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ASSESSMENT OF VARIABILITY AND CHARACTER ASSOCIATION IN URDBEAN (*VIGNA MUNGO* L. HEPPER) GENOTYPES

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ABSTRACT

The current study, entitled "Assessment of genetic variability for seed yield and it's contributing traits in urdbean genotypes" was conducted during the summer of 2024 at the Agricultural Research Station, Ummedganj, Kota, (Rajasthan). The experimental material consisted of forty-two urdbean genotypes including three check varieties (Pratap Urd-1, Kota Urd-3, Kota Urd-4), which were evaluated using a randomized block design with three replications. The analysis of variance (ANOVA) indicated that the differences among the 42 urdbean genotypes were highly significant for all 13 quantitative traits studied. A high magnitude of genotypic coefficients of variation (GCV), phenotypic coefficients of variation (GCV), heritability and genetic advance as per cent of mean was recorded for traits such as the number of clusters per plant, number of branches per plant, number of pods per plant and biological yield per plant, suggesting that direct selection based on these characters would be effective in improving seed yield. The association study revealed that highly significant and positive correlation of biological yield per plant, number of clusters per plant, number of pods per plant, harvest index, plant height and number of seeds per pod exhibited a true relationship with seed yield per plant. The genotypes like KPU-2420, KPU-2414**,** KPU-2418 can be used as promising donor parents in recombination breeding programme for obtaining high heterotic response and better segregates.
Keywords **:** Urdbean, GCV, PCV, heritability, Correlation.

Introduction

Urdbean (*Vigna mungo* (L.) Hepper), occupies a unique place among pulses for its use as seed and it is grown both as pure and mixed crop. It is native to India, belong to the family Leguminosae. It also supplements the income of many small-scale farmers and contributes to the maintains of soil fertility by fixing nitrogen in the soil. Urdbean is rich protein food and consumed in various forms as dal (whole or split, husked and un-husked) (Bhargavi *et al*., 2022).

Urdbean is one of the most widely grown short-duration grain legume crops. It was domesticated using *Vigna mungo* var. silvestris (Lukoki *et al.,* 1980). With a genome size of 574 Mbp, it is a self-pollinating diploid species (2n = 2x = 22). In 2023–2024, India produced 23.2 lakh tonnes of urdbean, with an area of 35.3 lakh hectares and a productivity of 656 kg/ha. Rajasthan produced 1.49 lakh tonnes of urdbean with an area of 2.95 lakh hectares and a productivity of 505 kg/ha (Anonymous 2024-25). In the Kota zone, 0.59 lakh tonnes of Urdbean were produced on 1.38 lakh hectares of land, with a productivity of 427 kg/ha (Anonymous 2022-23).

To fulfil the requirement of growing population, production & productivity of urdbean needs to be enhanced. Selection of genotypes based on yield as such is difficult to the integrated structure of plant in which most of the characters are inherited and being governed by the large number of cumulative, duplicate and additive genes. Urdbean breeding strategy for the improvement involves generating genetic material, selection of superior genotypes from the variable genetic material to develop superior varieties. This necessitates a thorough knowledge on the nature of

relationship prevalent between yield contributory characters and grain yield and the extent of genetic variability. Therefore, the present investigation aims to assess the variability together with the relative contribution of different yield attributes to grain yield with heritability and genetic advance so as to select superior genotypes (Meshram *et al*., 2012).

Correlation coefficient analysis helps to determine both the strength and direction of relationships among yield-related traits. By assessing these interrelationships, it becomes possible to identify the key traits that can be targeted through selection to enhance yield. Understanding such character associations is critical for designing an efficient breeding strategy aimed at developing high-yielding genotypes.

