



Exploring Genetic Variability Parameters for Yield and Quality Traits in Urdbean Genotypes and Its Triple Test Cross F₁ Hybrids

Tarun Rathore^{a++*}, R.K. Yadav^{a#}, Sarvendra Kumar^{b#}, Lokendra Singh^{a†}, Geeta Rai^{b‡} and C.L. Maurya^{c#}

^a Department of Genetics and Plant Breeding, College of Agriculture, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.) 208002, India.

^b Department of Genetics and Plant Breeding, Legume Section, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.) 208002, India.

^c Department of Seed Science and Technology, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.) 208002, India.

Authors' contributions

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

Article Information

DOI: <https://doi.org/10.9734/jeai/2024/v46i72586>

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc. are available here: <https://www.sdiarticle5.com/review-history/118711>

Original Research Article

Received: 08/04/2024

Accepted: 12/06/2024

Published: 14/06/2024

⁺⁺ Ph.D. Research Scholar;

[#] Professor;

[†] Associate Professor;

[‡] Research Associate;

*Corresponding author: E-mail: tarunrathore777@gmail.com;

ABSTRACT

Pulses play a vital role in providing nutrition to billions of individuals globally. Improving yield in the urdbean faces a significant challenge due to its narrow genetic base and limited exploitable variation. This research explores the genetic variability, heritability, and genetic advance among 111 diverse lines of urdbean. 27 lines, three testers, and Eighty-one F₁ hybrids were grown in a Randomized Block Design (RBD) with three replications during Kharif 2023 at the Crop Experimental Research Farm of Chandra Shekhar Azad University of Agriculture and Technology, Kalyanpur, Kanpur (U.P.). The analysis of variance for parents (27 lines and three testers) and their 81 triple test cross hybrids indicated highly significant genotypic differences across all traits under study. The PCV was higher compared to GCV for all the traits, While Maximum GCV and PCV were observed for primary branches per plant, number of pods per plant, seed yield per plant, biological yield per plant, and harvest index. Broad-sense heritability (h^2_b) was high for all the traits examined ranging from 73.27% to 98.05%. Further, high heritability coupled with high genetic advance as percent over mean were recorded for all the traits except day to 50% flowering, day to 75% maturity, and protein content, where high heritability is observed with moderate genetic advance. These findings suggest the involvement of additive genetic effects in shaping the inheritance of these traits and phenotypic selection of these characters would be effective for further breeding purposes.

Keywords: Genetic advance; genotypic; heritability; phenotypic; variability.

1. INTRODUCTION

“Urdbean [*Vigna mungo* (L). Hepper] widely known as blackgram, “mash kalai”, urd, or urad. It is a self-pollinated diploid grain legume ($2n=2x=22$), belongs to the family Fabaceae or Leguminosae, and subfamily Faboideae or Papilionoideae or Papilionaceae with a small genome size estimated to be 574 Mbp” [1]. “The wild progenitor of blackgram domesticated in India is believed to be *Vigna mungo* var. *silvestris*” [2,3]. “Among pulses, Urdbean is the fourth most important pulse crop after chickpeas, pigeon peas, and lentils. It is widely consumed as dry whole grain or split grain known as daal

and as unfermented and fermented flour” [4]. “It contains a high content of protein (25-28%), carbohydrates (62-65%), fiber (3.5-4.5%), ash (4.5-5.5%), oil (0.5-1.5%), as well as essential amino acids such as lysine, and vitamins including thiamine, niacin, and riboflavin, along with minerals like iron and phosphorus” [5]. “Black gram seeds include more protein and lysine content than cereals” [6]. In India, about 92% (percent) of urdbean production comes from 9 states Madhya Pradesh, Rajasthan, Uttar Pradesh, Tamil Nadu, Andhra Pradesh, Maharashtra, Jharkhand, Gujarat, and Karnataka (Fig. 1).

