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Mohd. Ataur Rehman
Department of Genetics and
Plant Breeding, Naini
Agricultural Institute, SHUATS,
Prayagraj, Uttar Pradesh, India

Gabrial M Lal
Department of Genetics and
Plant Breeding, Naini
Agricultural Institute, SHUATS,
Prayagraj, Uttar Pradesh, India

Indranil Bhattacharjee
Department of Genetics and
Plant Breeding, Naini
Agricultural Institute, SHUATS,
Prayagraj, Uttar Pradesh, India

Genetic variability for quantitative traits in F_4 generation of blackgram ([*Vigna mungo* (L.) Hepper]

Mohd. Ataur Rehman, Gabrial M Lal and Indranil Bhattacharjee

Abstract
The genetic materials consisted of thirty one Urdbean genotypes. A Randomizes block design (RBD) with three replications was used. Experiment was conducted at CRF Dept of Plant Breeding and Genetics at Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences Naini, Prayagraj Uttar Pradesh in *Zaid* season 2019. Analysis of variance revealed significant differences among the genotypes for all the traits except days of 50% pod setting. The maximum yield obtained was SU-URD 72, followed by SU-URD 82, SU-URD 83, U-5, and UH-85-5. High estimate of heritability were exhibited for seed yield per plant, seed index, days of maturity, plant height, harvest index, biological yield, pod length and number of primary branches per plant the character. Therefore, it is concluded that the characters which showed high heritability coupled with genetic advance should be considered for direct selection. Here, seed yield per plant and harvest index the character under study showed high heritability and genetic advance. Thus, one should select these characters for direct selection.

Keywords: genetic variability, heritability, genetic advance, agronomic characters and black gram

Introduction
Legumes represent the second largest family of higher plants, second only to grasses in agricultural importance (Doyle and Luckow, 2003) [6]. Pulses are the principle source of dietary protein among vegetarians and are an integral part of daily diet because of their high protein content and good amino-acid balance in several forms world-wide. On account of balanced amino acid composition of cereals and protein blend, which matches with the milk protein, pulses are often called as life line of human beings. Proteins of grain legumes are generally high in lysine, but deficient in sulphur containing amino acids *i.e.* methionine and cysteine [Wang *et al.* 2003] [19]. Legumes adapt well to various cropping systems, owing to their ability to fix atmospheric nitrogen in symbiosis with soil bacteria of *Rhizobium spp.* Legumes adapt well to various cropping systems owing to their ability to fix atmospheric nitrogen in symbiosis with soil bacteria of *Rhizobium spp.* Urdbean [*Vigna mungo* (L.) Hepper, $2n = 2x = 22$] are important legume crop widely cultivated in Asia. *V. mungo var. silvestris* is the wild proginator of urdbean. It is utilized in several ways, where seeds, sprouts and young pods are consumed as sources of protein, amino acids, vitamins and minerals, whereas plant parts are used as fodder and green manure. It is a rich source of protein, minerals and vitamins providing higher calories. Generally, urdbean seeds contain 24% protein, 67% carbohydrates, 3-5% fibre and 1.74% fat and a major portion of lysine in the vegetarian diet Elangaimannan *et al.* (2008).

Creation of genetic variability and selection for important traits is a crucial activity that any plant breeder should apply to achieve better yield and other desirable agronomic traits. However, to carry out effective selection, the information on available genetic variation among urdbean genotypes, the nature of component traits on which selection would be effective and the influence of environmental factors on each trait need to be known. Information on the nature and magnitude of variability as well as heritability in a population is one of the prerequisites for successful breeding program in selecting genotypes with desirable characters (Dudly and Moll, 1969). It is therefore, of great importance for breeders to know the heritability of the agronomical characters to improve the yield of the crop effectively.

According to Falconer and Mackay (1996), heritability is defined as the measure of the correspondence between breeding values and phenotypic values. Thus, heritability plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. It is the breeding value which determines how much of the phenotype would be passed onto the next generation (Tazeen *et al.*, 2009).

