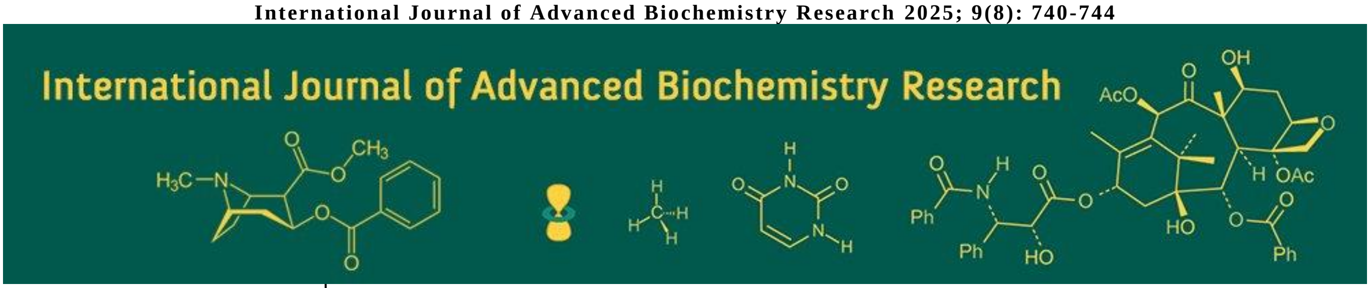
International Journal of Advanced Biochemistry Research 2025; 9(8): 740-744



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; 9(8): 740-744
www.biochemjournal.com
Received: 13-05-2025
Accepted: 16-06-2025

Anupriya Rana
Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

RK Panwar
Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

SK Verma
Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

Anju Arora
Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

Shubham Kumawat
Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

Ayushi Mehra
Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

Anu George
Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

Manavi Bisht
Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

Khyati Sengar
Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

Corresponding Author:
RK Panwar
Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India

Assessment of genetic variability, heritability and genetic gain for agro-morphological traits in lentil (*Lens culinaris* Medik.)

Anupriya Rana, RK Panwar, SK Verma, Anju Arora, Shubham Kumawat, Ayushi Mehra, Anu George, Manavi Bisht and Khyati Sengar

DOI: https://www.doi.org/10.33545/26174693.2025.v9.i8j.5304

Abstract

This study was conducted at the N.E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, India, during the *rabi* seasons of 2024-2025, to study the agro-morphological, genetic variability, heritability, expected genetic advance and inter-relationship of ten yield attributing traits for 50 genotypes. The genotypes showed highly significant ($p<0.01$) variations for all of the studied traits. For all the traits, analysis of variance indicated substantial genetic variability among genotypes. These characters also had higher phenotypic co-efficient of variation (PCV) than those of the corresponding genotypic co-efficient of variation (GCV). GCV ranged from 3.36% (days to maturity) to 43.99% (seed yield). High heritability (>75%) was recorded for seed yield, harvest index, and seeds per pod. Traits such as seed yield, harvest index, and biological yield exhibited both high heritability and high genetic advance as a percentage of mean. These results point towards the presence of additive gene effects influencing the inheritance of these traits, highlighting the efficacy of simple selection methods for yield enhancing focusing on these essential agronomic characteristics.

Keywords: Lentil, GCV, PCV, heritability, genetic advance, genetic advance mean

Introduction

Lentil (*Lens culinaris* L. Medik.) is a self-pollinated, annual diploid legume crop (2n = 14) belonging to the family Fabaceae, valued for its distinctive lens-shaped seeds and high nutritional content. With a haploid genome size of about 4, 063 Mbp (Kumar *et al.*, 2014) [13], lentil is one of the earliest domesticated pulse crops and continues to play a vital role in global food systems. Its seeds contain 60-67% carbohydrates, 20-36% protein, and around 4% fat (Johnson *et al.*, 2020) [11], making it a rich source of plant-based protein and micronutrients. In South Asian countries such particularly in India, Bangladesh, Nepal, and Sri Lanka, lentils are an integral component of daily diets, featuring prominently in traditional dishes such as "dahl" and soups.

