Original Research Article

Genetic parameters Analysis for Grain Yield and Related Traits in Urdbean [*Vigna mungo* (L.) Hepper] Genotypes

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A B S T R A C T

Keywords

Genetic advance, Heritability, urdbean, Selection

The present investigation was made to study urdbean germplasms with an objective to estimates genetic variability parameters such as coefficient of variation, heritability, and genetic advance for yield and its associated traits. Proposed experimental materials included twenty-one urdbean genotypes with single check UTTARA that were evaluated during *Kharif*-2017. An experimental perusal conducted mainly depended on the selection of superior along with high variable genotypes that were analyzed in Randomized Block Design (RBD) with three replications. The results of the Analysis of Variance(ANOVA) revealed that genotypes were significant for all of the traits except seeds per pod included for proposed investigation and found to be highly variable for clusters per plant (CPP) followed by seeds per pod(SPP) and Harvest Index (HI). High heritability coupled with high genetic advance as percent of mean was recorded for CPP(80.00, 21.21) followed by SYP (95.00, 12.96),Harvest Index (73.00, 17.86), and BYP (74.00, 15.86). Thus, the present findings could be beneficial to develop superior genotypes through selection in urdbean breeding program.

Introduction

Urdbean [*Vigna mungo* (L.) Hepper] (2n=2x=22) belongs to the family *Leguminaceae*, also known as blackgram is an excellent source of easily digestible proteins with low flatulence which complements the staple rice diet in Asia. The major portion of seeds is utilized in making dal, curries, soup, sweets, and snacks. The sprouted seeds contain a good amount of vitamins such as Thiamine, Niacin, and Ascorbic acid (Dahiya *et al.,* 2015). Thus, urdbean sprouts are increasingly becoming popular in certain vegetarian diets. The grains contain approximately 25-28% protein, 1.0-1.5% oil, 3.5-4.5% fibre, 4.5-5.5% ash content and 62-65% carbohydrates on dry

weight basis. Blackgram also contains vitamin A, vitamin C, iron, calcium, magnesium, phosphorus, potassium, zinc, and foliate. Unlike other pulses, it free from flatulent effects in the stomach (Dahiya *et al.,* 2015).

Therefore, it is fed to babies and as a convalescent to elders. Urdbean crop is widely cultivated throughout South Asia including India, Pakistan, Bangladesh, Sri Lanka, Thailand, Cambodia, Vietnam, Indonesia, Malaysia, and South China. It is grown mainly as a *Kharif* seasonal crop. However, it can be cultivated in the *Rabi* season that is restricted to the eastern and southern parts of the country. Due to its short duration, it fits in rotation, intercropping, and mixture.

In a crop improvement program, variability present in crop plants is a pre-requisite, because it provides the base for effective selection and for selecting desirable genotypes towards the desirable direction.

A clear understanding of variability in various quantitative characters existing in the breeding material helps plant breeders for selecting superior genotypes based on different genetic parameters such as genotypic variation, heritability, genetic gain, etc. to understand the nature and magnitude of variation for the available plant characters Burton and DeVane (1953).

Hence, it is necessary to estimate the relative amount of genetic and non-genetic variability exhibited by the traits under the study. The average yield of urdbean is very low in India and year-to-year variation in yield is remarkably high. Therefore, there is an urgent need to design a breeding program that can enhance productivity and stabilize the yield. It has also been well established that the greater the genetic variability in the population greater will be the chance of obtaining desirable gene contribution. Previous studies have been made in consonance with the present study in respect of urdbean Chauhan *et al.,* (2007), Konda *et al.,* (2008), Kumar *et al.,* (2003), Natarajan and Rathinasamy (1999), Punia *et al.,* (2014) in urdbean, in mungbean Kushwaha *et al.,*(2013), Degefa *et al.,*(2014), Jebaraj *et al.,* (2015), Baisakh *et al.,* (2016) and Kumar *et al.,* (2020) and Sahoo *et al.,* (2019) in mothbean.

