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Exploring Genetic Variability Parameters for Yield and its Contributing Traits in Lentil (*Lens culinaris* L. Medik)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

This research outlines into exploring the genetic variability, heritability, and genetic advance among 33 diverse lentil genotypes for 11 quantitative traits in the rabi season of 2022-2023 in Punjab, India. Three replications of each of the 33 genotypes of lentil were planted in a randomized block

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design. The Analysis of Variance was found significant for all the traits under study, this implies that a significant amount of variation is present among these genotypes. The estimates of PCV and GCV were found to be moderate for most of the traits under study. Heritability estimates ranged from 96.80% to 45.08%, with a high heritability observed for traits like Days to maturity, No. of primary branches per plant, No. of secondary branches per plant, seed yield per plant, No. of pods per plant, Biological yield, No. of seeds per pod, Harvest index, and Day to 50% flowering. The traits with the highest estimates of genetic advance included Seed yield per plant, No. of primary branches per plant, No. of secondary branches per plant, and No. of seeds per pod. The study identified a significant genetic variability among the lentil genotypes, characterized by high heritability and genetic advance for key traits such as Seed yield per plant, No. of primary branches per plant, No. of secondary branches per plant and No. of seeds per pod. These results point towards the presence of additive gene effects influencing the inheritance of these traits, highlighting the efficacy of simple selection methods for enhancing lentil quality focusing on these essential agronomic characteristics.

Keywords: Lentil; GCV; PCV; heritability; genetic advance.

1. INTRODUCTION

The lentil (*Lens culinaris* L. Medik.) is an annual diploid (2n=14) of the pea family (Fabaceae), known for its lens-shaped seeds. It is self-pollinating species with a haploid genome size of an estimated 4063 Mbp [1]. Typically, lentils are eaten as soup or “dahl”, a Southeast Asian meal that is popular in Bangladesh, Sri Lankan, Indian and Nepal. Lentil seed is made up of 60%–67% carbohydrates, 20%–36% protein, and 4% fat [2]. Of all the edible pulse production worldwide, lentils come in fifth place, behind chickpeas, pigeon peas, beans, and mung beans. With a global annual production of 5.6 million tons in 2021, the average yield of lentils is approximately 850-1100 kg/ha [3]. Lentils are a crucial legume crop cultivated during the winter (rabi) season in India. They account for a significant portion, around 5%, of the total area devoted to pulse cultivation as well as the overall pulse production in the country. In India, lentil production totalled 13.43 lakh tons during 2022-23, with U.P (36%), M.P (35%), West Bengal (10%), and Bihar (9%) contributing significantly, which makes up about 90% of the nation's overall cultivation of lentils [4].

The main reason for poor yield performance of lentils are the unavailability of high-yielding varieties, the cultivation of low-yielding cultivars with limited genetic bases, the impacts of various biological and environmental stresses, and the cultivation of lentils on marginal land using inadequate cultivation methods [5,6]. Reducing biotic and abiotic stresses with chemicals is not economically feasible [7]. Moreover, growing crop varieties that possess resilience to various biotic and abiotic stresses, which can be accomplished by utilizing the diverse genetic resources available, it is the most effective strategy to tackle these challenges. Conventional breeding methods and modern biotechnological approaches could enhance crop plants by either pyramiding multiple advantageous genes or introducing desirable genes into improved cultivars [8-10]. However, a major obstacle in fully realizing the yield potential of crops is the limited insight into genetic variation and the constraints of molecular techniques for genetic improvement. [7]. In the past, numerous investigations have been carried out globally to evaluate genetic diversity in lentils and other legumes using phenotypic analysis [11,12,13]. A valuable resource that contains a vast amount of genes that are desirable for crop improvement is the germplasm repository, however, this can only be used with an understanding of the extent of genetic diversity [14]. A wide range of methods involving the measurement and analysis of morphological characteristics have been employed to evaluate and categorize different genotypes across various crop species, including alfalfa, cowpea, lentil, soybean, mustard, peas, and mungbean [15–20]. The assessment of genetic diversity can be carried out by evaluating both qualitative and quantitative traits. This study aimed to unveil the untapped potential of lentil genetic resources by employing various statistical methods to analyze the genetic diversity present in agromorphological characteristics. The novel genotypes identified through this research will serve as a foundation for future lentil breeding programs, either by incorporating them into hybridization efforts or by implementing straightforward selection strategies based on multi-location field trials.