Material and Methods

The experimental material of the current study comprised of forty-two genotypes including three checks of urdbean grown in Randomized Block Design at Agriculture Research Station, Ummedganj, Agriculture University, Kota during *summer*, 2024. Geographically, Kota lies in the Humid South-Eastern Plain Zone (Zone V) and situated between 75° 50' E longitude and 25° 11' latitude with an altitude of 258 m above the mean sea level. The plants were grown in 4m x 1.2m plot with a row-to-row spacing of 30cm and plant-to-plant spacing of 10 cm. Data were recorded on thirteen characters, in which days to 50% flowering, days to maturity were recorded on plot basis, whereas plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g), biological yield per plant (g), harvest index (%), protein content (%) and seed yield per plant (g) were recorded on five randomly selected plants of each genotype for these characters in each replication. Protein content of urdbean was estimated as per the procedure given by Lowery *et al.* 1951 at Central Laboratory of Ummedganj-Kota. The data sets were subjected to statistical analysis for ANOVA (Analysis of variance) as per Panse and Sukhatme (1985). Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were calculated using the standard formula suggested by Burton (1952) and Johnson *et al.* (1955) and heritability in broad sense was estimated as per Hanson *et al.* (1956). Besides, genetic advance and genetic gain as a percentage of mean were calculated using the formula suggested by Johnson *et al.* (1955). Genotypic and phenotypic correlation coefficients were worked out by the method described by Singh and Chaudhary (1979).

Result and Discussion

Analysis of variance

The analysis of variance revealed that the mean sum of squares due to genotypes were highly significant for all the studied traits. These traits included days to 50% flowering, days to maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, biological yield per plant, seed yield per plant, and protein content. The mean sum of squares for the different sources of variation of the thirteen characters is given in Table 1. Singh *et al*. 2023 and Punia *et al*. 2020 also find similar results of availability of sufficient variability in the urdbean genotypes.

Mean performance

On the basis of mean performance of genotypes days to 50 per cent flowering ranged from 42.33 to 49.00 days, days to maturity ranged from 72.33 to 78.00 days, plant height ranged from 19.70 to 39.43 cm, number of branches per plant ranged from 1.17 to 4.63, number of clusters per plant ranged from 1.13 to 6.20, number of pods per plant ranged from 10.00 to 35.40, pod length ranged from 3.06 to 4.42 cm, number of seeds per pod ranged from 4.46 to 6.82, 100-seed weight ranged from 3.52 to 5.16 g, biological yield per plant ranged from 5.54 to 19.64 g, harvest index ranged from 18.79 to 47.57%, protein content ranged from 21.59 to 24.52% and seed yield per plant ranged from 1.57 to 9.21 g.

Phenotypic and genotypic variations

Phenotypic coefficients of variation were marginally higher than the corresponding genotypic coefficients of variation, which indicates the little environmental effect on the characters expression (Table 2). The higher value of genotypic coefficients of variation and phenotypic coefficients of variation were observed for number of clusters per plant (41.56%, 45.02%), seed yield per plant (40.11%, 43.06%), number of branches per plant (32.63%, 37.21%), number of pods per plant (29.73%, 31.05%) and biological yield per plant (29.40%, 30.74%). Similar findings were obtained by Bandi *et al.* (2018), Blessey *et al*. (2018) and Sushmitharaj *et al*. (2018) for number of clusters per plant, Seed yield per plant, number of branches per plant and number of pods per plant. Moderate value of genotypic coefficients of variation and phenotypic coefficients of variation were observed for Harvest index (15.63%, 20.66) and Plant height (15.26%, 17.04%). Similar outcomes were proclaimed by Kondagari *et al.* (2017) for plant height. Low genotypic coefficients of variation and phenotypic

coefficients of variation were recorded for number of seeds per pod (8.63%, 14.02%), pod length (7.77%, 10.47%), 100-seed weight (6.04%, 9.28%) and protein content (3.63%, 4.07). Bal and Lal *et al.* (2021) found similar results for 100-seed weight, Rathore *et al.* (2024) found low GCV and PCV for protein content and Aftab *et al.* (2018) found for number of seeds per pod and pod length.

Heritability and genetic advance as per cent of mean

Heritability governs the resemblance between parents and their progenies whereas the genetic advance provides the knowledge about expected gain for a particular character (Table 2). High heritability was observed for number of pods per plant (91.26%), biological yield per plant (91.48%), Seed yield per plant (86.74%), number of clusters per plant (85.23%), plant height (80.24%), protein content (79.54%), number of branches per plant (76.88%), days to 50% flowering (76.56%) and days to maturity (70.06%). Similar findings for this parameter were observed by Bal and Lal (2021) and Vanniarajan *et al.* (2022) for days to 50% flowering and Days to maturity. Barik and Lenka (2021) for number pods per plant, Seed yield per plant, number of clusters per plant, plant height and biological yield per plant, Rathore *et al.* (2024) for protein content. Moderate value of heritability was estimated for harvest index (57.22%) and pod length (55.04%). A comparable trend for this parameter was also reported by Barik *et al.* (2021), Chaitainya *et al.* (2019) and Rehman *et al.* (2021) for pod length, Bal and Lal (2021) and Chaitainya *et al.* (2019) for harvest index, Vanniarajan *et al.* (2022) for number of branches per plant. Low heritability was observed for 100-seed weight (42.32%) and number of seeds per pod (37.94%). Bal and Lal *et al*. (2021) also concurred with finding for this parameter for 100-seed weight and number of seeds per pod.