On a global scale, lentil ranks fifth among pulse crops, following chickpea, pigeon pea, common bean, and mung bean occupying around 5.0 million hectares. And the top 5 countries are Canada, India, Australia, Türkiye and Nepal (FAO, 2020) [9]. In Nepal, lentil is the principal pulse crop, accounting 62.64% of the total legume cultivation area and 64.35% of total production (Darai *et al.*, 2017) [7]. In India, lentil is the second most important *rabi* pulse after chickpea, cultivated during the winter season from November to March. The country accounts for nearly 40% of the global lentil cultivation area and about 28% of global output. The country contributes nearly 40% of the world's lentil area and about 28% of total production, with a cultivated area of approximately 1.94 million hectares and an annual output of 1.65 million tons (FAO, 2024) [8]. The bulk of production comes from Madhya Pradesh, Uttar Pradesh, West Bengal, and Bihar, which together account for almost 90% of national output.

Despite it's prominence, India's average lentil productivity (766 kg/ha) remains below the global mean (1, 015 kg/ha). Major productivity constraints include the use of low-yielding varieties with narrow genetic bases, high susceptibility to diseases and insect pests, sensitivity to drought and temperature extremes, and cultivation on marginal lands with limited input use.

Chemical-based stress management strategies are often uneconomical and environmentally unsustainable, underscoring the need for genetic improvement as a sustainable alternative. Harnessing the existing genetic variability within lentil germplasm offers a viable pathway to developing high-yielding and stress-resilient cultivars.

Genetic variability forms the foundation of any crop improvement program. Effective crop improvement hinges on the selection of genetically diverse parents for hybridization, guided by an understanding of genetic parameters such as variance, heritability, coefficient of variation, and genetic advance (Idris, 2012) [10]. Yield, a complex phenotypic trait, is influenced by multiple contributing traits, (e.g., branches per plant, pods per plant, seeds per pod, 100-seed weight, plant height), and knowledge of their genetic architecture is essential for designing efficient breeding strategies. Biometrical analyses, including variance, standard error, and heritability estimates, provide insights into the extent of genetic variability and environmental influence within a population. High heritability combined with substantial genetic advance typically indicates additive gene action, suggesting that traits can be improved effectively through simple selection and enable breeders to predict genetic gains through selection by identifying traits with high heritability for targeted improvement. Well-characterized Germplasm repositories, rich in diverse genetic resources, are invaluable for crop improvement, provided the extent of genetic variability is well-characterized. This study aims to evaluate the genetic variability and interrelationships among morphological traits and yield in lentil to identify key attributes contributing significantly to yield variation. By characterizing these traits, the research seeks to pinpoint those with the greatest potential for enhancement through targeted breeding programs, thereby facilitating the development of high-yielding lentil varieties.

Materials and Methods

Experimental Site Design and Material

The present study was conducted during the *rabi* seasons of 2024-25 at the N.E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Uttarakhand. The experimental material consisted of 50 lentil genotypes mentioned in Table.1 provided by G.B. Pant University of Agriculture and Technology, Pantnagar. The genotypes that were employed varied in terms of various morphological and quantitative traits. Two replications of each of the 50 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.

Data on Yield and Yield Contributing Components

For recording observations five randomly selected plants from each genotype are selected in each replication for ten quantitative traits viz., Days to 50% flowering (DFF), Days to maturity (DM), Plant height(cm) (PH), No. of primary branches/plant (NPB), 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).

Table 1: List of genotypes

S. No	Genotype
1.	ILL7663
2.	PL8/PL063
3.	K75
4.	DPL58
5.	KLS218
6.	PL7/PL024
7.	PL639
8.	LL875
9.	L4147
10.	L4188
11.	PL406
12.	DPL15
13.	LL864
14.	DPL62
15.	PL234
16.	PL5
17.	PL4
18.	L4076
19.	FLIP-96-51
20.	PRECOZ
21.	PL-6
22.	LL-1161
23.	L4710
24.	L4603
25.	LL1374
26	LL1122
27	IC201738
28	ILWL 118
29	PL9
30	LL1373
31	L4727
32	BANKA LOCAL
33	IPL321
34	LL1694
35	TITVA
36	LL931
37	VL514
38	PL14
39	PL15
40	ILWL 35
41	PL029
42	PL02
43	IC22670
44	PL12
45	PL010
46	IC201648
47	IC201675
48	IC201707
49	IC296889
50	IC201799

Statistical analysis

MS Excel 2007 was used to process experimental data and R-stat 3.5.was used to analyze it. The PCV and GCV of (Singh and Chaudhary, 1985) [18], Heritability (in the broad sense) (Johnson *et al.*, 1955) [12], genetic advance (Burton, 1952) [5], and genetic advances as percentage of the mean (Johnson *et al.*, 1955) [12] were all calculated by using the following formulas:

a) Phenotypic coefficient of variation

$PCV = \sqrt{\sigma p^2}/\bar{X} \times 100$b)

b) Genotypic coefficient of variation

$GCV = \sqrt{\sigma g^2}/\bar{X} \times 100$

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

Estimation of heritability

Broad sense heritability was calculated by using the formula given by Weber and Moorthy (1952) [19]

Heritability (h^2) = $\sigma^2{}_{gi}/\sigma^2{}_{pi} \times 100$

Estimation of genetic advance

The expected genetic advance under selection for various characters was calculated according to the formula given by Allard *et al.* 1960 [1].

