Genetic Variability, Heritability, and Genetic Advance in Mung Bean [*Vigna radiata* (L.) Wilczek] Genotypes

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Abstract

Assessment of genetic variability in crop species is one of the major activities to meet the diversified goals in plant breeding programs. However, there is a lack of sufficient information on the genetic variability study of mung bean. Therefore, field experiment was conducted on sixty mung bean genotypes with the objectives to assess the genetic variability, heritability, and genetic advance for desirable traits that have a vital role in determining and designing breeding strategies. The experiment was conducted at Jinka Agricultural Research Center laid out in a 6 × 10 alpha lattice design with two replications during the 2018 cropping season. The analysis of variance revealed highly significant ($P \leq 0.001$) differences for most of the traits indicating the existence of high genetic diversity among the genotypes. High estimates of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) was observed for harvest index (48.77% and 59.73%). The lowest GCV and PCV estimates were obtained for days to flowering (3.26% and 6.82%), days to maturity (2.08% and 4.20%), seed yield per hectare (0.34% and 0.45%), and biomass yield per hectare (0.08% and 0.13%). Terminal leaf length, terminal leaf width, peduncle length, plant height, number of primary branches per plant, seeds per pod, seed yield per plant, hundred seed weight, seed yield per hectare, biomass yield, and harvest index exhibited high heritability values. High heritability coupled with high GAM estimates was recorded for plant height, the number of primary branches per plant, hundred seed weight, and harvest index. In general, the observed variability could help to develop breeding schemes for mung bean.

Keywords: Diversity, Heritability, Phenotypic variation, Quantitative traits, Selection

Introduction

Mung bean [*Vigna radiate* (L.) Wilczek] is an important legume crop. It is a self-pollinated crop with a diploid chromosome number of 2n = 2x = 22 and a genome size of 579 Mb (Parida *et al.,* 1990). Mung bean seed is rich in easily digestible protein which makes it an important component of a balanced diet. Seeds are also a very good source of the minerals calcium, iron, zinc, potassium, phosphorus, and vitamins such as vitamin K and dietary fibers (Keatinge *et al.,* 2011). It can restore soil fertility through nitrogen fixation. Mung bean is one of the most important grain legumes extensively cultivated in arid, semi-arid, and subtropics of the world. It is one of the most important pulse crops and becoming the most important cash crop in Ethiopia after the common bean.

Assessment of genetic diversity in mung bean genotypes would facilitate the development of elite cultivars. Omima *et al.* (2018) suggested that having information on the magnitude of genetic variability is the number one criterion for successful breeding. Genetic variability is a key for the success of a plant breeding program since it provides an opportunity to breeders to make the selection for desirable superior individuals from a genetically diverse base population (Partap *et al*., 2019). Understanding the level of genetic variability might support plant breeders' decision on the selection of parental genotypes with a broad genetic base for further genetic improvement and amenities in the development of the breeding strategy (Souza and Sorrells, 1991; Singh, 2002; Denton and Nwangburuka, 2011; Prasanthi *et al.,* 2012; Omima *et al*., 2018). The lack of adequate variability has been considered as one of the major bottlenecks in mung bean improvement and the success of its improvement needs the use of wide genetic variability in respect of important economic characters present in the population (Bhanu *et al*., 2016).

Estimates of genetic parameters indicate the relative importance of the various types of gene effects affecting the total variation of a plant character. Heritability plays a significant role in plant breeding and serves as an extrapolative guide to realize the breeding value. The estimation of heritability along with genetic advance is more applicable than the heritability value alone (Johnson *et al.,* 1955; Shukla *et al*., 2006). There is a direct relationship between heritability and response to selection, which is referred to as genetic advance (Nwangburuka and Denton, 2012; Ogunniyan and Olakojo, 2015; Omima *et al.,* 2018). Genetic advance used as a measure to predict the expected progress and to find the actual gain expected under selection (Larik *et al.,* 2000; Nwangburuka and Denton, 2012; Ogunniyan and Olakojo, 2015). If the value of genetic advance is large in the succeeding generation, there will be good progress over the population mean. Genotypic and phenotypic coefficients of variation along with heritability plus genetic advance are very essential to improve traits of interest (Denton and Nwangburuka, 2011; Gbaguidi *et al.,* 2013).