Heritability and genetic advance are the important genetic parameters for selecting a genotype that permit greater effectiveness of selection by separating out environmental influence from total variability (Table 3). Heritability estimates along with genetic advance are normally more useful in predicting the genetic gain under selection than that of heritability alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al.* 1955).The high genetic advance as per cent of mean was recorded for number of clusters per plant (78.65%), Seed yield per plant (76.58%), number of pods per plant (58.36%), biological yield per plant (57.65%), Number of branches per plant (67.76%), plant height (28.03%) and harvest index (24.24%).Comparable outcomes for this parameter were noted by Barik *et al.* (2021) and Singh *et al*. (2014) for number of pods per plant, number of branches per plant and plant height. It is suggested that these traits are strongly influenced by genetics and can be effectively improved through breeding programs.

Moderate value of genetic advance as per cent of mean was observed for pod length (11.81%) and number of seeds per pod (10.90%). Findings of Barik *et al.* (2021) for pod length and number of seeds per pod and Singh *et al.* (2014) for number of seeds per pod were also in accordance for this parameter. Moderate amount of improvement can be expected in a population through selective breeding for these particular traits. Low value of genetic advance as per cent of mean estimated for 100-seed weight (8.06%) followed by protein content (6.64%), days to 50% flowering (4.28%) and days to maturity (3.11%). A comparable trend for this parameter was also reported by Bal and Lal *et al.* (2021) and Barik *et al.* (2021) in relation to days to maturity and days to 50% flowering.

Correlation of attributing characters with seed yield

Correlation coefficients of various characters with seed yield per plant and among themselves at both genotypic and phenotypic levels were estimated and are presented in Table 4. Seed yield per plant exhibited highly significant and positive correlation at both genotypic and phenotypic levels with biological yield per plant, number of clusters per plant, number of branches per plant, number of pods per plant, pod length, harvest index, plant height, number of seeds per pod and 100-seed weight. Findings of Punia *et al.* (2020) for number of branches per plant and number of pods per plant and Singh *et al.* (2009) for biological yield per plant, number of clusters per plant, harvest index, plant height, number of seeds per pod and 100-seed weight also cognate to the present results. Conversely, seed yield showed a significant negative correlation with days to maturity, days to 50% flowering and protein content at both genotypic and phenotypic levels. Resemblant findings for this parameter were also noted by Dheeraj *et al*. (2020) for days to maturity and days to 50% flowering.

Table 1 : Analysis of variance (ANOVA) for yield contributing traits in urdbean genotypes

Source of variation	Degree of freedom	Mean sum of square					
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Pod length (cm)	Protein content (%)
Replication	2	0.798	0.217	9.805	0.374	0.078	0.105
Genotypes	41	4.16**	6.45**	51.66**	2.342**	0.30**	2.25**
Error	82	0.385	0.804	3.918	0.213	0.064	0.178

**Significant at 1 per cent

Table 2 : Analysis of variance (ANOVA) for seed yield and its contributing traits in urdbean genotypes

Source of variation	d.f.	Number of Cluster/plant	Number of Pods/plant	Number of Seed/pod	Seed yield /plant (g)	100 – seed weight (g)	Biological yield/plant (g)	HI (%)
Replication	2	0.395	3.329	0.285	1.618	0.121	7.985	4.072
Genotypes	41	5.757**	140.44**	0.92**	10.59**	0.25**	40.94**	118.14**
Error	82	0.314	4.128	0.325	0.513	0.078	1.231	23.56

**Significant at 1 per cent

Table 3 : Genetic variability parameters for seed yield and its contributing characters in urdbean genotypes

