Exploring Genetic Variability Parameters for Yieldand Quality Traits in Urdbean Genotypes and itsTriple Test Cross F_1 Hybrids.

ABSTRACT

This research explores the genetic variability, heritability, and genetic advance among 111 diverse lines of urdbean. 27 lines, three testers, and Eighty-one F_1 hybridswere 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^2b) was high for all the traits examinedranging 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: Variability, genotypic, phenotypic, heritability, ~~and~~ genetic advance.

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, andsubfamily Faboideae or Papilionoideaeor Papilionaceae with a small genome size estimated to be574 Mbp**(Prakit Somta and Peerasak Srinives, 2007).**The wild progenitor ofblackgramdomesticated in Indiais believed to be *Vigna mungo var. silvestris* **(Lukoki et al., 1980,Chandel et al., 1984).**It is widely consumed as dry whole grain or split grain known as daal and as unfermented and fermented flour **(Khan et al., 2021).**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 **(Gnanasekaran et al., 2024).**Black gram seeds include more protein and lysine content than cereals **(Gomathi *et al.* 2021).**In India, about 92 % (per cent) of urdbean production comes from 9 states Madhya Pradesh, Rajasthan, Uttar Pradesh, Tamil Nadu, Andhra Pradesh, Maharashtra, Jharkhand, Gujarat, and Karnataka ~~*(Fig. 1).*~~

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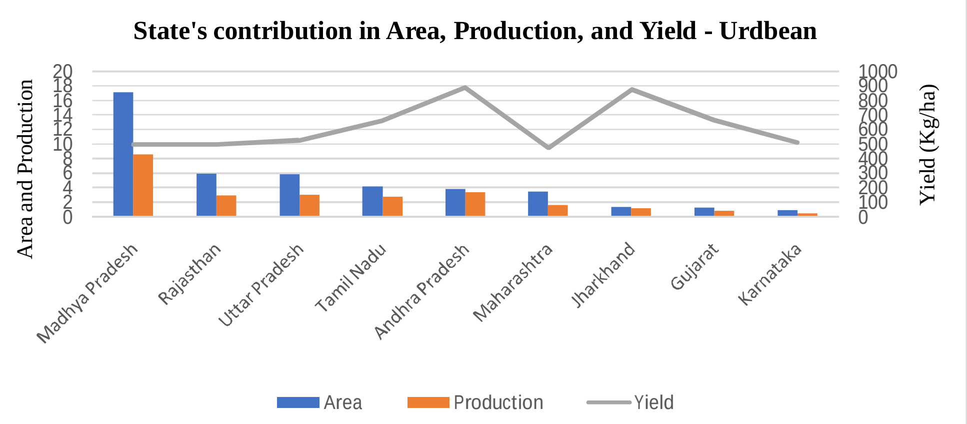

Fig:1 Area-lakh ha, Production-lakh tons, Yield-kg/ha.

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The urdbean 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).**Despite its great importance, the productivity of urdbean 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**(Souframanien and Gopalakrishnan, 2004).**The achievement of high yield mainly depends on the magnitude of yield-contributing traits and the nature of genetic variability present in the crop **(Johnson and Bernard, 1962).**To increase the productivity and production of this crop, developing new high-yielding genotypes is a prime goal of urdbean breeding**(Kumar et al. 2022).** 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 yieldand 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 F_1TTC hybrids for future application in breeding programs or through straightforward selection strategies based on multi-location field trials.

2. MATERIALS AND METHODS:

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The present investigation was conducted during*Kharif,* 2023at 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 urdbean, 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 (L_1), Azad-3 (L_2)**,**and F_1 of KU-96-7 × Azad-3 i.e., L_3, to produce 81 triple test cross (TTC) progenies. TTC progenies in the form of 54 single crosses and 27three-way crosses.Therefore,27 lines, three testers, and Eighty-one F_1 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 (1984).**The analysis of variance followed the linear model proposed by **Fisher (1954).**

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

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}genotypein 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 (1952),**

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, $\sigma^2 g$ = Genotypic variance.

$\sigma^2 p$ = phenotypic variance.

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

2.2.2 Estimation of Heritability (h²b) broad sense:

Heritability in a broad sensewas calculated using the formula suggested by **Allard (1960).**

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

where **h²b** = Heritability in a broad sense;

$\sigma^2 g$=Genotypes variance;

$\sigma^2 p$ = Phenotypic variance.

2.2.3 Estimation of Genetic Advance:

It was computed with the help of the following formula given by **Johnson *et al.* (1955).**

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

Where, G.A.= Genetic advance

K = Selection differential(K = 2.06 at5%selectionintensity)

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.* (1955).**

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

3. RESULT AND DISCUSSION:

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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.* 2022;Singh*et al.* 2022; and Gomathi*et al.* 2021**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 **(Burt and Austin, 2000).**

Table1: Analysis of variance for randomized block design.

S.no.	Source of Variation→	Mean sum of square		
		Replication	Treatment	Error
	Trait↓ df→	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.