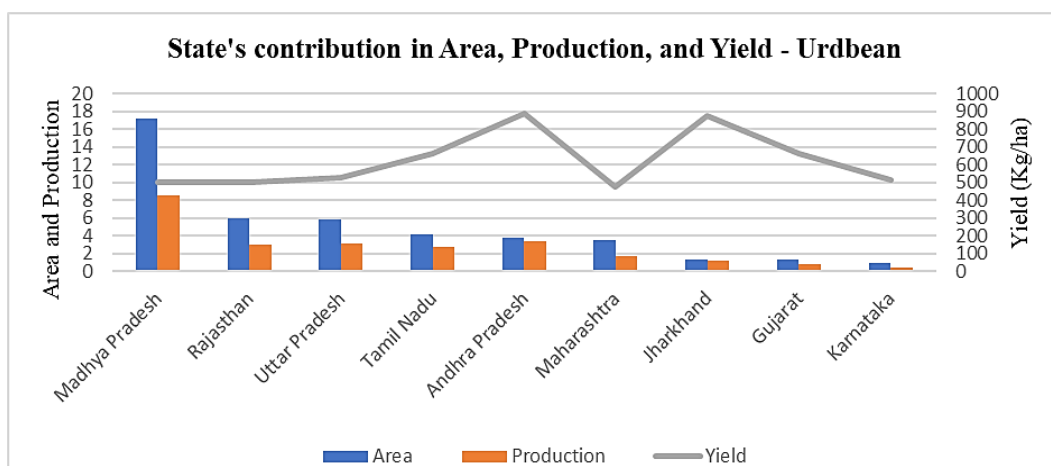


Fig. 1. Area-lakh ha, production-lakh tons, Yield-kg/ha.

“The urbean production of India was 2.78 million tonnes from the acreage of 4.63 million hectares with a productivity of 600 Kg/ha”. (Agricultural Statistics Division, DES, MoAF&W, 2022) [7]. Despite its great importance, the productivity of urbean in India continues to be low due to several factors including limited genetic diversity for developing high-yielding varieties, lack of variability, inadequate plant ideotype, suboptimal crop management, weed infestation, and vulnerability to both biotic and abiotic stresses [8]. “The achievement of high yield mainly depends on the magnitude of yield-contributing traits and the nature of genetic variability present in the crop” [9]. To increase the productivity and production of this crop, developing new high-yielding genotypes is a prime goal of urbean breeding [10]. Understanding the inheritance of various quantitative and qualitative traits by estimating genetic parameters, such as phenotypic and genotypic coefficients of variability, heritability, and genetic advance, is crucial for establishing selection criteria to improve seed yield and effective breeding programs. With these factors in mind, this present investigation aims to assess variability, broad-sense heritability, and genetic advance to identify superior black gram genotypes and F₁ TTC hybrids for future application in breeding programs or through straightforward selection strategies based on multi-location field trials.

2. MATERIALS AND METHODS

The present investigation was conducted during *Kharif, 2023* at the Crop Experimental Research Farm of Chandra Shekhar Azad University of Agriculture and Technology, Kalyanpur, Kanpur (U.P.). The material for the investigation comprised 111 diverse lines of urbean, namely; Shekhar-1, Shekhar-2, KU-14-1, KU-16- 4, KU 17-4, KU-17-9, KU-19-10, KU-20-12, KU-48, KU-88-1, KU-88-31-2, KU-99-12, KU-99-19, KU-96-05, KU-321, KU-333, KU-717, KUG-818, KPU-1720-140, Azad-2, IPU-17-1, IPU-12-5, IPU-13-3, PU-13-15, Pant-431, SBC-50, and VBG-13-003. These lines were crossed with three testers *viz.*, KU-96-7 (L₁), Azad-3 (L₂), and F₁ of KU-96-7 × Azad-3 *i.e.*, L₃, to produce 81 triple test cross (TTC) progenies. TTC progenies in the form of 54 single crosses and 27 three-way crosses. Therefore, 27 lines, three testers, and Eighty-one F₁ hybrids were grown in a Randomized Block Design (RBD) with three replications respectively. Standard production techniques were followed to get a healthy crop. The data on

12 quantitative traits *viz.*, days to 50% flowering (DFF), days to 75% maturity(DM), plant height (cm) (PH), number of primary branches per plant (NPB), pods per plant (NPP), pod length (cm) (PL), seeds per pod (NSP), seed yield per plant (g) (SY/P), biological yield per plant (g) (BY/P), and harvest index (%),(HI), 100-seed weight (HSW), and protein content (%) (PC) were recorded.

2.1 Analysis of Variance for Randomized Block Design

The data for the various characters were analyzed according to Panse and Sukhatme [11]. The analysis of variance followed the linear model proposed by Fisher [12].

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = phenotypic observation of the i^{th} genotype in the j^{th} replication.

μ = general population mean

g_i = effect of i^{th} genotype.

r_j = effect of j^{th} replication.

e_{ij} = random error (error associated with i^{th} genotype in the j^{th} replication).

2.2 Estimation of Genetic Parameters

2.2.1 Genotypic and phenotypic coefficient of variation

The various genetic estimates *viz.*, GCV and PCV were calculated by adopting the formulae given by Burton [13],

a. Genotypic Coefficient of Variation: GCV (%)

$$= \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100$$

b. Phenotypic Coefficient of Variation: PCV (%)

$$= \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100$$

Where,

σ^2_g = Genotypic variance.