S. No.	Characters	Range		Mean	GCV (%)	PCV (%)	H^2	Genetic advance	GAM
		Min.	Max.						
1.	Days to 50% flowering	42.33	49.00	47.01	2.38	2.72	76.56	2.01	4.28
2.	Days to maturity	72.33	78.00	75.60	1.81	2.16	70.06	2.35	3.11
3.	Plant height (cm)	19.70	39.43	26.13	15.26	17.04	80.24	7.32	28.03
4.	Number of branches per plant	1.17	4.63	2.58	32.63	37.21	76.88	1.51	58.64
5.	Number of Cluster per plant	1.13	6.20	3.24	41.56	45.02	85.23	2.55	78.65
6.	Number of Pods per plant	10.00	35.40	22.67	29.73	31.05	91.67	13.23	58.36
7.	Pod length (cm)	3.06	4.42	3.61	7.77	10.47	55.04	0.42	11.81
8.	Number of Seed per pod	4.46	6.82	5.16	8.63	14.02	37.94	0.56	10.90
9.	100 – seed weight (g)	3.52	5.16	3.98	6.04	9.28	42.32	0.32	8.06
10.	Biological yield per plant (g)	5.54	19.64	12.37	29.40	30.74	91.48	7.13	57.65
11.	Harvest index (%)	18.79	47.57	35.92	15.63	20.66	57.22	8.70	24.24
12.	Protein content (%)	21.59	24.52	22.90	3.63	4.07	79.54	1.52	6.64
13.	Seed yield per plant (g)	1.57	9.21	4.57	40.11	43.06	86.74	3.49	76.58

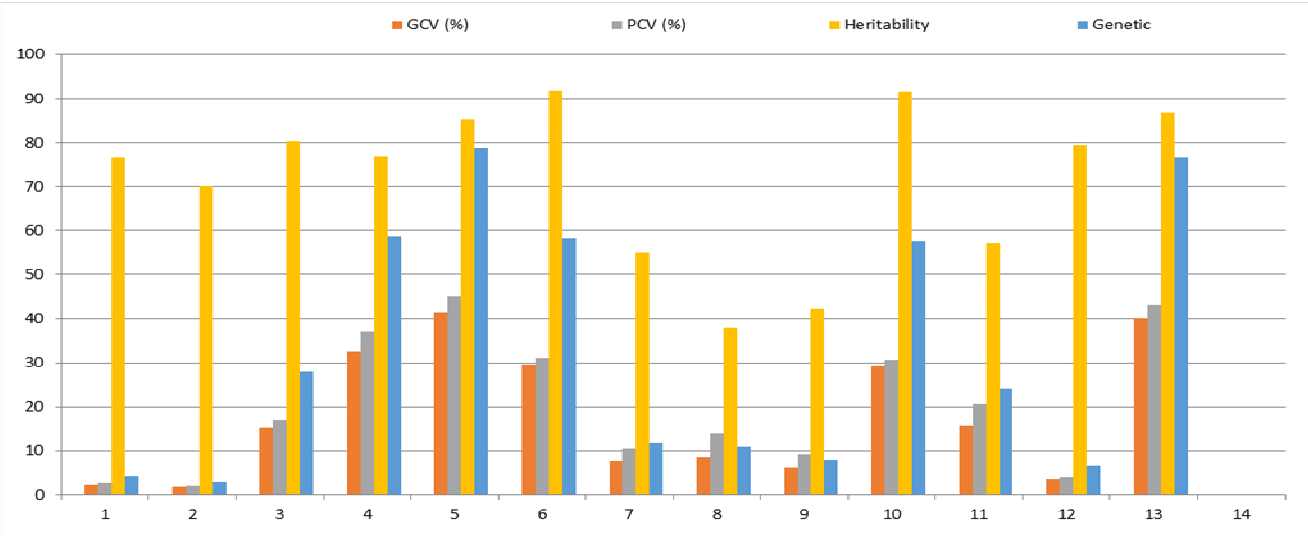

Fig. 1 : Chart representation of variability parameters, heritability and genetic advance as per cent of mean

Table 4 : Estimates of genotypic and phenotypic correlation coefficients between thirteen characters in urdbean

