In addition, they are utilised in salads, casseroles, soups, stews, snacks, and vegetarian meals. Unlike other pulses, it doesn't need to be pre-soaked and cooks more quickly. This contrasts with the Recommended Dietary Allowances (RDA) for adult males and females, which are 55 grams and 60 grams per day, respectively (Tewari

and Shivhare, 2016).

Materials and Methods

The present investigation was conducted at the Crop Research Centre-I (CRC-I), ITM University, Gwalior, Madhya Pradesh, which falls under the Gwalior–Chambal agro-ecological zone of Madhya Pradesh, India. The experimental material comprised 53 lentil (*Lens culinaris* Medik.) genotypes procured from the Indian Institute of Pulses Research (IIPR), Kanpur.

The genotypes were evaluated during the experimental season using an augmented design. Observations were recorded on randomly selected representative plants from each plot for various phenological, morphological, and yield-related traits. The traits studied included days to 50 per cent flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of pods per

plant, number of seeds per pod, 1000-seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g). Observations for each trait were recorded at the appropriate crop growth stage following standard procedures and the mean values of the randomly selected plants were used for subsequent statistical analysis.

Descriptive statistics were computed for all the quantitative traits under study. The statistical parameters included mean, standard deviation (SD), standard error of the mean (SE), minimum and maximum values, range, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). The analysis was performed using the augmentedRCBD package in R statistical software (RStudio) following the methodology described by Aravind *et al.* (2023). These statistical parameters were used to assess the magnitude and extent of variability present among the evaluated lentil genotypes.

Results and Discussion

The present investigation revealed the existence of substantial genetic variability among the 53 lentil genotypes for most of the quantitative traits studied, indicating ample scope for selection and crop improvement. Significant differences observed through ANOVA (Tables 1a and 1b) for traits such as days to 50% flowering, days to maturity, number of primary and secondary branches, number of pods per plant, number of seeds per pod, 1000-seed weight, biological yield and seed yield per plant confirmed the presence of considerable genetic diversity among the genotypes.

Genetic variability parameters

The parameters of genetic variability such as mean, range, coefficient of variation, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV), heritability in broad sense (%), genetic advance and

Table 1a : Analysis of Variance of Quantitative Traits in Lentil Genotypes.

Source	Df	Mean. Sq				
		Days to 50 % flowering	Days to Maturity	Number of primary branches	Number of secondary branches	Number of pods per plant
Block (ignoring Treatments)	4	14.4**	29.4*	0.3 ^{ns}	1.2**	57.1**
Treatment (eliminating Blocks)	52	12.2**	22.7*	0.5*	1.7**	32.9**
Treatment: Check	2	6.64 ^{ns}	45.6*	1.7**	2.1**	34.5**
Treatment: Test and Test vs. Check	50	12.5**	21.8*	0.5*	1.6**	32.9**
Residuals	8	1.69	7.05	0.1	0.1	2.64
CD 5%		1.06	3.13	3.79	7.74	6.43
Std. Error		0.51	0.7	0.1	0.17	0.72

^{ns} P > 0.05; * P ≤ 0.05; ** P ≤ 0.01

Table 1b : Analysis of Variance of Quantitative Traits in Lentil Genotypes.

Source	Df	Mean. Sq				
		Number of seeds per pod	1000 seed weight (g)	Biological yield (g)	Harvest index%	Yield per plant (g)
Block (ignoring Treatments)	4	0.03**	6.13**	11.6**	3.8 ^{ns}	0.2 ^{ns}
Treatment (eliminating Blocks)	52	0.1**	15**	31.2**	5.8 ^{ns}	1.1**
Treatment: Check	2	0.9**	13.3**	49.3**	5.1 ^{ns}	2.1**
Treatment: Test and Test vs. Check	50	0.1**	15**	30.4**	5.9 ^{ns}	1.1**
Residuals	8	0	0.13	1.15	4.9	0.1
CD 5%		1	4.74	0.76	0.14	1.05
Std. Error		0.04	0.47	0.7	0.33	0.13

^{ns} P > 0.05; * P ≤ 0.05; ** P ≤ 0.01

Table 2 : Mean, Range and C.V. of quantitative traits in lentil genotypes.

Trait	Mean	Range		CV
		Min	Max	
Days to 50% flowering	84.35	77.79	89.89	2.13
Days to Maturity	133.68	124.82	141.56	1.99
Number of primary branches	3.31	1.57	4.38	10.77
Number of secondary branches	9.95	8.16	12.96	2.67
Number of pods per plant	79.25	67.48	87.68	2.08
Number of seeds per pod	1.71	1.16	2.04	2.91
1000 seed weight (g)	26.82	21.55	33.04	1.39
Biological yield (g)	25.49	18.12	34.93	1.96
Harvest index	14.6	9.36	18.66	13.5
Yield per plant (g)	3.73	1.94	5.91	10.15

Table 3 : GCV and PCV of quantitative traits in lentil genotypes.

