RESEARCH ARTICLE

Study on Genetic Variability and Selection Strategy for Enhancing Productivity in Urdbean [*Vigna mungo* (L.) Hepper]

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Abstract

Twenty-two genotypes were evaluated for thirteen biometric traits to assess available genetic variability and formulate a selection strategy for enhancing productivity in urdbean. The analysis of variance revealed significant differences among the genotypes for all agro-morphological characters, including seed yield under study. VBN 08 is sorted out as a top-yielding (3.95 g/plant) test genotype among the materials tested. Besides, IC-106-176 and the local land race "Barabanki" also managed to have high yield performance (>3.0 g/plant) almost at par with "Shekhar-2" (3.26 g/plant). All these high-yielding genotypes had shown improved mean performance for major yield contributing traits viz., pods per plant, seeds per pod, and 100-seed weight. VBN 08 bore longer pods (4.11cm) and bold seeds (100-seed wt=4.30g) with a maximum number of seeds/pod (6.25). The high Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were displayed by the number of primary branches per plant (PBPP), seed yield per plant, biological yield per plant, number of clusters per plant and number of pods per plant. The highest estimates of heritability in a broad sense and genetic gain (% of mean) were exhibited by the number of primary branches per plants followed by seed yield per plant, biological yield per plant, and pods per plant. A regression equation was shown to be fit to Y (seed yield) = -3.774 + 0.183 (clusters/plant) + 0.487 (pods/plant) + 0.271 (seeds/pod) + 0.206 (100-seed wt.) + 0.034 (harvest index) to serve as selection model for enhancing seed yield in urdbean.

Keywords: Genetic advance, Genetic variability, Heritability, Regression analysis, Seed yield, Urdbean.

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Introduction

Urdbean (*Vigna mungo* (L.) Hepper, Chromosome number 2n = 22) is an important pulse crop of rainfed agriculture in Asia. Urdbean is a good source of calorific value (341 Kcal), dietary fiber (18.3 g), calcium (138 mg), phosphorous (379 mg), iron (7.57 mg), easily digestible protein (25.21 g), essential amino acids and vitamins per 100 g of seeds (Baisakh *et al*., 2021). The crop thrives well in marginal lands besides fortifying nitrogen to the soil by fixing atmospheric N_2-fixation (22.10 N/ha) through root nodules (Kachave *et al*., 2018) and also is used as green fodder for cattle. India shares 70% to global urdbean production. In India, black gram is grown on 47.26 lakh hectares of area, producing 23.63 lakh tonnes and 500 kg/ha in 2018-19 (Kharif pulses prospects-DPD, Bhopal). Maharashtra, Andhra Pradesh, Madhya Pradesh, Uttar Pradesh, Tamil Nadu, Karnataka, and Rajasthan are the leading states for urdbean production. However, India is still behind in productivity compared to the world average (902 kg/ha), and as such, urdbean is being imported in large amounts to meet the demand. The major reason for low productivity is the least emphasis for breeding and co-ordinated consortium (Ghafoor *et al*., 2000), diverting its cultivation in marginal lands, lack of widely adaptable cultivars, severe sensitivity to abiotic (cold, salinity, high temperature, waterlogging, and drought) and biotic (YMV, powdery mildew, and *Cercospora* leaf spot) stresses. In any crop improvement program, germplasm plays an important source of valuable genes. In fact, the crop faces a narrow range of genetic variation, plausibly due to genetic erosion of landraces under high selection pressure for the desired trait (seed yield) and cultivation of a limited number of varieties in the marginal lands prone to adverse climatic conditions. Nevertheless, the existing genetic variation is not fully exploited, and there is a vast scope of genetic improvement in urdbean for enhancing yield potential.

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High-yielding varieties' development requires information on the nature and magnitude of genetic variability present in the available population, which is a prerequisite to formulating an effective breeding program. Hence, an attempt was undertaken to assess the status of genetic variability of agro-morphological traits and formulate a realistic selection strategy for enhancing seed yield of urdbean in Indian perspective.