Character		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of Clusters per plant	Number of Pods per plant	Pod length (cm)	Number of seeds per pod	100 – seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Protein content (%)	Seed yield per plant (g)
Days to 50% flowering	G p	1.000 1.000	0.923** 0.732**	-0.200* -0.123^{NS}	-0.458** -0.297**	-0.400** -0.320**	-0.279** -0.208*	-0.774** -0.537**	-0.834** -0.486**	-0.534** -0.394**	-0.512** -0.413**	-0.410** -0.278**	0.054^{NS} 0.009^{NS}	-0.492** -0.395**
Days to maturity	G p		1.000 1.000	-0.442** -0.285**	-0.700** -0.526**	-0.725** -0.515**	-0.582** -0.466**	-0.893** -0.636**	-0.902** -0.518**	-0.668** -0.434**	-0.753** -0.618**	-0.697** -0.479**	0.231** 0.159^{NS}	-0.778** -0.639**
Plant height (cm)	G p			1.000 1.000	0.586** 0.455**	0.604** 0.525**	0.566** 0.490**	0.753** 0.477**	0.664** 0.402**	0.713** 0.347**	0.675** 0.574**	0.565** 0.435**	-0.061^{NS} -0.045^{NS}	0.712** 0.623**
Number of branches per plant	G p				1.000 1.000	0.941** 0.813**	0.966** 0.820**	0.786** 0.555**	0.435** 0.231**	0.543** 0.349**	0.893** 0.757**	0.767** 0.487**	-0.522** -0.337**	0.931** 0.756**
Cluster per plant	G p					1.000 1.000	0.984** 0.894**	0.747** 0.555**	0.489** 0.240**	0.565** 0.380**	0.873** 0.778**	0.861** 0.625**	-0.547** -0.406**	0.946** 0.835**
Pods per plant	G p						1.000 1.000	0.602** 0.500**	0.348** 0.182*	0.418** 0.301**	0.814** 0.786**	0.870** 0.653**	-0.533** -0.426**	0.919** 0.855**
Pod length (cm)	G p							1.000 1.000	0.957** 0.549**	0.910** 0.610**	0.941** 0.758**	0.595** 0.345**	-0.210* -0.081^{NS}	0.869** 0.675**
Seed per pod	G p								1.000 1.000	0.853** 0.259**	0.771** 0.462**	0.395** 0.314**	-0.001^{NS} 0.027^{NS}	0.691** 0.479**
100 – seed weight (gm)	G p									1.000 1.000	0.737** 0.551**	0.476** 0.218*	-0.133^{NS} -0.043^{NS}	0.659** 0.455**
Biological yield per plant (gm)	G p										1.000 1.000	0.642** 0.452**	-0.303** -0.221*	0.954** 0.903**
Harvest index (%)	G p											1.000 1.000	-0.479** -0.260**	0.821** 0.765**
Protein content (%)	G P												1.000 1.000	-0.399** -0.277**
Seed yield per plant (gm)	G P													1.000 1.000