Corresponding Author:
Mohd. Ataur Rehman
Department of Genetics and
Plant Breeding, Naini
Agricultural Institute, SHUATS,
Prayagraj, Uttar Pradesh, India

There is a direct relationship between heritability and response to selection, which is referred to as genetic advance. High genetic advance with high heritability estimates offer the most effective condition for selection (Larik *et al.,* 2000). The utility of heritability therefore, increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection programme. Knowledge of the extent and pattern of variability, heritability of the trait and genetic gain present in a population of Urdbean. The productivity of pulse crop is very low when compared to cereals, which have been selected for high grain yield under high input conditions, while the selection pressure in case of pulses have been focused on the adaptation to both biotic and a biotic stresses. Hence, this study was done with the objective to assess the variability, heritability and genetic advance of grain yield and some of its related components to select a more desired trait that may contribute towards the improvement of Urdbean.

Methods and Materials
Location and source of experiment
The experiment was conducted at Central Research Farm, Dept of Plant Breeding and Genetics at Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences Naini, Prayagraj, Uttar Pradesh in *Zaid* season 2019. The genetic materials consisted of thirty one Urdbean genotypes. A Randomizes block design (RBD) with three replications was used. Each genotype was sown in six rows with a row length of 4m in each plot. The Plant were spaced 10 cm within a row and 30 cm between rows. A basal dose of 20 kg N and 40 kg P_2O_5 ha^{-1} was applied at sowing time; all the recommended agronomic inputs and practices were applied to the crop during the season, to raise a healthy crop.

Observations
The data on seed yield and its components were recorded on five randomly plants taken in each genotypes from each replication for thirteen characters *viz.,* plant height, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, number of primary branches per plant, seed index, biological yield, harvest index and seed yield per plant. Days to 50% flowering, days of 50% pod setting and days of maturity were recorded on plot basis. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability and genetic advance in percent of mean were computed as per standard formulas.

Estimation of variability parameters
The magnitude of genetic and phenotypic variation *i.e.,* Genetic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) existing in a character was estimated by the formula given by Burton (1952) [3]. Heritability in broad sense (h^2) was calculated using the formula suggested by Burton and De Vane (1953) [4]. Expected genetic advance ($\overline{Ga}$) was estimated by the method suggested by Johnson *et al.* (1955) [8].

Result and Discussion
Variability parameters
Analysis of variance revealed significant differences among the genotypes for all the traits except days of 50% pod setting under study indicating the presence of substantial genetic variability in Urdbean (Table-1).

Table 1: Analysis of variance for seed yield and its component traits in Urd bean

Characters Source of variation	Mean sum of square		
	Replications	Treatments	Error
d. f.	2	30	60
Days of 50 % flowering	2.78**	2.88**	0.53
Days of 50% pod setting	8.35**	2.23	1.58
Days of maturity	1.00	16.53**	1.08
Plant height	21.96*	60.08**	4.86
No. of clusters per plant	10.84**	3.65**	1.12
No. of pods per plant	9.50	25.66**	9.59
Pod length	1.90**	0.08**	0.01
No. of seeds per pod	1.50**	0.08**	0.02
No of primary branches	0.92**	0.58**	0.11
Seed index	0.04	0.36**	0.02
Biological yield	0.42	11.48**	1.37
Harvest index	2.02	53.43**	4.73
Seed yield per plant	0.05	1.60**	0.05

* Significant at 5% L.S.
** Significant at 1% L.S.

Per se performance of genotypes and its range
For each of the traits evaluated, the descriptive statistics including the extreme genotype mean values and the means together with their standard errors obtained on the basis of average data are summarized in (Table-2). In general, Urdbean genotypes showed wide range of variability for most of the characters and all the traits exhibited broad spectrum of ranges between the maximum and minimum genotype mean values. For instance, days to 50% flowering ranged from 42.00 to 45.66 with a mean of 43.38, days to 50% pod setting ranged from 50.33 to 54.00 with mean of 51.77 days to maturity ranging from 60.33 to 68.66 with a mean of 64.19.