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

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

Results and Discussion

Analysis of Variance

The analysis of variance (ANOVA) demonstrated that all evaluated traits exhibited highly significant differences ($p \leq 0.01$) among the genotypes studied for all the traits *viz.*, DFF, DM, PH, NPB, NPP, NSP, HSW, SY/P, BY/P, HI (Table.2), indicating plentiful genetic variation in the material studied. Such diversity is necessary for effective breeding and selection as reported in previous crop improvement research (Brady, 2015) [15]. The coefficient of variation (CV%) values indicated the precision and stability of trait measurement. Phenological traits such as DM (2.35%), DFF (5.01%), and NSP (8.67%) showed notably low CVs, indicating minimal environmental influence and high measurement reliability. These genetically controlled traits are well suited for early-generation selection (Moore, 2023) [16].

Moderate CV values were recorded for morphological traits like plant height (8.74%) and primary branches per plant (12.33%), reflecting acceptable stability. These traits contribute to plant architecture and biomass formation, which are important considerations in ideotype breeding (Araújo, 2003) [2]. Yield-related traits including NPP (15.44%), BY/P (16.33%), HI (17.60%), and particularly SY/P (21.84%) exhibited higher CVs, revealing greater environmental sensitivity. Despite this, significant genotypic effects for these traits confirm the presence of exploitable genetic variability, underscoring the necessity of multi-environment testing to identify stable, high-yielding genotypes (Brady, 2015; FAO, 2024) [15, 8].

Genetic Variability

The evaluation of genetic variability parameters including GCV, PCV, ECV, heritability in the broad sense, genetic advance (GA), and GAM provides critical insights into the inheritability and improvement potential of traits in a breeding program. In this study, the traits exhibited a range of variability and heritability estimates that reflect their genetic control and environmental influence.

Table 2: ANOVA for various traits under study in lentil

Trait	Rep. (DF = 1)	Entries (DF = 49)	Error (DF = 49)	CD 5%	CD 1%	C.V. (%)
DFF	7.8400 NS	49.1135**	14.8604	7.7484	10.331	5.0142
DM	26.0100 NS	43.0141 **	8.4998	5.86	7.8134	2.359
PH	12.3201 NS	72.6610 **	14.0119	7.5239	10.032	8.7379
PB	0.3469 NS	0.7226 **	0.1269	0.7161	0.9548	12.3285
PPP	92.1600 NS	260.8808 **	52.2008	14.522	19.363	15.4447
SPP	0.0497 NS	0.1636 **	0.022	0.2984	0.3979	8.6744
HSW	0.0313 NS	0.3926**	0.0723	0.5406	0.7208	11.9802
BY	0.8409 NS	4.9060**	0.8686	1.8733	2.4977	16.3312
SY	0.0161 NS	1.4816**	0.1626	0.8104	1.0806	21.843
HI	0.014 NS	0.0205**	0.00205	0.1001	0.1335	17.6028

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

Phenological traits such as DFF and DM showed moderate GCVs (5.38% and 3.36%, respectively) and relatively low PCVs, resulting in narrow differences between GCV and PCV, indicating limited environmental effect on these traits. The heritability estimates for these traits were moderate to high (53.54% for DFF and 67.00% for DM), and the genetic advance as percentage of mean ranged from 5.67% to 8.11%, suggesting that selection for these traits would be moderately effective and reliable in early generations (Bhagasara *et al.*, 2017; Kumar *et al.*, 2018) [3, 14].

Morphological traits such as PH and PB demonstrated higher GCVs (12.64% and 18.90%) and PCVs (15.37% and 22.59%), with moderate environmental coefficients of variation, illustrating moderate environmental influence. Heritability was high for both traits (>67%), and GAM was substantial (21.43% and 32.58%), indicating these traits are primarily governed by additive gene effects and can be effectively improved through selection (Chacko *et al.*, 2023; Meena *et al.*, 2017) [6, 3].