*, ** = Significant at 5% and 1% significance level, respectively

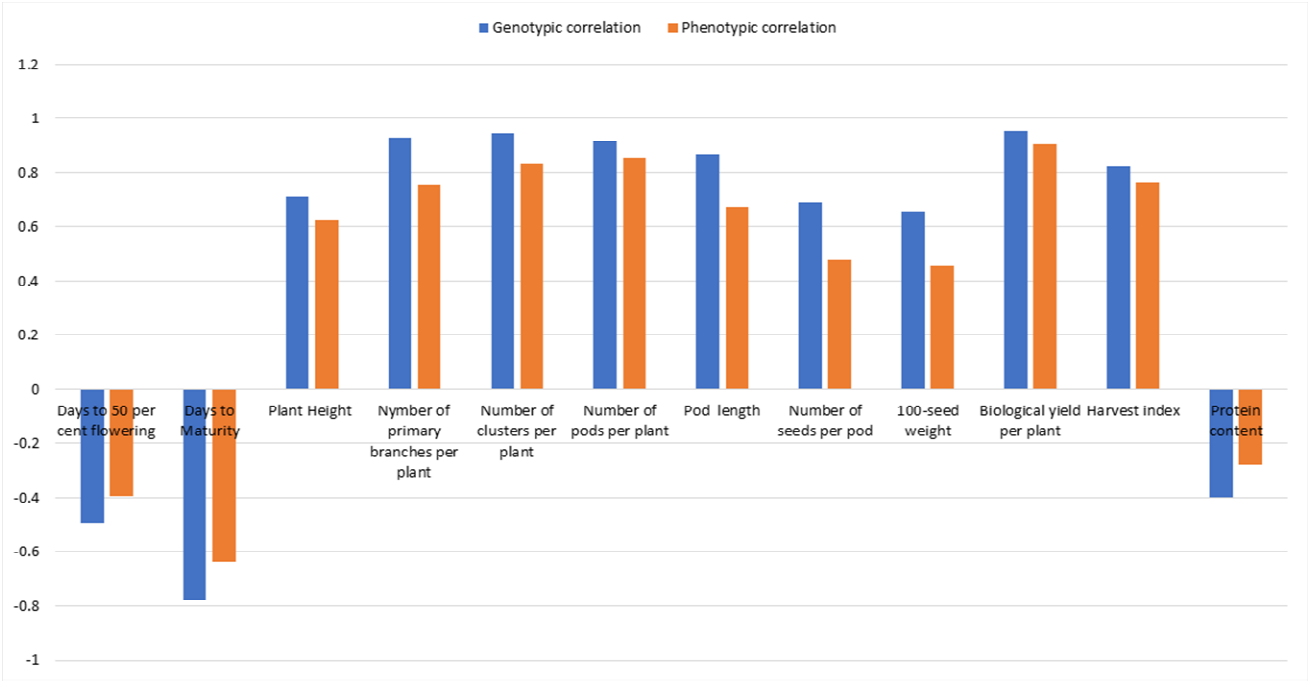

Fig. 2 : Estimates of genotypic and phenotypic correlation coefficients between thirteen characters in urdbean.

Conclusion

The analysis of variance revealed highly significant differences among the genotypes for all the traits under investigation. The evaluated genotypes exhibited ample variability across most of the traits. This wide range of variation provides a valuable opportunity for the selection of superior genotypes aimed at enhancing yield potential. A high magnitude of genotypic coefficients of variation, phenotypic

coefficients of variation, heritability and genetic advance as per cent of mean was recorded for traits such as the number of clusters per plant, number of branches per plant, number of pods per plant and biological yield per plant, suggesting that direct selection based on these characters would be effective in improving seed yield. The correlation analysis revealed that seed yield per plant exhibited a significant and positive association with biological yield per plant followed by number of clusters per plant**,** number of branches per plant**,** number of pods per plant**,** pod length, harvest index, plant height**,** number of seeds per pod and 100-seed weight at both phenotypic and genotypic levels. These findings suggest that seed yield in Urdbean can be effectively enhanced by selecting genotypes that show superior performance for these yield-contributing traits.

References

Aftab, N., Lal, G.M., Sheera, A., Bose, N.C.and Tripathi, A.M. (2018). Evaluation of genetic variability in black gram [*Vigna mungo* (L.) Hepper] germplasm. *Journal of Plant Development Sciences*, **10**(8),445-452.

Anonymous (2023). Directorate of Economics and Statistics (DES), 2023. Ministry of Agriculture & Farmers Welfare (MoA&FW), Government of India.

Anonymous (2024-25). Project Coordinator's report, All India Coordinated Research Project on Kharif Pulses, ICAR-IIPR, Kanpur of Jammu region, indianjournals.com, 319-327.

Bal, S. and Lal, G.M. (2021). Study on genetic variability and selection strategy for enhancing productivity in urdbean [*Vigna mungo* (L.) Hepper]. *International Journal of Plant and Environment***, 7**(02),151-155.

Bandi, H.R.K., Rao, K.N., Krishna, K.V. and Srinivasulu, K. (2018). Correlation and path-coefficient estimates of yield and yield component traits in rice fallow blackgram [*Vigna mungo* (L.) Hepper]. *International Journal of Current Microbiology and Applied Sci*ence, **7**(3),3304-3309.

Barik, B.R., Lenka, D., Agarwal, A.K., Mishra, A., Nayak, G. and Tripathy, S.K. (2021). Genetic variation and extent of genetic diversity in urdbean [*Vigna mungo* (L.) Hepper]. *Biological Forum-An International Journal,* **13**, 556.

Bhargavi, M. and Rai, P.K. (2022). Standardization of selected organics seed treatments on growth yield and yield attributing traits of black gram (*Vigna mungo*) var. PU-19.*Environment and Ecology,***40** (4D), 2807-2811.

Blessy, V. and Pavan Naik, B. (2018). Studies on correlation and path analysis in black gram [*Vigna mungo* (L.) Hepper]. *International Journal of Current Microbiology and Applied Sciences,***7**(8), 1991-1997.

Burton,G.W. (1952).Quantitative inheritance in grasses. Proc. 6th International. *Grassland Crosses*,**1,** 227-283.