Materials and Methods

A field experiment comprising of twenty-two genotypes including one check variety (Shekhar 2) was laid out in Randomized Block Design (RBD) with three replications at the Field Experimentation Centre, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology & Sciences, Prayagraj, Uttar Pradesh, during Zaid 2021. The genotypes were grown in the field row to row and plant to plant spacing of 30 cm x10 cm in each plot (1-m^2). The recommended package of practices was followed to raise the crop. The set of genotypes were assessed for genetic variability based on thirteen biometrical traits *viz*., days to 50% flowering (DF), days to 50% pod setting (DPS), days to maturity (DM), plant height (PHT)(cm), number of primary branches per plant (NPB/Pl.), number of clusters per plant (NC/PL), number of pods per plant (NP/Pl.), pod length(PL) (cm), number of seeds per pod(NS/pod), 100-seed weight (g), harvest index (HI)(%), biological yield per plant (BY/Pl.) (g) and seed yield per plant(SY/Pl.) (g). 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 broad-sense heritability was estimated as per Burton and Devane (1953). Besides, genetic advance and genetic gain as a percentage of mean were calculated using the formula suggested by Johnson *et al*. (1955).

RESULTS AND DISCUSSION

Analysis of Variance

Analysis of variance revealed significant differences among the genotypes for all the agro-morphological traits studied at 1% level of significance except pod length, which turns to be significant at 5% only (Table 1), indicating a considerable amount of variability in the present set of materials. Whereas, block effect was found to be non-significant for all biometric traits under study except days to 50% flowering, pod length, a number of seeds/pod, harvest index and seed yield per plant indicating requirement of blocks to eliminate the appreciable amount of environmental influence on these traits to judge the genotypic potential in the materials.

The estimate of the coefficient of variation was less than 5% for days to 50% flowering, pod setting and to attain maturity; and around 7-11% for pod length, number of seeds per pod, 100-seed weight, and harvest index (Table 1) justifying the experimental precision. Characters *viz.,* plant height, number of primary branches/plant and number of pods/plant had shown relatively high coefficient of variation (CV) and higher CV (24-25%) was recorded for a number of clusters/plant, biological yield/plant and seed yield/plant suggesting their highly versatile nature of expression under micro-changes of environment.

Mean performance

Among the test genotypes, UH 10 followed by IC 106-176 and LBG 20 produced more number of branches per plant (Table 2). VBN 08 recorded the highest number of clusters/plant (5.07), followed by IC 106-176. Pods per plant, seeds per pod, and 100-seed weight reflect direct bearing on seed yield. The genotypes VBN 08 (15.13) and IC 106 176 (14.46) recorded a higher number of pods per plant. VBN 08 produced longer pods (4.11cm) and bold seeds (100-seed weight=4.30 g) with a maximum number of seeds/pod (6.25). The said genotype, therefore, emerged as promising with the highest and statistically significant single plant seed yield (3.95 g) over the grand mean and even appreciably higher than the standard check “Shekhar 2” (3.26 g). The superiority in seed yield and other yield attributes in few test genotypes was also reported by Kumar *et al*. (2018). Higher number of primary branches and over-all canopy growth usually reflect high biomass production and biological yield. Genotypes with efficient partitioning of biomass to sink during seed filling are known to enhance seed yield potential. In the present study, seed yield per plant ranged from 0.65g in PBG 107 to as high as 3.95 g in VBN 08. Besides, IC 106-176 and the local land race “Barabanki” had high yield performance (>3.0 g/plant), almost at par with “Shekhar-2” (3.26 g/plant). VBN 08, IC 106-176 and Barabanki produced higher magnitude of biological yield coupled with high seed yield. Hence, the above genotypes with excellent genotypic worth can be utilized in future hybridization programmes for yield enhancement in genotypes.

Genetic Variability

Variation and selection are the two basic requirements of genetic improvement in any crop.

Table 1: Analysis of variance for agro-morphological traits among 22 genotypes of urdbean

		Mean sum of squares		
Sl. No.	*Characters*	*Replication (df=2)*	*Treatment (df=21)*	*Error (df=42)*
1.	Days to 50% flowering	8.770**	15.031**	0.503
2.	Days to 50% pod setting	0.242	12.124**	0.496
3.	Days to maturity	0.545	16.569**	0.879
4.	Plant height(cm)	1.662	19.519**	6.198
5.	No. of primary branches per plant	0.529	9.000**	0.374
6.	Number of clusters per plant	1.077	1.687**	0.630
7.	Number of pods per plant	7.034	15.802**	3.164
8.	Pod length(cm)	0.290*	0.166*	0.084
9.	No. of seeds per pod	1.303*	0.820**	0.311
10.	100-seed weight(g)	0.142	0.472**	0.131
11.	Harvest index (%)	66.859*	82.040**	18.793
12.	Biological Yield (g)	5.180	8.184**	2.008
13.	Seed yield per plant (g)	0.988**	1.102**	0.168