σ^2_p = phenotypic variance.

\bar{x} = General mean of the character under study.

2.2.2 Estimation of Heritability (h²b) broad sense:

Heritability in a broad sense was calculated using the formula suggested by Allard [14].

$$h^2b (\%) = \frac{\sigma^2g}{\sigma^2p} \times 100$$

where,

h^2b = Heritability in a broad sense;

σ^2g = Genotypes variance;

σ^2p = Phenotypic variance.

2.2.3 Estimation of genetic advance

It was computed with the help of the following formula given by Johnson *et al.*, [15].

$$GA = K \cdot h^2 \cdot \sigma_p \text{ or } GA = K \cdot \frac{\sigma^2g}{\sigma^2p} \cdot \sqrt{\sigma^2p}$$

Where,

G.A. = Genetic advance

K = Selection differential (K = 2.06 at 5% selection intensity)

h^2 = Coefficient of heritability estimates.

σ_p = Phenotypic standard deviation.

Genetic advance as a percentage of mean:

The genetic advance as a percentage of the mean to facilitate comparison between different characters was estimated as suggested by Johnson *et al.*, [15].

$$\text{Genetic advance as \% of mean} = \frac{G.A}{\bar{x}} \times 100$$

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance (ANOVA)

The analysis of variance revealed significant differences in the 27 parents, 3 Testers, and the 81 cross combinations for all the traits, indicating that the parents were genetically diverse and sufficient variability was generated through hybridization *i.e.*, sufficient genetic variability among crosses for all the traits, *viz.*, DFF, DM, PH, NPB, NPP, PL, NSP, SYPP, BYPP), HI, HSW, and PC (Table 1) indicated ample genetic variability in the existing genetic materials. Earlier Bharathi *et al.*, [16], Singh *et al.*, [17], and Gomathi *et al.*, [6] also had similar findings about significant genetic variability for all the characters. Understanding the extent of variability within crop species is crucial as it forms the foundation for the effective selection of desired traits [18].

3.2 Estimation of Mean, Range, and Genetic Parameters

Mean values and the variance components were used to compute other genetic parameters *viz.*, genotypic coefficient of variation (GCV),

phenotypic coefficient of variation (PCV), and Genetic advance as percent (%) over mean were estimated for all traits Table 2. The mean values and ranges are shown in Graph 1, while GCV and PCV are illustrated in Graph 2.

The phenotypic variance was high as compared to genotypic variance for all the traits studied which was also observed earlier by Panigrahi *et al.*, [19], Priyanka *et al.*, [20], Thirumalai and Murugan [21], Gnanasekaran *et al.*, [5], The estimates of GCV, and PCV are low (10%), moderate (10-20%), and high (more than 20%) as suggested by Burton and DeVane [22]. Maximum GCV and PCV were observed for primary branches per plant (51.52%, 52.68%), number of pods per plant (44.76%, 45.52%), seed yield per plant (38.48%, 39.44%), biological yield per plant (34.83%, 35.67%), and harvest index (31.75%, 32.06%) in the present study, which aligns with the findings of Hemalatha *et al.*, [23]. Further, the phenotypic and genotypic coefficient of variance was recorded as low for days to 50% flowering (6.60%, 7.33%), days to 75 % maturity (5.52%, 6.02%), and protein content (6.95%, 7.03%). Meanwhile, moderate GCV and PCV were observed for Plant Height, Pod length, Seeds Per Pod, and 100-seed weight (Table 2). These results conformed with earlier reports by Kumar *et al.*, [10]. These estimates provided a clear understanding of the variability present among the different genotypes.

3.3 Heritability and Genetic Advance as a % of Mean

The broad-sense heritability estimates for yield and its contributing characters are presented in Table 2. Predictions regarding heritability were categorized following Robinson's (1949) [24] guidelines: low (less than 50%), moderate (50-70%), and high (more than 70%) heritability estimates. In the present study, broad-sense heritability (h^2b) was high for all the traits, *viz.*, DFF, DM, PH, NPB, NPP, PL, NSP, SYPP, BYPP), HI, HSW, and PC (Table 2).