Since the human population is increasing, therefore, there is an urgent need to provide high yield varieties to meet demand.

Therefore, the present study has been undertaken to study genetic variability for different quantitative characters in urdbean germplasms.

Materials and Methods

The research experiment was carried out during *Kharif*-2017 comprising twenty-one genotypes including single check UTTARA at the Experimental Farm, the Department of Genetics and Plant Breeding, (SHUATS) Sam Higgin bottom University of Agriculture, Technology and Sciences, Allahabad. Recommend agronomic packages of practices were followed for a good crop.

The technique of random sampling was adopted for recording the observations of various quantitative characters of blackgram. Five plants of each treatment from each replication were selected at random at the time of recording the data on various characters. Data of five plants per replication were averaged and mean data was used for statistical analysis of the present investigation. Observations were recorded for twelve characters *viz.,* days to 50% flowering (DF), days to maturity (DM), plant height

(PH), number of primary branches per plant (BPP), number of clusters per plant (CPP), number of pods per plant (PPP), pod length (PL), seeds per pod (SPP), biological yield per plant (BYP), Seed Index (SI), Harvest Index (HI) and seed yield per plant (SYP).

Analysis of Variance (ANOVA)

The analysis of variance was estimated to test the differences among genotypes by F-test. It was carried out according to the procedure of Randomized Block Design for each character as per the methodology advocated by Panse and Sukhatme (1985).

Genetic variability parameters

Following genetic variability parameters worked out:

Mean

Mean value of each character was determined by dividing the total value by the corresponding number of observations included for the present study.

Range

Difference between the maximum and minimum mean value for each trait.

Components of variance

Two types of variance components (additive and dominance variance) were estimated as suggested by Burton and DeVane (1953).

Coefficients of variation

It is the measure of variability evolved. The coefficient of variation is the ratio standard deviation of the variable traits to its mean and expressed in percentage which was suggested by Sivasubramanian and Madhavamenon (1973).

Heritability

Heritability (broad sense) is the ratio of genotypic variance to the phenotypic variance that was suggested by Lush (1949) and Burton and DeVane (1953).

Genetic Advance

Improvement in the mean performance of selected plants over the base population is known as Genetic Advance, which was estimated as suggested by Johanson *et al.,* (1955).

Results and Discussion

Analysis of Variance (ANOVA)

Genetic variability in any plant breeding program is the first major requirement for deeming the effectiveness of selection. Its existence is crucial for resistance to abiotic and biotic stresseslikewise for wide adaptability also. The evaluation of genetic variability was the main objective of the present investigation. The analysis of variance mentioned in Table 1 indicated that the mean sum of squares of genotypes was significantly different at a 5% level of significance for DF, DM, PH, PBP, CPP, PPP, PL, BYP, SI, HI, and SYP except for SPP. The results indicated a wide range of variability among genotypes. Similar observations were recorded by Chauhan *et al.,* (2007), Konda *et al.,* (2008), Kumar *et al.,* (2003), Natarajan and Rathinasamy (1999), Punia *et al.,* (2014) in urdbean, Byregowda *et al.,*(1997), Das and Chakraborty (1998), Kapoor *et al.,* (2005), Eswari and Rao (2006), Hanif *et al.,* (2006), Wani *et al.,* (2009), Khan *et al.,* (2008), Kamleshwar *et al.,* (2013), Kushwaha *et al.,* (2013), Degefa *et al.,*(2014), Jebaraj *et al.,* (2015), Baisakh *et al.,* (2016) and Kumar *et al.,* (2020)in mungbean.

Genetic variability parameters

One of the important considerations in any crop improvement is the detailed study of genetic variability. Absolute variability is measured by the estimation of the phenotypic and genotypic coefficient of variation (PCV & GCV), heritability, genetic advance (GA), and genetic gain.