Yield-related traits including PPP, SPP, HSW, BY, SY, and HI displayed high GCV and PCV values, reflecting considerable genetic variability but also notable environmental influence as seen by relatively high ECV values. Heritability estimates for these traits ranged from approximately 66% to 80%, indicating good genetic control. GAM was particularly high for SY/P (81.18%) and HI (61.10%), signifying that these traits hold significant potential for improvement via selection. The high magnitude of GA coupled with high heritability suggests additive gene action predominates, which is essential in breeding for quantitative traits like yield (Meena *et al.*, 2017; Bhagasara *et al.*, 2017; Chacko *et al.*, 2023) [3, 6].

Overall, the close proximity of GCV and PCV values in many traits suggests minor environmental influence, underscoring the genetic basis of variability. Traits with high heritability and GA, especially seed yield and its components, are promising candidates for selection in breeding programs aimed at improving productivity. This aligns with prior studies highlighting the importance of combining genetic variability and heritability measures to predict the efficiency of selection strategies (Bhagasara *et al.*, 2017) [3].

Table 3: Estimation of genetic parameters for quantitative traits in fifty lentil genotypes

Trait	GCV	PCV	ECV	Heritability (%)	Genetic Advance	GA as% of Mean
DFF	5.383	7.3565	5.0142	53.5423	6.24	8.114
DM	3.3613	4.1064	2.359	67	7	5.6677
PH	12.6433	15.3686	8.7374	67.6783	9.18	21.4265
PB	18.9051	22.5949	12.3744	70.0065	0.94	32.5849
PPP	21.8356	26.7457	15.4447	66.6535	17.17	36.7235
SPP	15.5013	17.7831	8.7149	75.9836	0.48	27.8352
HSW	17.8228	21.475	11.9802	68.8786	0.68	30.4709
BY	24.8973	29.7755	16.3312	69.9172	2.45	42.8856
SY	43.9956	49.1196	21.843	80.2251	1.5	81.1768
HI	33.5053	37.8479	17.6028	78.3688	0.17	61.1015

Estimation of heritability and genetic advance

Heritability in a broad sense estimates the proportion of total phenotypic variance attributable to genetic variance and serves as an indicator of how reliably a trait can be passed from parents to offspring. In this study as depicted in Fig.1, heritability values ranged from moderate to high, with SY/P showing the highest heritability (80.23%), followed by HI (78.37%), and NSP (75.98%). High heritability coupled with a high GAM indicates that these traits are predominantly controlled by additive gene effects, making them excellent candidates for selection. For example, SY/P's GAM was 81.18%, signifying substantial expected improvement if selection is based on phenotypic performance. Traits with moderate heritability such as DFF (53.54%) also exhibited modest GA, suggesting selection would be somewhat effective but may be influenced by environmental factors. Traits with high heritability and GA (e.g., SY/P, HI, BY/P) are more responsive to selection and should be prioritized in breeding programs (Bhagasara *et al.*, 2017; Meena *et al.*, 2017) [3]

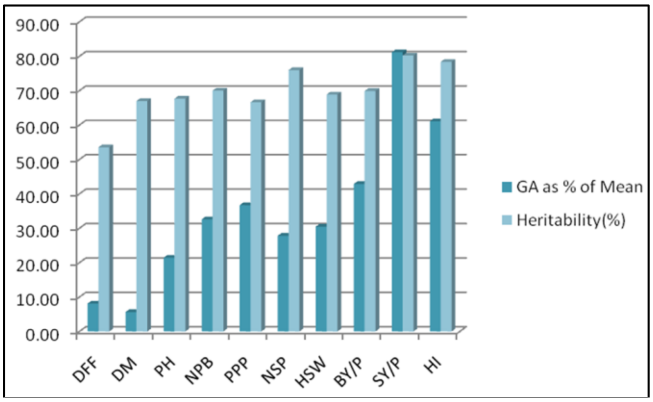


Fig 1: Graphical representation of comparative data for H^2 & GA as % of Mean

Conclusion

The present investigation evaluated 50 genotypes for ten agro-morphological and yield-related traits to assess variability, heritability, and genetic advance. Phenological traits (DFF, DM) exhibited low coefficients of variation (CV = 2.36-5.01%), suggesting stable expression and high experimental precision. In contrast, yield and yield-contributing traits, especially SY/P (CV = 21.84%), recorded higher variability, implying greater environmental influence.

