Estimates of genetic variability for yield its component trait in Urdbean (Vigna mungo *L.*) germplasm

ABSTRACT

Genetic variability among thirty urdbean germplasm was assessed for twelve quantitative traits. These genotypes along with two checks 'Indira Urd Pratham' and 'KU-96-3' were evaluated in randomized block design with three replications during *Kharif* 2023.Wide range of variability was observed for quantitative traits. The high value of genotypic coefficient of variation and phenotypic coefficient of variation was obtained by seed yield per plant, whereas, number of branches per plant showed high value of GCV and PCV.High heritability and high genetic advance as percent of mean was shown by trait plant height, number of branches per plant, number of pods per cluster and number of clusters per plant

INTRODUCTION

Black gram [*Vigna mungo* (L.) Hepper], popularly known as urdbean, urid or mash is an important self-pollinating diploid grain legume and is originated in India from wild progenitor *Phaseolus sublobatus* and found domesticated in South Asian countries. Total blackgram production in the world is about 3.4 million tons whereas, India produces about 2.23 million tons of black gram annually from about 4.14 million hectares of area with an average productivity of 538 kg ha^{-1} (Anonymous, 2021-22). 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). To strengthen urdbean breeding program, study of available natural genetic variation is of immense importance. The knowledge of certain genetic parameters is also essential for proper understanding and their manipulation in any crop improvement programme. Therefore, present study was planned to assess variability, broad-sense heritability, and genetic advancetoidentify superior urdbean genotypes with best yield traits for future application in breeding programs

MATERIAL AND METHOD

The research material consists of thirty germplasm of blackgram including check varieties namely Indira Urd Pratham and KU-96-3. The experiment was carried out during *Kharif* 2023 in randomized complete block design (RCBD) with three replications.Each genotype was accommodated in a row of 2m length with row to row spacing of 30 cm and plant to plant distance is 10 cm apart. Observations were recorded for twelve quantitative traits *viz.*, days to 50% flowering, days to maturity, plant height, number of branches/ plant, number of cluster/ plant, number of pod/ cluster, number of seeds/ pod, pod length, 100 seed weight, harvest index, biological yield and seed yield/ plant. Alltheobservationswererecordedon fiverandomly selected plants fromeach entry in threereplications and mean value was used for analysis.

RESULTS AND DISCUSSION

The genetic parameters for twelve different quantitative characters revealed considerable amount of variability among the 30 urdbean germplasm (Table 1). Among the twelve quantitative characters, biological yield (from 50.0 to 85.0g) had maximum variation followed by plant height (from 32.4 to 67.6 cm),harvest index (15.2 to 29.2%) and seed yield per plant from 10.2 to 22.50g) showed high variation.

The variation for these traits can be exploited for yield improvement in breeding programme. On the other hand, low variation was observed for number of clusters per plant, number of branches per plant, number of pods per cluster and 100 seed weight. Improvement of these traits through simple selection might be limited from germplasm used in the present study. Hence, the genes for these important traits should be explored through more germplasm collections. (Ghafoor et al., 2001).

The phenotypic variance was found higher to genotypic variance for all the quantitative traits studied which was also observed by earlier workers Thirumalai and Murugan, 2020 and Gnanasekaran *etal.*, 2024.High values of GCV and PCV were observed for seed yield (20.69 and 26.37), number of branches per plant (21.70 and 25.08) respectively, suggesting possibility of improvement in these traits through direct selection which aligns with the findings of Hemalatha *et al.*, 2017.

Further, the genotypic and phenotypic coefficient of variance was recorded as low for days to 50% flowering (4.72 and 5.45), days to maturity (2.67 and 3.16), number of seeds/ pod (4.77 and 6.32), pod length (5.90 and 7.39) and 100 seed weight (8.50 and 9.44). Meanwhile, moderate GCV and PCV were observed for plant height (19.34 and 19.77), number of cluster/ plant (14.02 and 17.18), number of pod/ cluster(14.76 and 16.88),harvest index (13.50 and 19.50) and biological yield(10.57 and 13.93).These results conformed with earlier reports by Kumar *et al.*, [10].Theseestimates provided a clear understanding of the variability present among the different genotypes.

The broad-sense heritability estimates for yield and its contributing characters are presented in Table 1. In the present study, broad-sense heritability (h^2b) was high for the traits, viz., DFF, DM, PH, NBP, NPC and 100 SW (Table 1). 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. Therefore, heritability estimates combined with genetic advances are more informative.

Higher genetic advance coupled with high heritability was observed for plant height, number of branches per plant and number of pods per cluster indicating the influence of additive gene effects therefore, simple selection would be effective for improvement of these traits.These results conformed with those of, Gnanasekaran *et al.*, 2024 and Kumar *et al.*, 2022. Presence of high genetic advance as % of mean for seed yield per plant (27.28%) and number of cluster/ plant (23.58%) indicated that it is governed by additive genes action and selection would be more effective.

Top priority should be given for these characters while formulating selection strategies and selection of these characters may be effective. Similar results were reported in blackgram by Vijaya Kumar *et al.*, 2015 for seed yield per plant, clusters per plant and pods per plant.

CONCLUSION

The phenotypic coefficient of variation was significantly higher than the genotypic coefficient of variation indicating the influence of environment in the expression of characters. Characters with high heritability values are less impacted by their environment and have more potential for genetic improvement through selection. High heritability with high genetic advance as percent of mean was shown by trait plant height, number of branches per plant, number of pods per cluster and number of clusters per plant, suggesting that this character is more stable, controlled by additive gene action, and less impacted by the environment. These results outlined the importance of yield contributing traits in determining the grain yield of different urdbean genotypes.

Table 1. Genetic variability parameters for yield attributing traits in urdbean

Characters	**Mean**	**Range**		**GCV(%)**	**PCV (%)**	**h^2(%)**	**GA aspercent ofmean**
		Max	**Min**				
DF	41.94	46	38.3	4.72	5.45	74.75	8.40
DM	79.52	83.3	75.0	2.67	3.16	71.30	4.64
PH(cm)	49.74	67.6	32.4	19.34	19.77	95.67	38.97
NBP	2.17	3.8	1.4	21.70	25.08	74.86	38.67
NCP	5.07	6.8	3.4	14.02	17.18	66.64	23.58
NPC	2.36	3.8	2.0	14.76	16.88	76.48	26.60
NSP	6.98	7.5	6.2	4.77	6.32	57.02	7.43
PL (cm)	4.72	5.5	4.2	5.90	7.39	63.84	9.72
100SW(g)	4.27	4.8	3.1	8.50	9.44	81.20	15.79
HI(%)	22.74	29.2	15.2	13.50	19.50	47.94	19.26
BY (g)	67.62	85.0	50.0	10.57	13.93	54.44	15.63
SYPP	15.47	22.5	10.2	20.69	26.37	50.21	27.28

DF = days to 50% flowering
DM = days to maturity
PH= plant height
NBP = number of branches/ plant
NCP = number of cluster/ plant
NPC = number of pod/ cluster
NSP = number of seeds/ pod
PL= pod length
100 SW = 100 seed weight
HI% = harvest index
BY = biological yield
SYPP= seed yield/ plant

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