The environment also plays an important role in the expression of phenotype and genotype, a fact which are inferred from phenotypic observation. Therefore, variability can be observed through biometric parameters like the genotypic coefficient of variation, heritability, and genetic advance. These genetic variability parameters would be of great help to a breeder in evolving efficient selection programs for crop improvement.The estimates of varance, coefficient of variation, heritability, and genetic advance for all the thirteen characters studied have been presented in Table 2 and Figure 1 explained here as under:

Phenotypic and genotypic coefficient of variation

In the present investigation, it is depicted from Table 2 that in general, estimates of the phenotypic coefficient of variation (PCV) were found higher than their corresponding genotypic coefficient of variation (GCV), indicating that the little influence of environment on the expression of these characters.

However, good correspondence was observed in the genotypic coefficient of variation (PCV) and phenotypic coefficient of variation (GCV) in all the characters. The result of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) presents are summarized as under: A wide range of phenotypic coefficient of variation

(PCV) was observed for all the traits ranged from 12.92 (clusters per plant) to 3.66 (pod length).

A higher quantum of PCV was observed for clusters per plant (12.92), seeds per plant (11.96), harvest index (11.88), pods per plant (10.91), and biological yield per plant (10.37). A moderate value of PCV was observed for the number of primary branches per plant (7.24) and seed yield per plant (6.65). Whereas the rest of the traits depicted the least phenotypic coefficient of variation.

High phenotypic coefficient of variation (PCV) for the number of clusters per plant and seed yield per plant was reported earlier by Loganathan *et al.,* (2001) and Kumar *et al.,* (2010) also reported moderate phenotypic coefficient of variation (PCV) for the number of seeds per plant followed by the number of pods per plant and number of branches per plant.

Genotypic coefficient of variation (GCV) ranged from 11.53 (clusters per plant) to 2.14 (pod length). A higher magnitude of GCV was recorded for CPP (11.53), HI (10.15), pods per plant (9.00), and BYP (8.94).

A moderate value of GCV was observed for the seed yield per plant (6.47), the number of primary branches per plant (5.95). Whereas the rest of the traits depicted the least genotypic coefficient of variation. Sirohi *et al.,* (2006) observed significant GCV for number of clusters per plant, number of effective branches per plant, number of pods per plant, biological yield per plant, and seed yield per plant.

Kumar *et al.,* (2010) also reported a moderate genotypic coefficient of variation (GCV) for the number of seeds per plant, followed by seed yield per plant, number of pods, and number of branches per plant.

Table.1 Analysis of Variance (ANOVA) for twelve characters of urdbean

Characters	Replication	Treatment	Hybrids	Parents	Hybrids vs. Parents	Checks vs. Hybrids	Checks vs. Parents	Error
Degree of freedom	**2**	**20**	**9**	**9**	**1**	**1**	**1**	**40**
DF	3.57	7.45**	4.52	5.98	40.01	5.60	25.64	1.23
DM	1.85	13.20**	12.89	14.99	13.07	0.88	0.36	2.84
PH	0.10	6.00**	4.05	7.08	6.33	9.25	16.95	1.12
PBP	0.02	0.09**	0.08	0.08	0.24	0.05	0.20	0.01
CPP	0.06	3.93**	2.24	5.26	10.41	2.22	0.01	0.30
PPP	5.79	19.79**	13.31	7.41	45.24	0.00	7.91	2.68
PL	0.01	0.03*	0.03	0.03	0.00	0.02	0.01	0.01
SPP	0.06	0.54	0.53	0.47	0.81	0.59	1.33	0.36
BYP	0.25	9.74**	8.85	12.11	0.12	5.35	6.07	1.01
HI	0.97	20.13**	16.04	21.86	61.08	5.19	1.11	2.21
SI	0.00	0.06**	0.06	0.04	0.15	0.07	0.19	0.01
SYP	0.01	0.26**	0.14	0.13	2.50	0.02	0.68	0.01

*, ** significant at 5% and 1 % of the level of significance

Table.2 Estimates of genetic variability parameters for all the traits to be used under present investigation