Since many characters of economic importance are highly influenced by environmental conditions; the improvement of a crop mainly depends upon the amount, nature, and magnitude of genotypic variability present in the population. Yimram *et al*. (2009) suggested that the quantitative nature of agro-morphological traits like the genotypic variance, phenotypic variance, heritability, and the genetic advance are the most important traits for phenotypic selection of crops. However, proper evaluation of the extent of genetic variation available for yield components, their heritability values, and genetic advance could be of great significance for the breeders to choose the best genotypes for improvement (Itefa *et al.,* 2014).

Mung bean is a highly self-pollinated crop lacks natural variability for seed yield and yield-related traits is very narrow in mung bean which makes the selection ineffective. Saeed *et al*. (2007) observed low genetic variability in mung bean genotypes due to the narrow genetic backgrounds of local collections. Genetic diversity studies on black gram genotypes have been reported by different authors (Sharma *et al.,* 2006; Konda *et al.,* 2009; Senapati and Mishra, 2010; Reddy *et al.,* 2011; Meshram *et al.,* 2013; Deepshikha *et al.,* 2014; Ramya *et al.,* 2014; Kumar *et al.,* 2015; Patel *et al.,* 2015; Gowsalya *et al.,* 2016; Patidar *et al.,* 2018). Though, information on the genetic diversity, heritability, and genetic advance of mung genotypes in Ethiopia is limited. Therefore, the present study was conducted to assess the genetic variability, heritability, and genetic advance of mung bean genotypes.

Materials and Methods

Descriptions of the Study Area

The field experiment was conducted at Jinka Agricultural Research Center (JARC) during the main cropping season from March to June 2018. Jinka Agricultural Research Center is located 729 km southwest of Addis Ababa at 36^0 33’ 02.7” E, 05^0 46’ 52.0” N, and at an altitude of 1420 meters above sea level. The maximum, minimum, and average temperatures of the center are 27.68^0C, 16.61^0C, and 22.14^oC, respectively with the mean annual rainfall of 1381 mm. The soil type of the center is Cambisols (Mesfin *et al*., 2017).

Experimental Materials

The experimental materials consisting of sixty mung bean genotypes were used for this study, fourty four genotypes were obtained from Melkassa Agricultural Research Center (MARC) and 16 genotypes were collected from Southern Nations, Nationalities, and People’s (SNNP) (Table 1).

Table 1. List of genotypes used for diversity study in 2018

Genotype	Code	Genotype	Code	Genotype	Code	Genotype	Code
VC6489-9-1	G38	N-26	G43	NLLP-MGC-04	G4	Acc003	G47
NLLP-MGC-10	G10	NLLP-MGC-16	G16	NVL-1	G44	Acc004	G48
NLLP-MGC-06	G6	VC2778A(KPS2)	G29	NLLP-MGC-15	G15	Acc005	G49
NLLP-MGC-20	G20	VC6469-12-34A	G37	HARSHA	G39	Acc006	G50
NLLP-MGC-14	G14	NLLP-MGC-09	G9	NLLP-MGC-08	G8	Acc007	G51
NLLP-MGC-19	G19	VC6368(46-40-4)	G34	NLLP-MGC-05	G5	Acc008	G52
NLLP-MGC-21	G21	NLLP-MGC-01	G1	NM92(VC6370-92)	G31	Acc009	G53
NLLP-MGC-11	G11	NLLP-MGC-24	G24	NLLP-MGC-23	G23	Acc0010	G54
NLLP-MGC-12	G12	VC6492-59A	G35	V2709 BG	G42	Acc0011	G55
VC1973A	G28	VC6370(30-65)	G33	NLLP-MGC-27	G27	Acc0012	G56
VC6510-151-1	G36	NLLP-MGC-07	G7	VC3890A	G30	Acc0013	G57
CN9-5	G41	NLLP-MGC-26	G26	NLLP-MGC-25	G25	Acc0014	G58
NLLP-MGC-02	G2	NLLP-MGC-17	G17	NLLP-MGC-22	G22	Acc0015	G59
NM94(VC6371-94)	G32	NLLP-MGC-18	G18	Acc001	G45	Acc0016	G60
BARI-MUNG 2	G40	NLLP-MGC-03	G3	Acc002	G46	NLLP-MGC-13	G13