2. MATERIALS AND METHODS

The current study was conducted at the School of Agriculture, LPU, Punjab, during the *rabi* season in 2022–2023. 33 genotypes of lentil were obtained from GBPUAT, Pantnagar, Uttarakhand, and used as experimental material in the current study. The genotypes that were employed varied in terms of various morphological and quantitative traits. Three replications of each of the 33 genotypes of lentil were planted in a randomized block design. Each of the genotype was planted in a 2-meter-long row with a 30-centimeter gap between rows and a 10-centimeter gap between plants.

For recording observations five randomly selected plants from each genotype are selected in each replication for eleven quantitative traits viz., Days to 50% flowering (DFF), Days to maturity (DM), Plant height(cm) (PH), No. of primary branches/plant (NPB), No. of secondary branches/plant (NSB), No. of pods/plant (NPP), No. of seeds/pod (NSP), 100-seed weight(g) (HSW), Seed yield/ plant(g) (SY/P), Biological yield/plant(g) (BY/P), Harvest index (%) (HI).

2.1 Estimation of Genetic Parameters

2.1.1 Genotypic and phenotypic coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated based on formulas given by Burton and De Vane [21] using estimate of genotypic and phenotypic variance:

a) Phenotypic coefficient of variation

$$PCV=\frac{\sqrt{\sigma p2}}{\bar{X}} \times 100$$

b) Genotypic coefficient of variation

$$GCV=\frac{\sqrt{\sigma g2}}{\bar{X}} \times 100$$

Were,

$\bar{X}$ = General mean of the character
σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance

2.1.2 Estimation of heritability

Broad sense heritability was calculated by using the formula given by Weber and Moorthy [22]:

$$h^2 = \frac{\sigma^2_{gi}}{\sigma^2_{pi}} \times 100$$

Were,

h^2 = Heritability in broad sense
σ^2_{gi} = Genotypic variance
σ^2_{pi} = Phenotypic variance

2.1.3 Estimation of genetic advance

The expected genetic advance under selection for various characters was calculated according to the formula given by Allard et al. [23].

$$G.A._{(S)} = h^2_b \times \sigma_p \times k$$

Were,

$G.A._{(S)}$ = expected genetic advance under selection
h^2_b = heritability in broad sense
σ_p = phenotypic standard deviation
k = selection differential under 5% selection intensity
G.A. as % of mean = *G.A.* / General mean × 100

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance (ANOVA)

The analysis of variance revealed that significant differences were present among the genotypes studied for all the traits viz., DFF, DM, PH, NPB, NSB, NPP, NSP, HSW, SY/P, BY/P, HI (Table 1). Therefore, it can be observed that there exists ample amount of opportunity and potential for the identification and enhancement of a wide array of quantitative characteristics in the context of lentil cultivation. Various studies have highlighted the presence of notable genetic variations among the different lentil genotypes as documented by [24-26] in their respective research endeavors. These findings underscore the significance of genetic diversity within lentil populations, shedding light on the intricate genetic makeup and potential implications for breeding programs and crop improvement strategies. Moreover, the insights provided by these studies contribute to a better understanding of the genetic makeup of lentil genotypes, offering valuable information for future research and practical applications in the field of lentil genetics and breeding.

3.2 Genetic Variability Parameters

Genetic variability parameters like PCV, GCV, ECV, heritability, genetic advance and genetic value as % mean for different traits under study are given in Table 2.

Table 1. ANOVA for various traits under study in lentil

S. No.	Character	Mean sum of squares		
		Replications	Genotypes	Error
1	DFF	9.36	70.72**	10.87
2	DM	22.98	222.99**	14.11
3	PH	2.24	16.38**	3.68
4	NPB	0.09	0.70**	0.33
5	NSB	0.006	5.50**	0.059
6	NPP	3.49	63.98**	2.26
7	NSP	0.001	0.11**	0.014
8	HSW	0.002	0.015**	0.004
9	SY/P	0.00	0.026**	0.001
10	BY/P	0.02	0.37**	0.014
11	HI	2.54	15.10**	1.97