Character	GV	PV	GCV	PCV	h^2	GA	GA as % of mean
DF	2.07	3.31	3.71	4.69	63.00	2.35	6.04
DM	3.45	6.30	2.87	3.87	55.00	2.84	4.38
PH	1.62	2.75	2.82	3.67	59.00	2.02	4.46
PBP	0.03	0.04	5.95	7.24	67.00	0.27	10.06
CPP	1.21	1.52	11.53	12.92	80.00	2.02	21.21
PPP	5.70	8.39	9.00	10.91	68.00	4.06	15.28
PL	0.01	0.02	2.14	3.66	34.00	0.10	2.58
SPP	0.06	0.42	4.51	11.96	14.00	0.19	3.51
BYP	2.91	3.92	8.94	10.37	74.00	3.03	15.86
HI	5.97	8.19	10.15	11.88	73.00	4.30	17.86
SI	0.02	0.03	3.90	4.57	73.00	0.24	6.86
SYP	0.09	0.09	6.47	6.65	95.00	0.59	12.96

Fig.1 Graphical representation of genetic parameters under study
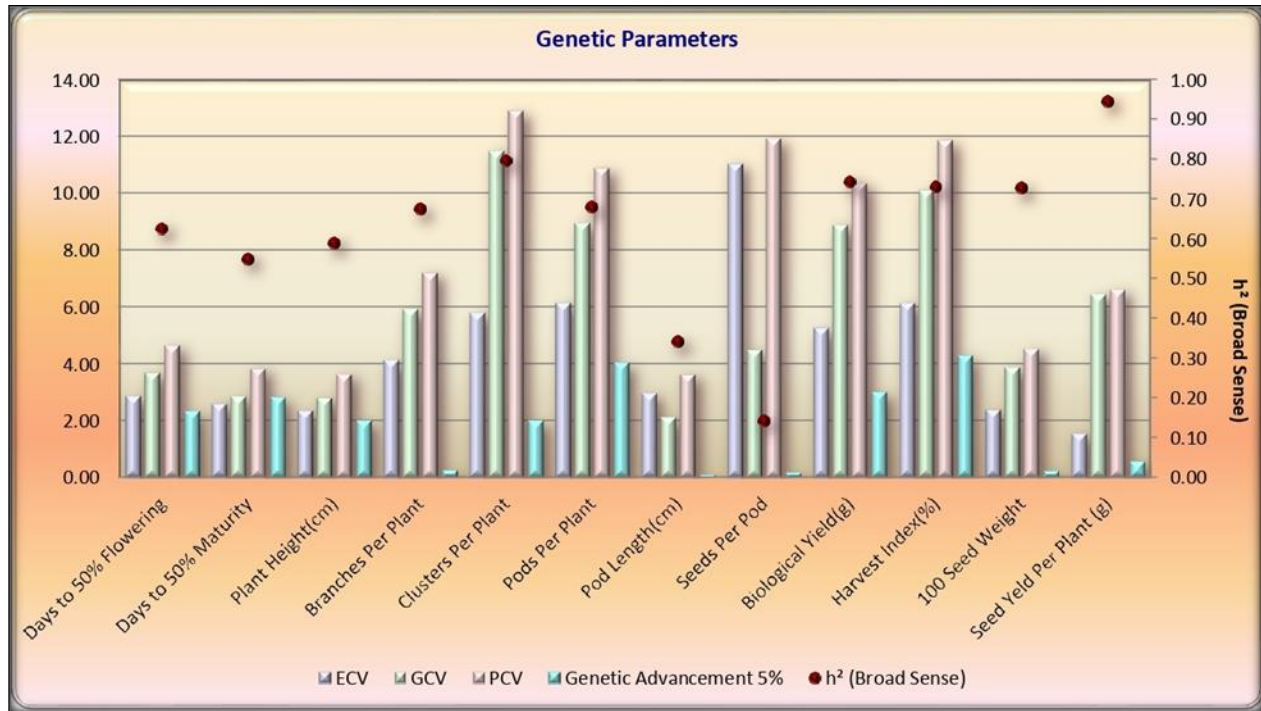
Das *et al.,* (1998) reported that plant height,number of branches per plant pods per plant, pod length, and yield per plant had a high genotypic coefficient of variance (GCV) suggesting the possibility of improvement of urdbean by selective breeding.Similar findings were reported by Das *et al.,* (1998); Neelavati and Govindarasu (2010) suggesting sufficient variability and thus scope for crop improvement through selection for these traits. Therefore, the studies on GCV and PCV indicated that the presence of a high amount of variation and the role of the environment on the expression of these traits. The differences between PCV and GCV were less to moderate for most of the characters indicating a lesser contribution of environment towards an expression of these characters.