GCV were highest for SY/P (43.99%), followed by HI (33.51%) and BY/P (24.90%), indicating wide genetic variation. High heritability coupled with high GA as a percentage of mean was observed for SY/P (80.22%, GA = 81.18%), HI (78.37%, GA = 61.10%), and BY/P (69.92%, GA = 42.89%), suggesting the predominance of additive gene action and scope for improvement through direct selection. Moderately high heritability coupled with moderate GAM was observed in traits like NPP, HSW, and NSP, which also recorded moderate GCV and PCV values. These traits can respond to selection, but progress may be slower compared to traits with higher genetic variability and heritability. The findings highlight SY/P, HI, NSP, and BY/P as key traits for selection in breeding programs aimed at yield enhancement

References

1. Allard RW. Principles of plant breeding. New York: John Wiley & Sons; 1960. p. 224-233.
2. Araújo AP. Statistical analysis of growth curves in plant breeding. Euphytica. 2003;31(1):51-64.
3. Bhagasara VK, Ranwah BR, Meena BL, Khan R. Estimation of GCV, PCV, heritability and genetic gain for yield and its related components in sorghum (*Sorghum bicolor* L. Moench). International Journal of Current Microbiology and Applied Sciences. 2017;6(5):1015-1024. doi:10.20546/ijcmas.2017.605.110
4. Brady SM. Reassess the t test: Interact with all your data via ANOVA. The Plant Cell. 2015;27(8):2047-2049. doi:10.1105/tpc.15.00586
5. Burton GH. Quantitative inheritance in grasses. Proceedings of the 6th International Grassland Congress. 1952;1:277-283.
6. Chacko A, Jayalekshmy VG, Shahiba AM. Studies on PCV, GCV, heritability, and genetic advance in rice genotypes for yield and yield components. International Journal of Plant & Soil Science. 2023;35(16):324-330. doi:10.9734/ijpss/2023/v35i163266
7. Darai R, Sarker A, Sah RP, Pokhrel K, Chaudhary R. AMMI biplot analysis for genotype × environment

interaction on yield trait of high Fe content lentil genotypes in Terai and mid-hill environment of Nepal. Annals of Agricultural and Crop Sciences. 2017;2(1):1026-1034.

8. Food and Agriculture Organization of the United Nations. Analysis of variance (ANOVA) and estimation of variance components in plant breeding. Rome: FAO; 2024. Available from: https://www.fao.org/4/y4391e/y4391e07.htm
9. Food and Agriculture Organization of the United Nations. FAOSTAT. Rome: FAO; 2020. Available from: https://www.fao.org/faostat/en/#data/QCL
10. Idris A. Genetic variability and interrelationship between yield and yield components in some rice genotypes. American Journal of Experimental Agriculture. 2012;2(2):233-239. doi:10.9734/ajea/2012/961
11. Johnson N, Johnson CR, Thavarajah P, Kumar S, Thavarajah D. The roles and potential of lentil prebiotic carbohydrates in human and plant health. Plants, People, Planet. 2020;2(4):310-319.
12. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 1955;47(7):314-318.
13. Kumar S, Hamwieh A, Manickavelu A, Kumar J, Sharma TR, Baum M. Advances in lentil genomics. In: Legumes in the omic era. New York: Springer; 2014. p. 111-130.
14. Kumar S, *et al*. Genetic variability, heritability, and genetic advance in rice mutant lines. The Pharma Journal. 2018;10(10S):128-248.
15. Meena BL, Das SP, Meena SK, Kumari R, Devi AG, Devi HL. Assessment of GCV, PCV, heritability and genetic advance for yield and its components in field pea (*Pisum sativum* L.). International Journal of Current Microbiology and Applied Sciences. 2017;6(5):1025-1033. doi:10.20546/ijcmas.2017.605.111
16. Moore K. The analysis of variance (ANOVA). Ames (IA): Iowa State University Press; 2023. Available from: https://iastate.pressbooks.pub/quantitativeplantbreeding/chapter/the-analysis-of-variance-anova/
17. Narkhede G. Genetic variability in plant breeding. LinkedIn Articles. 2025.
18. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetics analysis. Rev ed. New Delhi: Kalyani Publishers; 1985.
19. Weber CR, Moorthy HR. Heritable and non-heritable relationship and variability of oil content and agronomic characters in the F_2 generation of soybean crosses. Agronomy Journal. 1952;44(4):202-209.