Similarly, plant height and number of clusters per plant ranged from 51.32 cm to 67.21 cm and 6.17 to 10.47, respectively while, number of pods per plant varied from 17.45 to 31.25 with of 25.29. Pods length ranged from 3.94 to 4.63 with a mean of 4.22, number of seeds per pod of the test genotypes varied from 6.34 to 7.17 with mean of 6.66. Number of primary branches per plant ranged from 4.72 to 6.37 with mean of 5.71, seed index ranged varied from 3.61 to 5.14 with mean of 4.32. Similarly, biological yield ranged

from 14.77 to 25.62 with mean of 19.37 and harvest index varied from 17.81 to 38.51 with mean value of 27.09.

The maximum yield obtained was SU-URD 72 (6.82g) followed by SU-URD 82 (6.68g), SU-URD 83 (6.35g), U-5 (6.08g) and UH-85-5 (6.05) and it ranged varied from 3.68 to 6.82 with mean of 5.19. Thus, it is possible to succeed in improving seed yield by direct selection. Similar results were reported by Kumar *et al.* (2015) [9], Sushmitharaj *et al.* (2018) [17], Chaithanya *et al.* (2019) [5], and Anuradha *et al.* (2020) [1]. In the present investigation character studied exhibited low, moderate and high PCV and GCV values, (Table-3). None of traits exhibited high GCV and PCV. The moderate genotypic and phenotypic coefficient of variation was recorded for the characters seed yield per plant (13.82 and14.51) followed by harvest index (14.87 and 16.89), number of clusters per plant (10.95 and 16.69), number of pods per plant (9.15 and 15.29)

and biological yield (9.48 and 11.24) while lowest recorded for days of 50% pod setting (0.90 and 2.59), followed by days of 50 % flowering (2.04 and 2.64), days of maturity (3.54 an d3.89), number of seeds per pod (2.12 and 3.07) and number of primary branches per plant (6.99 and 9.02). The moderate to high magnitude of phenotypic variation were composed of high genotypic coefficient of variations and less of the environment variations, which indicated high genetic variability for different traits and less influence of environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. Similar, results for low to moderate values of GCV and PCV were also found by Kumar *et al.* (2013) [10] Singh *et al.* (2013) [14], Srivastava and Singh (2012) [16], Sushmitharaj *et al.* (2018) [17] and Anuradha *et al.* (2020) [1].

Table 2: *Per se* performance of 31 genotypes for seed yield and its component traits in Urd bean