Heritability

Heritability is a measure of the extent of phenotypic variation caused by the action of genes (Lush, 1949). For making effective improvement in the character for which selection is practiced, heritability has been adopted by a large number of workers as a reliable indicator.In the present investigation heritability and genetic advance have been worked out for all the thirteen quantitative characters and are presented in table 2.

High estimates of heritability in a broad sense were recorded for all the characters under study, which ranged from 95.00 (seed yield per plant) to 14.00 (seeds per pod). High heritability was observed for most of the traits *viz.*seed yield per plant (95.00), clusters per plant (80.00), biological yield per plant (74.00), harvest index (73.00), and seed index length (73.00).Moderate heritability was observed for the traits *viz.* pods per plant (68.00), the number of primary branches per plant (67.00), and plant height (59.00) whereas the rest of the traits were showed low heritability. High heritability was recorded for the seed yield per plant, clusters

per plant, biological yield per plant, harvest index, and seed index lengthindicating that these traits are likely to be controlled by an additive geneaction. Previously, Das *et al.,* (1998) and Loganathan *et al.,* (2001) also reported similar findings in mungbean genotypes.

Genetic advance as percent of mean

The estimate of genetic advance (GA) as a percent of mean ranged from 21.21 (clusters per plant) to 2.58 (pod length). Whereashigh GA as a percent of mean was observed for CPP (21.21), HI (17.86), BYP (15.86), PPP (15.28), and SYP (12.96). High heritability with high genetic advance was recorded for SYP, CPP, BYP, and HI suggesting that these traits were under the control of additive gene action and selection will be more useful for yield improvement. Moderate heritability with high genetic advance was found for PPP, showing the lesser influence of environment with additive gene action, hence, amenable for selection. High heritability with moderate genetic advance (GA) as a percent of mean was observed for seed index indicating that these traits were less influenced by the environment but governed by both additive and non-additive gene action. Therefore, the selection is suggested for the improvement of these traits in the later generations. Wani *et al.,* (2007), Jebaraj *et al.,* (2015), Baisakh *et al.,* (2016), and Kumar *et al.,* (2020) found similar results for plant height, branches per plant, and seed yield in mungbean.

Estimates ofanalysis of variance (ANOVA) revealed that sufficientsignificant genetic variability was found among urdbean genotypes. In general, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all the quantitative traits. High magnitude of GCV and PCV were observed

for CPP, HI, PPP, and BYP. High heritability coupled with high genetic advance (GA) as a percent of mean was observed for SYP followed by CPP, BYP, and HI. Therefore, these characters can be used for effective selection. It has been concluded that biological yield per plant, clusters per plant, pods per plant and seed yield per plant apart from a high genotypic coefficient of variation, estimates of heritability with genetic advance (GA) as a percent of mean were high, therefore, direct selection may be rewarded for these two traits.

Authors' contribution

Conceptualization of research; designing of the experiments; execution of field experiments and data collection; analysis of data and interpretation; preparation of the manuscript.

Acknowledgement

Conflicts of Interest

The authors declare no conflict of interest.

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