*,**Significant at $P_{0.05}$ and $P_{0.01}$, respectively

Table 2: Mean performance of 22 urdbean genotypes for agro-morphological biometric traits

Sl. No	*Genotypes*	*DF (days)*	*DPS (days)*	*DM (days)*	*PHT (cm)*	*NPB/Pl.*	*NC /Pl.*	*NP/ Pl.*	*PL (cm)*	*NS/ Pod*	*100-seed wt.(g)*	*H.I. (%)*	*BY/ Pl.(g)*	*SY/ Pl.(g)*
1.	IC-106-176	51.33	56.33	73.33	20.35	4.20	4.13	14.46	3.88	5.43	4.00	35.24	9.30	3.19
2.	AKU-16-03	51.67	57.33	74.33	17.94	3.67	2.66	9.60	3.59	5.00	3.99	38.22	5.11	1.93
3.	KU-96-7	51.00	57.00	73.33	17.87	3.80	3.33	11.13	3.79	5.22	4.00	44.40	5.25	2.35
4.	LBG-20	52.00	58.00	74.67	18.88	4.20	3.33	12.20	3.76	5.06	3.99	40.04	6.26	2.48
5.	LBG-645	49.33	55.33	71.33	16.33	3.00	2.80	10.06	3.73	5.24	3.97	48.66	4.05	1.96
6.	PDV-2	53.33	57.33	75.67	16.20	3.47	2.13	9.30	3.62	4.97	4.43	38.10	5.23	1.97
7.	BARABANKI	54.33	59.33	76.67	18.34	4.03	3.63	13.36	4.21	5.89	4.00	33.85	9.74	3.16
8.	PLU-1016	53.67	58.67	76.00	15.38	2.77	3.33	10.70	3.68	4.82	4.01	34.44	5.99	2.08
9.	IPU-99-16	52.33	58.33	74.67	14.92	2.90	2.27	8.13	3.55	4.80	4.00	40.10	3.88	1.57
10.	VBN-08	56.67	62.00	78.67	23.28	3.73	5.07	15.13	4.11	6.25	4.30	44.79	8.88	3.95*
11.	UH-10	51.33	57.00	74.00	16.57	4.67	3.67	12.40	3.29	5.53	4.20	41.08	7.34	2.99
12.	IPH-98-1	51.67	58.33	73.33	13.73	3.13	3.13	11.73	3.65	5.02	3.67	38.34	5.76	2.19
13.	PBG-107	56.00	61.33	78.67	12.88	3.00	1.87	5.60	3.47	4.40	2.93	43.78	1.52	0.65
14.	NDUK-13-4	56.67	62.67	79.00	21.21	3.97	2.53	7.20	3.47	4.97	3.63	23.13	5.63	1.30
15.	MU-06	51.33	57.33	73.33	19.41	3.47	2.70	10.86	3.47	4.56	4.01	39.92	5.33	2.09
16.	JU-2	51.33	56.67	73.00	15.02	2.67	2.93	9.87	3.47	4.32	3.60	34.67	4.72	1.60
17.	TBG-104	51.67	58.00	74.00	19.35	3.47	3.43	12.66	3.43	4.55	3.60	40.04	5.71	2.14
18.	IPU-02-43	51.33	57.33	73.33	14.46	3.67	2.87	8.67	3.35	4.51	3.33	40.99	3.29	1.31
19.	KU-321	51.67	57.67	74.00	18.77	2.70	3.23	11.33	3.76	4.39	3.66	44.70	5.08	2.30
20.	SN-2115	54.33	59.67	77.33	17.45	2.87	3.97	12.46	3.68	5.33	4.00	37.32	7.14	2.68
21.	IC-91-567	50.33	56.67	72.33	19.21	3.53	2.40	9.07	3.61	5.11	3.67	42.88	4.25	1.80
22.	SHEKHAR 2 (Check)	47.67	54.33	70.00	16.67	3.40	4.00	10.87	4.11	6.13	4.90	38.84	8.41	3.26
Grand Mean		52.30	58.03	74.59	17.47	3.47	3.16	10.76	3.67	5.068	3.905	39.25	5.81	2.23
$\text{CD}_{0.05\%}$		1.173	1.165	1.550	4.117	1.011	1.313	2.941	0.481	0.923	0.598	7.168	3.306	1.073
SE(m)±		0.409	0.407	0.541	1.437	0.353	0.458	1.027	0.168	0.322	0.209	2.503	1.154	0.374
SE(d)		0.579	0.575	0.765	2.033	0.499	0.648	1.452	0.238	0.456	0.295	3.540	1.632	0.530
C.V.(%)		1.355	1.214	1.257	14.254	17.626	25.152	16.52	7.884	10.90	9.259	11.04	24.391	24.146