Genotypes with initial “Acc” were obtained from Southern Nations, Nationalities, and People’s Region (SNNPR), and other genotypes were obtained from Melkassa Agricultural Research Center (MARC); G: Genotype.

Experimental Design and Procedures

The experiment was laid out using a 6 × 10 alpha lattice design. The plot size was 3 m long, 0.3 m between rows, and 0.05 m between plants. It consists of five rows accommodating 60 plants per row. The distance between plots, intra blocks, and replications was 1, 1.5, and 2 m, respectively.

Data Collection

The descriptor of mung bean developed by the International Board for Plant Genetic Resources (IBPGR, 1980) was followed for data collection. A plot basis data collected for days to flowering, days to maturity, and hundred seed weight (g), The data were collected from the central three rows for the determination of seed yield includes seed yield per plot (g), biomass yield (g), and harvest index (%). While, plant basis data collected for plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, pod length (cm), peduncle length (cm), number of pods per cluster, terminal leaflet length (cm) and terminal leaflet width (cm).

Data Analyses

The analysis of variance (ANOVA) was carried out by using the SAS computer software version 9.0 (SAS, 2007) as per the following linear model for alpha lattice design. The means were separated by using the Duncan procedure at 5%, 1%, and 0.1% levels of significance. The linear model for the alpha lattice design is as follows:

$Y_{ijk}=\mu+R_i+B_{ij}+T_k+e_{ijk}$

Where μ=the grand mean of trait Y; Ri= the effect of Replicate i; Bij= effect of Block j within Replicate I; Tk=Effect of treatment k., eijk=error

Estimation of phenotypic and genotypic variance components

The phenotypic and genotypic variance components and coefficient of phenotypic and genotypic variability were estimated based on the method suggested by Burton and De vane (1953) as follows:

Genotypic variance (σ^2g) = $\frac{MS_g - MS_e}{r}$

Environmental variance (σ^2_e) mean square = MS_e

Phenotypic variance (σ^2p) = $\sigma^2_g + \sigma^2_e$

Where: MS_g = mean square due to genotypes

MS_e = Environmental variance (error mean square)

r = Number of replications

The phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) was estimated following the procedure of Kumar *et al.* (1985) as:

Phenotypic coefficient of variation (PCV) = ($\sqrt{\sigma^2 p}$ /grand mean) x 100

Genotypic coefficient of variation (GCV) = ($\sqrt{\sigma^2 g}$ /grand mean) x 100

Estimation of broad-sense heritability and genetic advance

Broad sense heritability (H) expressed as a percentage of the ratio of the genotypic variance ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 p$) and was estimated on genotype mean base as described by Allard, (1999) as:

Heritability ($h^2 b$) = ($\sigma^2 g / \sigma^2 p$) x100

Genetic advance in the absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes were estimated following the methods illustrated by Johnson *et al.* (1955) as; GA= $K^*\sigma_P * h^2 b$

Where: K = the standardized selection differential at 5% selection intensity (k=2.063), σ_P = phenotypic standard deviation on mean basis, $h^2 b$ = heritability in broad sense

Genetic advance as percent of the mean was calculated to compare the extent of the predicted advance of different traits under selection, using the formula described by Comstock and Robinson (1952).

$GAM = \frac{GA}{\bar{X}} X100$ Where:

GAM=genetic advance as percent mean, GA=genetic advance under selection, $\bar{X}$ = Mean of the population in which selection employed.