** & ** represent significant at 5% and 1%*

Table 2. Genetic Parameters for various traits under study in lentil

S.No	Character	Mean	PCV (%)	GCV (%)	ECV (%)	H^2 (%)	GA	GAM (%)
1	DFF	77.7	7.13	5.74	4.24	64.72	7.40	9.51
2	DM	117.03	7.81	7.13	3.21	83.14	15.67	13.39
3	PH	30.15	9.33	6.82	6.37	53.44	3.09	10.27
4	NPB	3.09	16.39	15.28	5.94	86.83	0.90	29.33
5	NSB	11.33	12.08	11.88	2.15	96.80	2.73	24.09
6	NPP	45.41	10.52	9.98	3.31	90.09	8.86	19.53
7	NSP	1.42	15.16	12.66	8.35	69.66	0.30	21.76
8	HSW	2.07	4.41	2.96	3.27	45.08	0.08	4.10
9	SY/P	0.88	10.83	10.55	2.41	95.01	0.18	21.20
10	BY/P	3.43	10.67	10.08	3.50	89.23	0.67	19.62
11	HI	25.75	9.78	8.12	5.45	68.91	3.57	13.89

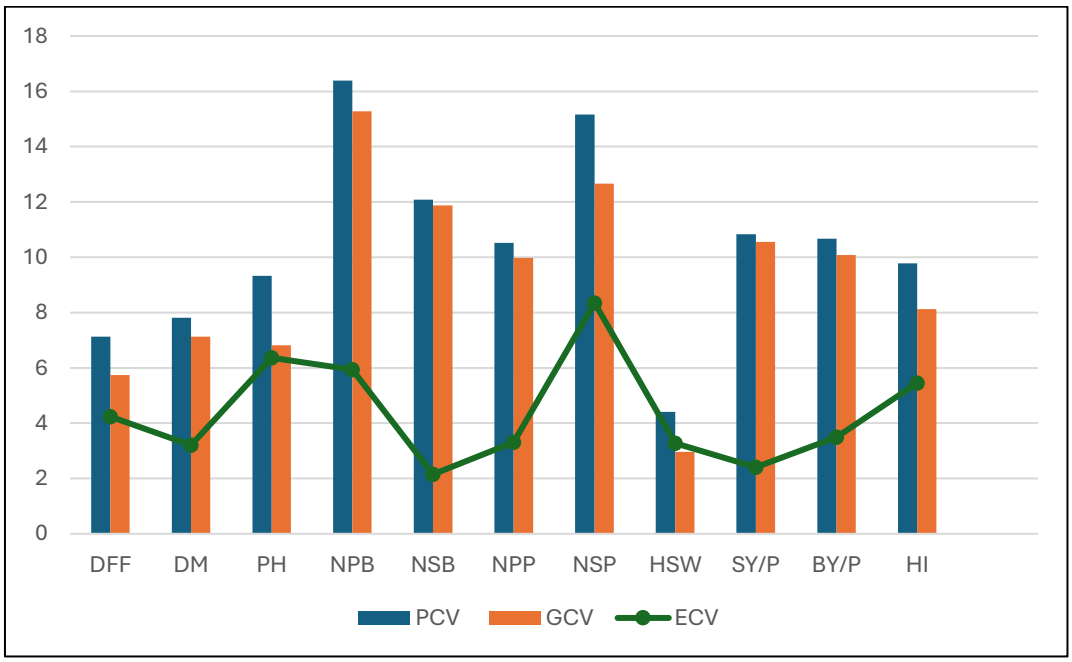

Fig. 1. Graphical representation of comparative data for GCV, PCV & ECV

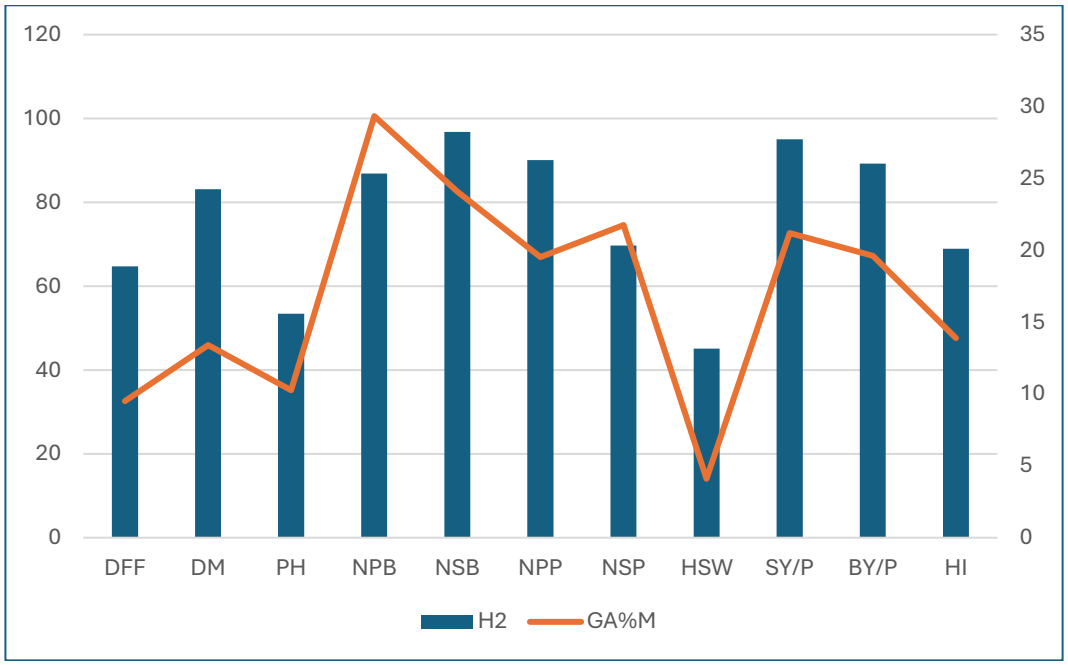

Fig. 2. Graphical representation of comparative data for H^2 & GA%M

3.2.1 Estimation of coefficient of variation

Moderate values of PCV and GCV was recorded for SY/P, NPB, NSP, NSB & BY/P, Similar studies of moderate PCV and GCV had been recorded for some of these traits by [27]. Low PCV and GCV was recorded for other traits like, DFF, DM, PH, HSW, HI. Similar studies of low PCV and GCV for these traits had been reported by [28,29].

For all traits studied, the GCV was lower than the PCV, whereas the PCV was higher than the ECV. Except for 100-seed weight, the GCV was greater than the ECV for all traits indicating a preponderance of heritable variation.

3.2.2 Estimation of heritability and genetic advance

The heritability estimates ranged from 96.80 to 45.08%. High heritability was found for traits like NSB (96.80%), SY/P (95.01%), NPP (90.09%), BY/P (89.23%), NPB (86.83%), DM (83.14%), NSP (69.66%), HI (68.91%), DFF (64.72%). Similar studies of high heritability for these traits were reported by [26,30]. While Moderate heritability was found for PH (53.44%), HSW (45.08%). High values of heritability indicates that the traits are less influenced by environmental conditions and controlled by additive gene effect, we can improve these traits by selection. Furthermore, heritability estimation is useful to determine the amount of heritable variations transmitted from parents to offsprings.