Broad sense heritability includes additive and non-additive gene effects (Hanson *et al.*, 1956).[25] Heritability estimates in a broad sense alone are insufficient for predicting the best individuals or genotypes because they include both additive and non-additive gene effects. High genetic advance is primarily due to additive gene action. Therefore, heritability estimates combined with genetic advances are more informative. As per reference Johnson *et al.*, [15] genetic

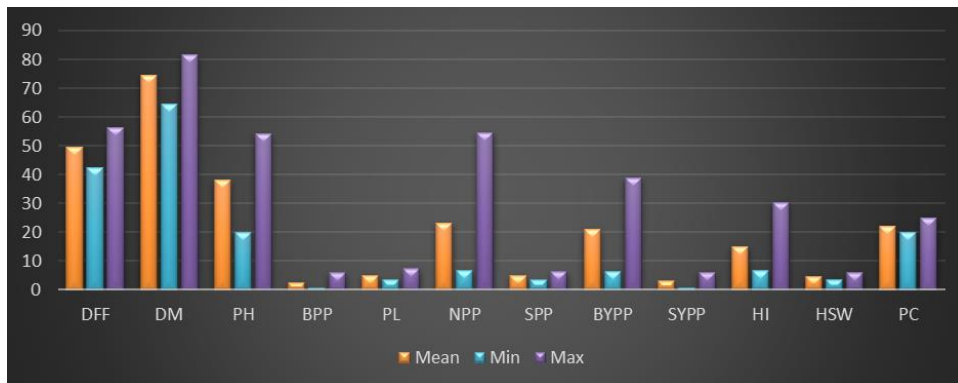
advance as a percentage of mean (GAM) was grouped if the values ranged from 0-10% are considered low, 10-20% are moderate and 20% and above are high. In the study, high heritability coupled with high genetic advance was observed

for plant height, number of primary branches per plant, pods per plant, pod length, seeds per pod, seed yield per plant, biological yield per plant, harvest index, and 100-seed weight. (Graph 3).

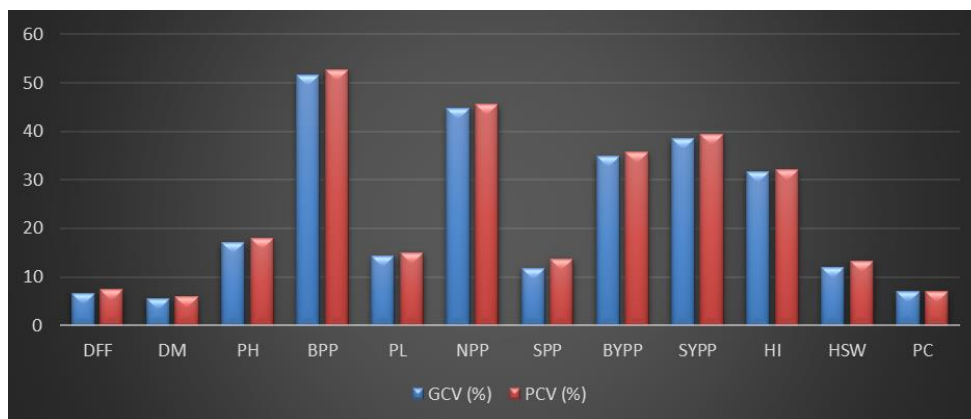
Table 1. Analysis of variance for randomized block design

S.no.	Source of Variation→ Trait↓	df→	Mean sum of square		
			Replication	Treatment	Error
			2	110	220
1.	Days to 50% flowering		2.17	34.45**	2.51
2.	Days to 75% Maturity		2.33	54.19**	3.14
3.	Plant Height (cm)		18.46	131.99**	4.43
4.	Primary Branches Per Plant		0.10	5.34**	0.08
5.	Pod Length (cm)		0.03	1.62**	0.06
6.	No. of Pods Per Plant		0.81	329.27**	3.71
7.	Seeds Per Pod		0.41	1.12**	0.12
8.	Biological Yield Per Plant (g)		1.24	166.23**	2.60
9.	Seed Yield / Plant(gm)		0.04	4.24**	0.07
10.	Harvest Index (%)		1.16	69.45**	0.46
11.	100-Seed Weight (gm)		0.03	1.03**	0.07
12.	Protein Content (%)		0.09	7.21**	0.06