Trait	GCV	GCV category	PCV	PCV category
Days to 50% flowering	2.75	Low	3.48	Low
Days to Maturity	3.03	Low	3.62	Low
Number of primary branches	16.14	Medium	19.2	Medium
Number of secondary branches	11.9	Medium	12.19	Medium
Number of pods per plant	6.47	Low	6.78	Low
Number of seeds per pod	15.59	Medium	15.85	Medium
1000 seed weight (g)	12.62	Medium	12.69	Medium
Biological yield (g)	19.43	Medium	19.52	Medium
Harvest index %	9.71	Low	16.52	Medium
Yield per plant (g)	23.16	High	25.1	High

genetic advance as percentage of mean for each trait are presented in Tables 2, 3 and 4.

Mean and Range

The mean number of secondary branches was 9.95 with a range of 8.16 to 12.96 branches per plant. The wide variation observed among the genotypes indicated the presence of useful variability for this yield contributing trait.

The number of pods per plant ranged from 67.48 to 87.68 with a mean value of 79.25 pods. The variation observed among the genotypes suggested the availability of sufficient genetic variability for improving pod bearing capacity.

The mean value for number of seeds per pod was 1.71 and ranged from 1.16 to 2.04 seeds per pod. The variability among the genotypes indicated the possibility of selecting superior genotypes with higher seed setting ability.

The mean 1000-seed weight was recorded as 26.82 g with a range from 21.55 g to 33.04 g. The wide variation

observed among the genotypes reflected the existence of substantial diversity for seed size and weight.

Biological yield exhibited a mean value of 25.49 g and ranged from 18.12 g to 34.93 g. The wide range indicated considerable variability among the genotypes for biomass production.

Harvest index recorded a mean value of 14.60% and ranged from 9.36% to 18.66%. The observed variation suggested moderate diversity among the genotypes for partitioning efficiency of assimilates towards economic yield.

Seed yield per plant exhibited a mean value of 3.73 g with a range from 1.94 g to 5.91 g. The wide range among the genotypes indicated the presence of substantial genetic variability for yield potential and provided scope for selecting high yielding genotypes.

Genotypic and phenotypic coefficient of variance

The genotypic and phenotypic coefficient of variance of ten quantitative traits are summarised in the Table 3. The phenotypic coefficient of variation was significantly higher in magnitude than that of genotypic coefficient of variation for all the traits in the present investigation.

Days to 50% flowering exhibited low GCV (2.75%) and PCV (3.48%) values, indicating low variability among the genotypes for this trait. The small difference between GCV and PCV values suggested limited environmental influence on trait expression.

Low GCV (3.03%) and PCV (3.62%) values were observed for days to maturity, indicating comparatively low genetic variability among the genotypes. The close proximity between GCV and PCV values indicated minimal environmental effect on this trait.

Number of primary branches showed moderate GCV (16.14%) and PCV (19.20%) values, indicating moderate variability among the genotypes. The slightly higher PCV compared to GCV suggested a minor environmental influence on the trait.

Moderate GCV (11.90%) and PCV (12.19%) values were observed for number of secondary branches. The narrow difference between the two values indicated that the trait was less influenced by environmental conditions.

Number of pods per plant exhibited low GCV (6.47%) and PCV (6.78%) values, indicating low variability among the genotypes for this character. The small difference between GCV and PCV values suggested limited

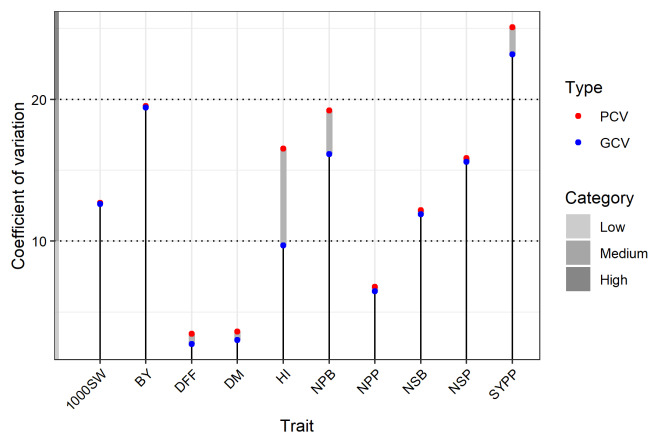


Fig. 1 : Graphical representation of PCV and GCV among different traits.

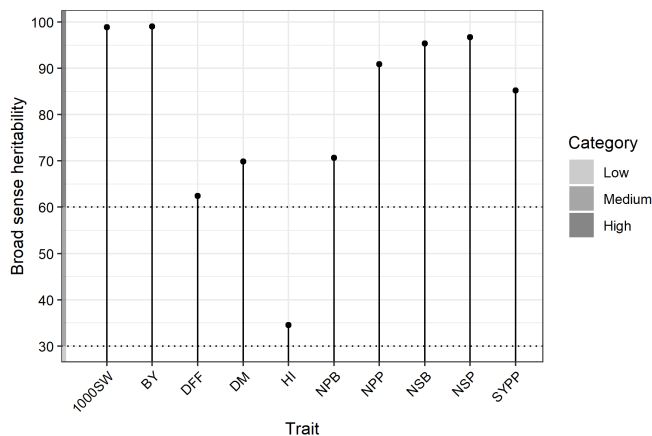


Fig. 2 : Graphical representation of heritability among different traits.

environmental influence.