Genotypes	Days to 50 % flowering	Days of 50% pod setting	Days to maturity	Plant height	Number of clusters per plant	Number of pods per plant	Pod length	Number of seeds per pod	Number of primary branches per plant	Seed index	Biological yield	Harvest index	Seed yield per plant
SU-URD72	44.67	51.00	65.33	65.91	8.73	25.32	3.99	6.78	5.75	4.60	21.87	31.20	6.82
SU-URD73	43.00	51.00	64.33	66.86	8.40	26.25	4.09	6.63	5.83	4.51	19.31	24.36	4.69
SU-URD74	45.00	50.67	66.67	62.10	7.60	25.05	4.39	6.87	6.17	5.14	18.53	29.15	5.22
SU-URD75	44.67	51.00	62.33	64.81	8.27	30.38	4.09	6.63	6.37	4.39	17.23	21.54	3.68
SU-URD76	45.33	51.67	66.33	59.42	8.80	28.72	4.06	6.67	5.97	4.20	21.29	23.58	5.02
SU-URD77	45.67	52.00	62.00	57.50	7.60	22.78	4.08	6.80	6.03	3.67	21.20	26.36	5.58
SU-URD78	44.33	51.33	60.67	62.55	7.53	24.52	4.06	6.60	5.57	4.42	19.05	25.42	4.85
SU-URD79	44.33	50.33	63.67	52.70	7.93	24.78	3.94	6.50	5.90	4.72	19.54	29.43	5.75
SU-URD80	43.33	52.00	66.33	67.21	10.00	25.05	4.39	6.40	6.03	3.86	18.70	26.20	4.89
SU-URD81	43.67	54.00	65.33	61.56	10.13	26.52	4.42	6.50	6.37	4.43	19.88	22.57	4.48
SU-URD82	43.33	52.00	65.67	65.28	10.13	24.32	4.40	6.47	6.10	4.43	19.99	33.42	6.68
SU-URD83	42.33	53.33	60.33	59.46	9.13	26.32	4.42	6.57	6.23	4.35	19.06	33.32	6.35
SU-URD84	42.67	52.00	62.67	52.54	8.80	25.65	4.45	6.57	6.23	4.46	18.64	23.90	4.45
SU-URD85	44.00	52.00	66.67	62.98	8.27	24.72	4.01	6.57	5.77	4.50	19.62	21.05	4.12
SU-URD86	43.67	51.00	61.67	65.42	8.53	24.72	4.11	6.63	5.17	3.62	25.62	17.81	4.56
SU-URD87	43.00	50.67	63.33	53.78	7.40	22.72	4.08	6.63	5.63	4.25	20.49	26.32	5.38
SU-URD88	42.33	51.67	61.33	58.44	8.00	25.12	4.16	6.63	5.63	4.38	18.79	29.19	5.48
SU-URD89	42.33	52.00	63.33	66.78	7.33	21.12	4.20	6.70	4.97	4.53	19.46	25.26	4.92
SU-URD92	42.33	52.00	61.00	59.41	7.47	23.05	4.22	6.57	5.63	4.16	19.61	28.85	5.65
SU-URD93	42.67	51.67	63.33	57.54	8.67	26.18	4.23	6.63	5.30	4.37	17.97	30.97	5.55
SU-URD94	42.33	51.00	61.67	65.03	8.73	26.98	4.21	6.73	5.97	4.36	17.87	25.23	4.50
U-5	43.00	51.00	66.33	63.64	10.47	31.25	4.11	6.60	5.50	3.76	20.52	29.71	6.08
UH-85-5	42.33	52.00	65.33	59.62	9.93	30.65	4.28	6.73	6.17	3.90	20.40	29.66	6.05
PKG-4-3	43.00	51.00	65.67	55.82	9.00	27.98	4.18	6.57	5.77	4.50	17.60	25.63	4.48
UH-10	44.00	51.67	61.67	59.49	8.60	24.92	4.21	6.83	5.43	4.32	19.67	26.80	5.25
UH-21-84	43.33	52.00	63.67	61.44	8.27	24.65	4.18	6.77	5.63	4.52	20.59	23.74	4.88
PU-38	42.00	53.33	62.67	59.73	9.07	27.05	4.36	6.83	5.77	3.61	19.64	24.70	4.85
PU-31	42.67	53.00	67.33	56.72	8.60	25.85	4.31	6.93	5.50	4.78	20.90	25.61	5.35
PU-11-14	43.33	53.00	66.67	64.65	6.33	19.25	4.16	6.34	4.85	4.34	14.77	38.51	5.65
L-6	42.67	52.00	68.67	59.35	6.17	24.78	4.28	6.77	4.99	4.49	16.75	31.96	5.35
Shekhar2(check)	43.33	51.67	68.00	51.32	6.27	17.45	4.63	7.17	4.72	4.49	15.92	28.46	4.53
Mean	43.38	51.77	64.19	60.62	8.39	25.29	4.22	6.67	5.71	4.32	19.37	27.09	5.20
C.V.	1.68	2.43	1.62	3.64	12.60	12.24	2.53	2.21	5.69	3.20	6.03	8.03	4.41
S.E.	0.42	0.73	0.60	1.27	0.61	1.79	0.06	0.09	0.19	0.08	0.67	1.26	0.13
C.D. 5%	1.19	2.05	1.70	3.60	1.73	5.06	0.17	0.24	0.53	0.23	1.91	3.55	0.37
C.D. 1%	1.58	2.73	2.26	4.79	2.30	6.73	0.23	0.32	0.71	0.30	2.54	4.72	0.50

Table 3: Estimates of variability, heritability and genetic advance as percentage of mean

Characters	Range		Grand mean (x̄) ±SE	Coefficients of variability		Heritability (H$_{bs}$) (%)	Genetic advance (GA)	Gen. adv. as % of means (5%)
	Lowest	Highest		GCV	PCV			
Days of 50% pod setting	50.33	54.00	51.77±0.73	0.90	2.59	12.10	0.34	0.65
Days of maturity	60.33	68.67	64.19±0.6	3.54	3.89	82.70	4.25	6.62
Plant height	51.32	67.21	60.62±1.27	7.08	7.96	79.10	7.86	12.97
No. of clusters per plant	6.17	10.47	8.39±0.61	10.95	16.69	43.00	1.24	14.80
No. of pods per plant	17.45	31.25	25.29±1.79	9.15	15.29	35.80	2.85	11.28