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



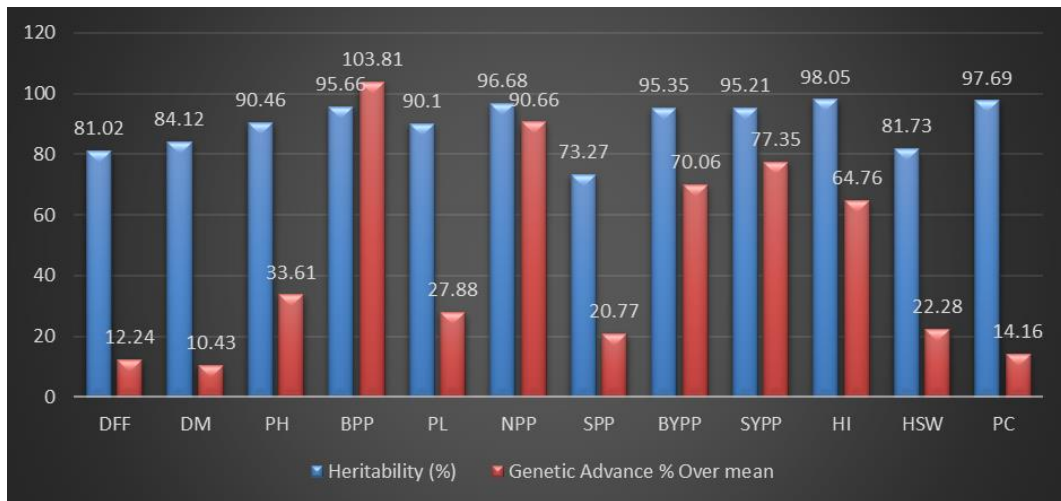
Graph 1. Mean, minimum, and maximum range for different traits



Graph 2. Genotypic and phenotypic coefficient of variance

Table 2. Mean, Range, Genotypic, Phenotypic coefficient of variance, Heritability, and Genetic advance as percent over mean for all the traits.

Traits ↓	Mean	Range		Coefficient of variance		Heritability h ² b (%)	Genetic Advance % Over mean
		Minimum	Maximum	GCV (%)	PCV (%)		
1. DFF	49.59	42.33	56.33	6.60	7.33	81.02	12.24
2. DM	74.46	64.33	81.67	5.52	6.02	84.12	10.43
3. PH	38.00	19.80	54.13	17.15	18.03	90.46	33.61
4. BPP	2.56	0.73	5.87	51.52	52.68	95.66	103.81
5. PL	5.04	3.54	7.25	14.26	15.02	90.10	27.88
6. NPP	23.18	6.73	54.60	44.76	45.52	96.68	90.66
7. SPP	4.91	3.40	6.33	11.78	13.76	73.27	20.77
8. BYPP	21.11	6.45	38.92	34.83	35.67	95.35	70.06
9. SYPP	3.05	0.76	6.07	38.48	39.44	95.21	77.35
10. HI	15.05	6.57	30.30	31.75	32.06	98.05	64.76
11. HSW	4.73	3.54	5.92	11.96	13.23	81.73	22.28
12. PC	22.11	20.01	24.97	6.95	7.03	97.69	14.16



Graph 3. Heritability and Genetic advance as % over mean

These results conformed with those of, Gnanasekaran et al. [5], Kumar et al. [10], Gomathi et al., [6], and Rolaniya et al., [26], observed high heritability coupled with high genetic advance for seed yield per plot, number of pods per plant, 100-seed weight, and plant height. Whereas, High heritability coupled with moderate genetic advance, for days to 50% flowering, days to 75% maturity, and protein content (Table 2) and (Graph 3). Some researchers found comparable results viz; Kumar et al. [10] and Singh et al. [17] demonstrated high heritability coupled with moderate genetic advance as a percentage of the mean for days to 50 percent flowering, days to maturity, number of branches/ per plants, and plant height. While Priya et al. [27] observed for 100 seed weight. Hence, High heritability (h^2b) coupled with high genetic advance suggests the predominance of additive gene action, indicating a greater response to phenotypic selection and potential for trait improvement. The selection of these traits was useful for further improvement in the plant breeding program [28-30].

4. CONCLUSION

The above experimentation concludes that the phenotypic variance was higher than the genotypic variance for all the traits studied, indicating the presence of environmental influence on the characters. This reveals the presence of exploitable genetic variance which can be improved through direct selection. Also, broad-sense heritability (h^2b) was high for all the traits, viz., DFF, DM, PH, NPB, NPP, PL, NSP, SYPP, BYPP), HI, HSW, and PC. Meanwhile, high heritability coupled with high genetic

advance was observed for PH, NPB, NPP, PL, NSP, SYPP, BYPP, HSW, and HI revealing that the presence of additive gene action and selection is rewarded for enhancing the seed yield. Whereas, high heritability with moderate genetic advance was observed for DFF, DM, and PC, could be improved by intermating superior genotypes of the population developed from combination breeding. Therefore, the genetic parameters estimated will guide effective selection strategies in urdbean breeding programs targeting yield enhancement.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of manuscripts.

COMPETING INTERESTS

The authors have declared that no competing interests exist.

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