Chaithanya, K., Rajesh, S., Suresh, B.G., Kumar, S. and Lal, G.M. (2019). Assessment of genetic variability parameter in black gram [*Vigna mungo* (L.) Hepper] germplasm. *International Journal of Current Microbiology and Applied Sciences***, 8**(8), 1853-1860.

Dheeraj, A.G., Lavanya, G.R., Kumar, P.P. and Sanadya, S.K. (2020). Mean performance and correlation coefficient analysis for seed yield and related traits in urdbean parents and crosses. *International Journal of Current Microbiology and Applied Sciences*, 1972-1977.

Hanson, G.H., H.F. Robinson and R.E. (1956). Biometrical studies on yield in segregating population of Korean lespedeza. *Agronomy Journal*, **48**, 476-490.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, **47**, 314–318.

Kondagari Hemalatha, S. S. L. and Lal, G. M. (2017). Study on genetic variability and correlation in blackgram [*Vigna mungo*(L). Hepper]. *Journal of Pharmacognosy and Phytochemistry*, **6**(4), 674-676.

Lukoki, L., Marechal, R. and Otoul, E. (1980).The wild ancestors of the cultivated beans *Vigna radiata* and *Vigna mungo*. *Bulletin Du JardinBotanique National De Belgique*,**28**,23–30.

Meshram, M.P., Sonone, N.G. and Patil, A.N. (2012). Genetic variability studies in urdbean. *PKV Research Journal*, **36**(2), 22-26.

Panse, V.G. and Sukhatme, P.V. (1985). Statistical methods for agricultural workers, *ICAR Publication*, New Delhi. pp 381.

Punia, S.S., Ram, B., Verma, P., Singh, K., Parihar, A.K. and Yadav, A.K. (2020). A recent overview of genetic variability and correlation studies in Urdbean (*Vigna mungo* (L.) Hepper]. *Cutting-edge Research in Agricultural Sciences*, **41.**

Punia, S.S., Ram, B., Verma, P., Singh, K., Parihar, A.K. and Yadav, A.K. (2020). A recent overview of genetic variability and correlation studies in Urdbean (*Vigna mungo* (L.) Hepper]. *Cutting-edge Research in Agricultural Sciences*, **41.**

Rathore, T., Yadav, R.K., Kumar, S., Singh, L., Rai, G. and Maurya, C.L. (2024). Exploring Genetic Variability Parameters for Yield and Quality Traits in Urdbean Genotypes and Its Triple Test Cross F1 Hybrids. *Journal of Experimental Agriculture International,* **46**(7),308-316.

Rehman, M.A., Lal, G.M. and Bhattacharjee, I. (2021). Genetic variability for quantitative traits in F4 generation of urdbean [*Vigna mungo* (L.) Hepper]. *Journal of Pharmacognosy and Phytochemistry*, **10**(1),252-256.

Singh, A.K. (2023). Genetic variability, correlation and path analysis for yield and yield attributes in Urdbean (*Vigna mungo* L.) under rainfed condition of Jammu.

Singh, A.K., Gautam, R.K., Singh, P.K., Kumar, K., Kumar, N., Swain, S. and Roy, S.D. (2014). Estimation of genetic variability and association analysis in the indigenous landraces of Urdbean [*Vigna mungo* (L.) Hepper] of Andaman Islands. *International Journal of Plant Research*, **27**(1),113-122.

Singh, D., Singh, A.K. and Singh, R.P. (2009). Genetic variability and character association in urdbean (*Vigna Mungo* (L.) Hepper). *Legume Research*, **32**(3),197-200.

Singh, R.K. and Chaudhary, B.D. (1979). Biometrical methods in quantitative genetic analysis. *Kalyani Publications.* Delhi and Ludhiana, India.

Sushmitharaj, D.V., Shoba, D. and Pillai, M.A. (2018). Genetic variability and correlation studies in black gram [*Vigna*

mungo (L.) hepper] with reference to YMV resistance. *International Journal of Current Microbiology and Applied Sciences*, **6**,2849-2856.

Vanniarajan, C. and Chandirakala, R. (2022). Genetic variability and diversity analyses in Electron Beam and Gamma Ray induced mutants for yield attributing traits in urdbean [*Vigna mungo* (L.)]. *Electronic Journal of Plant Breeding*, **13**(2), 512-518.