Pod length	3.94	4.63	4.22±0.06	3.48	4.30	65.50	0.25	5.80
No. of seeds per pod	6.34	7.17	6.67±0.09	2.12	3.07	48.00	0.20	3.03
No of primary branches	4.72	6.37	5.71±0.19	7.00	9.02	60.20	0.64	11.18
Seed index	3.61	5.14	4.32±0.08	7.80	8.43	85.60	0.64	14.87
Biological yield	14.77	25.62	19.37±0.67	9.48	11.24	71.20	3.19	16.48
Harvest index	17.81	38.51	27.09±1.26	14.87	16.90	77.40	7.30	26.96
Seed yield per plant	3.68	6.82	5.2±0.13	13.82	14.51	90.80	1.41	27.13

Heritability

In general sense, heritability specifies the proportion of the total variability that is genetic causes, or the ratio of genotypic variance to the total variance. It is a good index of the transmission of characters from parents to their offspring (Falconer, 1960) [7]. The reliability of the phenotypic value depends on the estimates of heritability for a particular character. Therefore, high heritability helps in the effective selection for a particular character. In the present investigation heritability in broad sense was calculated for all characters under study and is presented in (Table 3). Heritability is classified as high (above 60%), medium (30%-60%) and low (below 30%) as suggested by (Johnson et al. 1955) [8]. High estimate of heritability were exhibited for seed yield per plant (90.80) followed by seed index (85.6), days of maturity (82.70), plant height (79.10), harvest index (77.40), biological yield (71.20), pod length (65.50) and number of primary branches per plant (60.20) the character under study. Moderate heritability was expressed in days of 50 % flowering (59.70) followed by number of seeds per pod (48.00), number of clusters per plant (43.00) and number of pods per plant (35.80) while days of 50% pod setting (12.10) had exhibited lowest heritability. High heritability values indicate that the characters under study are less influenced by environment in their expression. The plant breeder, therefore adopt simple selection method on the basis of the phenotype of the characters which ultimately improves the genetic background of these traits. Similar results were also quoted by Kumar et al. 2013 [10], Singh et al. 2013 [14], Zaid et al. 2013, Srivastava and Singh 2012 [16], and Rahim et al. 2010 [12] and Sushmitharaj et al. 2018 [17].

Genetic advance

The estimates of genetic advance as per cent of mean provide more reliable information regarding the effectiveness of selection in improving the traits. Genetic advance is defined as the differences between the mean genotypic value of the selected lines and the mean genotypic value of the parental population (original population before selection). In other words genetic advance denotes the improvement in the genotypic value of the new population over the original population. Genetic advance is usually expressed as percent of mean. The range of genetic advance as percent of mean is classified as suggested by (Johnson et al, 1955) [8]. Low less than 10%, moderate 10-20% and high more than 20%. Genetic advance estimates are depicted in (Table-3). Among the studied characters the high, moderate and low estimates of genetic advance as percent of mean was recorded. The genetic advance as percentage of mean was highest for seed yield per plant (27.13) and harvest index (26.95) recorded. However it was recorded moderate for biological yield (16.48) followed by seed index (14.87), number of clusters per plant (14.80), plant height (12.96), number of pods per plant (11.28) and number of primary branches per plant (11.18). Lowest genetic advance as percent of mean recorded for days of 50% pod setting (0.65) followed by number of seeds per pod (3.033) and days of 50 % flowering (3.25). Similar results were also reported by Kumar et al. 2013 [10], Singh et al. 2013 [14], Srivastava and Singh 2012 [16], Rahim et al. 2010 [12], Sushmitharaj et al. 2018 [17], Chaithanya et al. 2019 [5], and Anuradha et al. 2020 [1].

Conclusion

Therefore, it is concluded that the characters which showed high heritability coupled with genetic advance should be considered for direct selection. Here, seed yield per plant and harvest index the character under study showed high heritability and genetic advance. Thus, one should select these characters for direct selection.

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