Estimation of genetic advance varied from 29.33 to 4.10%. The highest genetic advance value was recorded for NPB (24.09%), NSB (29.33%), SY/P (21.20%), NSP (21.76%). Similar studies of high heritability were reported by [24,31]. Moderate Genetic advance was recorded for BY/P (19.62%), NPP (19.53%), HI (13.89%), DM (13.39%), PH (10.27%), DFF (9.51%). while lowest value of genetic advance was recorded for HSW (4.10%).

High heritability combined with high genetic advance was found for several important traits like SY/P, NPB, NSB, NSP. High heritability combined with moderate genetic advance was found for NPP, BY/P, HI, PH, DFF. While high heritability with low genetic advance was found for rest of the traits. Selecting for traits with high heritability and genetic advance will be very effective and offer greater potential for improvement through selection by fixing additive genes, On the other hand, high heritability and low genetic advance indicates the prevalence of non-additive gene action because of strong environment influence. The study revealed that highly significant differences among the genotypes were observed for all the traits and presence of high amount of variability makes the generation of transgressive segregants possible by hybridization.

4. CONCLUSION

This study demonstrated significant genetic variability among 33 lentil genotypes for yield and yield-related traits. High heritability coupled with high genetic advance was found for seed yield, number of branches, and seeds per pod, indicating predominance of additive gene effects. Moderate estimates were observed for pods per plant, biological yield, harvest index. Promising genotypes identified can serve as parents for developing improved lentil varieties with desirable trait combinations. The genetic parameters estimated will guide effective selection strategies in lentil breeding programs targeting yield enhancement.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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