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.**

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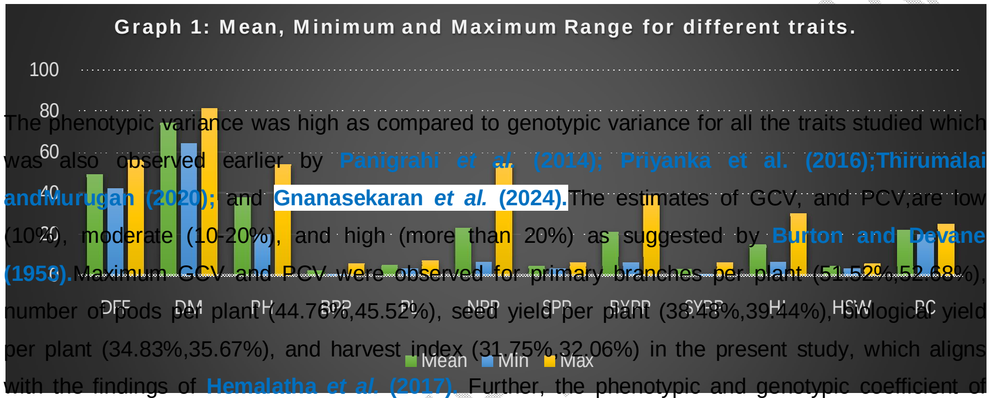

Graph 1: Mean, Minimum and Maximum Range for different traits.

The phenotypic variance was high as compared to genotypic variance for all the traits studied which was also observed earlier by **Panigrahi *et al.* (2014); Priyanka et al. (2016);Thirumalai andMurugan (2020);** and **Gnanasekaran *et al.* (2024).**The estimates of GCV, and PCV,are low (10%), moderate (10-20%), and high (more than 20%) as suggested by **Burton and Devane (1953).**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.* (2017).** 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.* (2022).**These estimates provided a clear understanding of the variability present among the different genotypes.

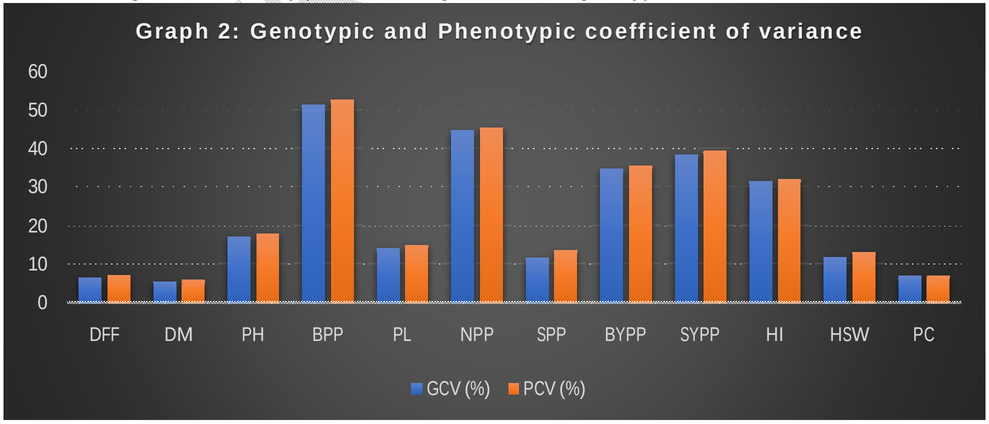

Graph 2: Genotypic and Phenotypic coefficient of variance

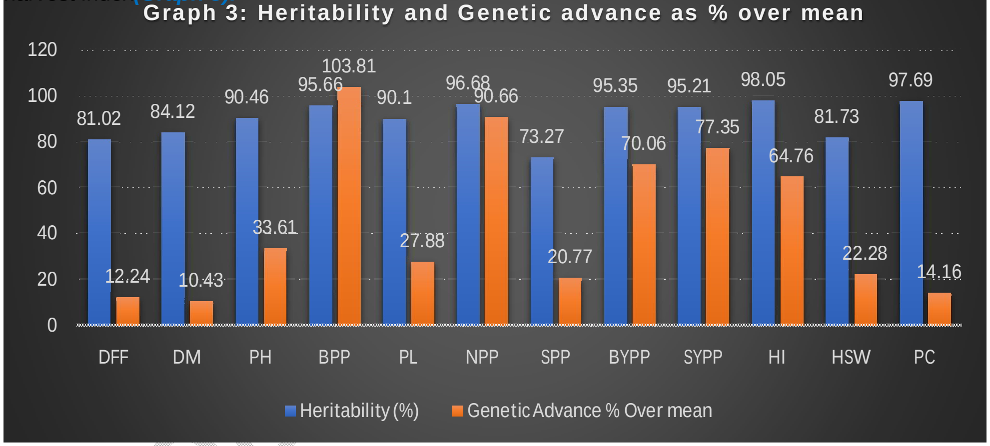
Table 2: Mean, Range, Genotypic, Phenotypic coefficient of variance, Heritability, and Genetic advance as percent over mean for all the traits.

		Range		Coefficient of variance		Heritability h^2b (%)	Genetic Advance % Overmean
Traits ↓	**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

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)**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 senseheritability includes additive and non-additive gene effects **(Hanson *et al.,* 1956).**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.,* (1955)**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, 100-seed weight,and harvest index***(Graph 3)***.


Graph 3: Heritability and Genetic advance as % over mean

These results conformed with those of, **Gnanasekaran *et al.* (2024)**; **Kumar *et al.* (2022); Gomathi et al., (2021); and Rolaniya *et al.,* (2017);**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.* (2022);**and**Singh*et al.* (2022)** demonstrated high heritability coupled with moderate genetic advance as a percentage of the mean fordays to 50 percent flowering, days to maturity, number of branches/ per plants, and plant height.While **Priya *et al.* (2018);** 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.

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 revealsthe 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,andHI 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.

5. REFERENCES:

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