*,** -Significant at $P_{0.05}$ and $P_{0.01}$, respectively

Without variation, selection becomes ineffective. Therefore, knowledge of the extent of genetic variability regarding various traits and their nature of transmission to the succeeding generations is indispensable for reliable selection.

A wide range of variation was observed for all the agro-economic traits, including seed yield per plant. The overall mean values, range, coefficient of variability, and critical difference (CD) were estimated and presented in Tables 2 & 3. The variance estimate may not give helpful information for comparison among agro-economic traits as it is not unit-free. Hence, the coefficient of variation, which is expressed in percentage, may be suitably used for comparison. In the present study, GCV gives an idea of the heritable component of variability, and it was highest for a number of primary branches/plant (48.85%), followed by seed yield per plant (24.97%), biological yield (24.68%), pod number (19.05%) and cluster number/plant (18.77%) suggesting wider scope for genetic augmentation in the crop. Estimates of GCV and PCV for days to flowering, pod setting, and maturity followed by pod length, seeds/pod, and 100-seed weight were negligible or narrow, and hence, selection for such traits may not be much effective compared to the rest of the traits, including seed yield per plant. Similarly, Ozukum and Sharma (2017) revealed sufficient genetic variability to justify selection for genetic improvement in this crop.

PCV was recorded higher than the GCV irrespective of the traits under study. However, the deviation was appreciably high in the case of pod length, number of clusters/plant, number of seeds/pod, and plant height, indicating significant genotype x environmental interaction for expression of these traits. These results are in accordance to the findings of Gowsalya *et al.* (2016), Mehra *et al.* (2016), Mohanlal *et al.* (2018) and Tank *et al.* (2018).

Heritability depends on the amount of genetic variation present in the population and the environmental conditions the population is evaluated (Allard, 1960).

Table 3: Estimates of variability parameters and expected genetic advance for 13 Agro-morphological biometric traits in urdbean

Sl. No.	*Characters*	*Mean*	*Range*	*GCV (%)*	*PCV (%)*	*h^2 (%)*	*$GA_{5\%}$*	*GA % of pop. mean*
1.	Days to 50% flowering	52.30	47.67–56.67	4.21	4.42	90.59	4.31	8.25
2.	Days to 50% pod setting	58.03	54.33–62.67	3.39	3.60	88.66	3.82	6.58
3.	Days to maturity	74.59	70.00–79.00	3.06	3.31	85.61	4.36	5.84
4.	Plant height (cm)	17.47	12.88–23.28	12.06	18.67	41.74	2.80	16.05
5.	No. of pry. branches /plant	3.47	2.67–4.67	48.85	51.93	88.49	3.28	94.66
6.	No. of clusters/ plant	3.16	1.87–5.07	18.77	31.33	35.87	0.73	23.15
7.	No. of pods/ plant	10.76	5.60–15.13	19.05	25.19	57.11	3.19	29.63
8.	Pod length(cm)	3.67	3.29–4.21	4.47	9.07	24.32	0.17	4.55
9.	No. of seeds per pod	5.07	4.32–6.25	8.13	13.67	35.34	0.50	9.95
10.	100-seed weight (g)	3.91	2.93–4.90	8.59	12.60	46.31	0.47	12.04
11.	Harvest index (%)	39.25	23.13–48.67	11.69	16.08	52.87	6.87	17.51
12.	Biological Yield/Pl.(g)	5.81	1.52–9.74	24.68	34.70	49.38	2.05	35.30
13.	Seed yield/ plant (g)	2.23	0.65–3.95	24.97	31.03	64.92	0.93	41.50