Moderate GCV (15.59%) and PCV (15.85%) values were recorded for number of seeds per pod. The close correspondence between GCV and PCV values indicated that the trait expression was mainly controlled by genetic factors.

1000-seed weight exhibited moderate GCV (12.62%)

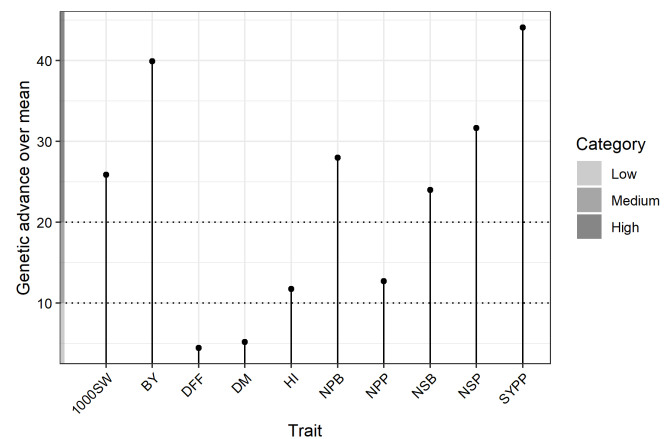


Fig. 3 : Graphical representation of genetic advance % of means among different traits.

and PCV (12.69%) values, indicating moderate variability among the genotypes. The negligible difference between GCV and PCV values suggested minimal environmental effect.

Biological yield showed moderate GCV (19.43%) and PCV (19.52%) values, indicating considerable variability among the genotypes. The close similarity between GCV and PCV values indicated negligible environmental influence.

Harvest index exhibited low GCV (9.71%) and moderate PCV (16.52%) values, indicating considerable environmental influence on the expression of this trait.

Seed yield per plant exhibited high GCV (23.16%) and PCV (25.10%) values, indicating the presence of high genetic variability among the genotypes for this important economic trait. The slightly higher PCV compared to GCV suggested a minor environmental influence on the trait.

The similar finding for most of the traits mainly in seed yield per plant, 1000 seed weight was also confirmed by Sakthivel *et al.* (2019). Similar findings for Harvest

Table 4 : Heritability and Genetic Advance (%) for Quantitative traits in Lentil genotypes.

Trait	Heritability	Heritability category	Genetic advance % of mean	Genetic advance % of mean category
Days to 50% flowering	62.41	High	4.48	Low
Days to Maturity	69.89	High	5.22	Low
Number of primary branches	70.66	High	27.99	High
Number of secondary branches	95.38	High	23.98	High
Number of pods per plant	90.86	High	12.72	Medium
Number of seeds per pod	96.74	High	31.64	High
1000 seed weight (g)	98.86	High	25.88	High
Biological yield (g)	99.07	High	39.9	High
Harvest index	34.56	Medium	11.77	Medium
Yield per plant (g)	85.17	High	44.1	High

Index, Pods per plant and seed yield per plant was confirmed by Bhattacharjee *et al.* (2023).

Heritability and genetic advance

In the present investigation, broad sense heritability, genetic advance and genetic advance (%) of mean have been estimated for different traits involved in the study are presented in Table 4. Heritability was classified as high (>60%), medium (50-70%) and low (<50%). Genetic advance as a percentage of mean was classified as high genetic advance (>20%), medium genetic advance (10%-20%) and low genetic advance (<10%).

Highest heritability was observed in biological yield (g) (99.07) followed by 1000 seed weight (g) (98.86), number of seeds per pod (96.74), number of secondary branches (95.38), number of pods per plant (90.86), yield per plant (g) (85.17), number of primary branches (70.66), days to maturity (69.89) and days to 50% flowering (62.41). Least was observed in harvest index (34.56).

Highest genetic advance as percent of mean was observed in yield per plant (g) (44.1) followed by biological yield (g) (39.9), number of seeds per pod (31.64), number of primary branches (27.99), 1000 seed weight (g) (25.88), number of secondary branches (23.98), number of pods per plant (12.72), harvest index (11.77), days to maturity (5.22) and least was observed in days to 50% flowering (4.48).

The similar results of heritability were obtained for traits days to 50% flowering, days to 50% maturity, Number of secondary branches, harvest index, pods/plant with Sowmya *et al.* (2020). Similar results of genetic advance were also recorded for seeds per pod and Seed yield per plant by Chowdhury *et al.* (2019).

Conclusion

The present investigation successfully demonstrated the existence of considerable genetic variability among lentil genotypes for yield and yield contributing traits. High heritability coupled with high genetic advance for important characters such as seed yield per plant, biological yield, number of seeds per pod, number of secondary branches and 1000-seed weight indicated the predominance of additive gene action and suggested good scope for improvement through direct selection. Overall, the study provided valuable information regarding the nature of variability in lentil and established a strong foundation for future breeding programs aimed at developing high yielding, stable, and genetically superior lentil varieties.

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