Table 4: Regression analysis of yield component traits on seed yield

Estimates of regression	*a-value*	*NC/plant (X_1)*	*NP/plant (X_2)*	*NS/pod (X_3)*	*100-seed wt. (X_4)*	*HarvestIndex (X_5)*
Standardized partial regression co-efficient(beta value)	-3.774	0.183*	0.49**	0.27**	0.206**	0.034
SE of partial regression coefficient	0.362	0.090	0.026	0.089	0.100	0.005
t- value of partial regression coefficient	-10.44	2.059	6.145	4.270	3.939	0.955
Partial regression equation	Y(Seed yield)= $-3.774 + 0.183 X_1 + 0.487X_2 + 0.271X_3 + 0.206X_4 + 0.034X_5$					

*,** -Significant at $P_{0.05}$ and $P_{0.01}$, respectively

The estimate of heritability (broad sense) alone is not used in predicting the resultant effect for selecting the best individuals or genotypes because it includes additive and non-additive gene effects. High genetic advance occurs only due to additive gene action (Panse, 1957). So, heritability estimates coupled with the genetic advance would be more useful than heritability alone. In the present investigation, heritability ranged from 24.32% for pod length to 90.59% in case of days to 50% flowering, whereas, genetic advance expressed as percentage of mean varied from 4.55% in pod length to as high as 94.66% in number of primary branches/plant (Table 3). Among the characters studied, number of primary branches/plant exhibited the highest genetic advance (94.66%) coupled with fairly high heritability (88.49%), indicating the presence of additive gene action for the character. So, the selection of genotypes basing on number of primary branches/plant can be fairly reliable. The finding corroborates Blessy et al.'s findings (2018) and Mohanlal *et al.* (2018). Seed yield per plant, biological yield per plant, number of pods per plant exhibited moderate heritability (50–65%) along with moderately high GA (% of mean), suggesting a role of both additive and non-additive mode of gene action. High heritability (85.6–90.6%) but with a very low genetic advance (6–8%) in case of days to flowering, pod setting, and maturity indicated the preponderance of non-additive gene action compared to additive mode. On the other hand, pod length and number of seeds per pod recorded low heritability with low genetic advance (% of mean), which envisaged the dominance and epistatic gene effects in inheritance of such traits and thus limited the scope for reliable selection of genotypes.

Selection Strategy

The knowledge of genetic variability and imposing a proper selection strategy is imperative for efficient sampling and utilization of germplasm. This warrants immediate genotypic characterization followed by pre-breeding to select valuable germplasm lines, resulting in a core germplasm collection. Morphological characterization of germplasm accessions for yield-related traits is an important step in this regard. Productivity *per se* is a complex character. Often, direct selection based on per se mean grain yield led to missing valuable breeding materials that otherwise have potential genotypic worth for some specific traits. Besides, the direct selection based on mean performance often leads to statistical error and a lack of precision. While regression analysis of yield component traits on seed yield could simultaneously establish a basis of selection based on important yield contributing characters. In the present set of test materials, the partial regression coefficients for the five most important yield determining traits were worked out (Table 4) to fit the regression equation Y (Seed yield) = $-3.774 + 0.183 X_1 + 0.487X_2 + 0.271X_3 + 0.206X_4 + 0.034X_5$; where, X_i –represents independent variables, e.g., number of clusters per plant (X_1), number of pods per plant (X_2), number of seeds per pod (X_3), 100-seed weight (X_4) and harvest index (X_5). Regression coefficients of all the above yield contributing traits were positive and significant, indicating that these have an appreciable influence on seed yield in urdbean. Further, the NP/Pl. seems to be the major contributing factor, followed by a number of seeds per pod and 100-seed weight for seed yield as revealed by the magnitude of partial regression coefficients (Table 4). Therefore, selection based on such component traits would enhance productivity in urdbean.

CONCLUSION

VBN 08 followed by IC-106-176 and "Barabanki" (a local land race) were the most promising genotypes with high yield potential as compared to standard check "Shekhar 2". The present set of materials retained a wide range of variations in the number of primary branches per plant, number of pods per plant, number of seeds per pod, and seed yield *per se*. Days to flowering, pod setting, maturity, and primary branches per plant were highly heritable in nature compared to seed yield per plant and its component traits. Genetic advance, a measure of expected genetic improvement due to the selection, was remarkably high for number of primary branches per plant, while it was moderately high for biological yield, seed yield, number of clusters per plant, and pods/plant. However, a regression equation formulated in this study considering all important yield contributing traits could be incredibly helpful for the realization of high yield potential genotypes through selection in urdbean breeding.

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