Results and Discussion

Analysis of Variance

The analysis of variance results showed significant differences among mung bean genotypes for all the studied traits (Table 2). The observed genotypic and phenotypic variations among the genotypes indicated the presence of genetic variability for yield improvement by selection. Similarly, the presence of variability among mung bean genotypes reported from different studies (Hemavathy *et al.*, 2015; Shiv *et al.*, 2017; Himabindu and Roopa Lavanya, 2017; Muthuswamy *et al.*, 2019; Dhunde *et al.*, 2021). Likewise, Garg *et al.* (2017) observed significant differences amongst 30 mung bean genotypes for days to flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, pod length, 100-seed weight, seed yield, biological yield, and harvest index. Similar results were reported by several authors (Rao *et al.*, 2006; Singh *et al.*, 2009; Reddy *et al.*, 2011; Dhoot *et al.*, 2017), who observed significant differences among the mung bean genotypes for the number of seeds per pod, hundred seed weight, seed yield per hectare, biomass yield and harvest index. Similar results were recorded (Balachandran *et al.*, 2010; Kumar *et al.*, 2015; Priyanka *et al.*, 2016; Nagmi and Lal, 2017; Rolaniya *et al.*, 2017; Partap *et al.*, 2019) on black gram genotypes, indicating that the presence of considerable genetic variability among the genotypes.

Simple Measure of Variability

The estimates of means, range, genotypic, and phenotypic variances and their coefficients of variation, heritability in a broad sense, genetic advance, genetic advance as a percentage of means, and standard errors of the studied traits for sixty mung bean genotypes were presented in (Table 3). High variability was recorded for peduncle length, seeds per pod, seed yield per plant, hundred seed weight, seed yield per hectare, biomass yield, and harvest index for the tested genotypes (Table 3). Therefore, the present finding showed that the presence of inherent genetic variability among the mung bean genotypes, suggesting a good opportunity for the selection of genotypes with desirable traits for further improvement. The existence of variability suggesting that the presence of additive gene effects is important for improving those traits through direct phenotypic selection. Similar study results were reported by Reddy *et al.* (2003) on 36 mung bean genotypes, Khairnar *et al.* (2003) on 22 mung bean genotypes, Rao *et al.* (2006) on 60 mung bean genotypes, and Makeen *et al.* (2007) on 646 mung bean genotypes.

The variance due to days to flowering showed that the genotypes differed significantly (Table 2) and the mean values ranged from 30 to 47 days with an overall mean of 41.68 (Table 3). Early flowering was recorded on most of the studied genotypes except in a few genotypes. The variance due to days to maturity depicted that the genotypes differed significantly (Table 2) and the mean values ranged from 75 to 97 days with an overall mean of 90.98 (Table 3). The present study showed that most of the genotypes attained their maturity early, suggesting a good opportunity to obtain drought escaping materials from the tested genotypes in the drought-prone areas of the country through simple phenotypic selection. This result is in line with the report of Mak and Yap (1980), who suggested that early maturity may provide an opportunity for selection for drought-stressed environmental conditions.

The analysis of variance results depicted that there were significant variations observed among the genotypes for the terminal leaf width (Table 2). As indicated in Table 3, the mean values for terminal leaf length ranged from 3.2 to 9.8 (cm) with a mean of 5.88 (cm), while the mean values for terminal leaf width ranged from 6.2 to 15.0 (cm) with the overall mean of 10.28 (cm). The analysis of variance results revealed that there were significant differences observed among the genotypes for plant height (Table 2). The mean for plant height (cm) ranged from 18.4 to 78.2 with an overall mean of 37.42 (Table 3). The values for peduncle length (cm) ranged from 4.6 to 13.0 with an overall mean of 8.35 (Table 3). The analysis of variance results for pod length showed that there were significant variations observed among the genotypes for pod length (Table 2). The mean for pod length (cm) ranged from 5.0 to 13.6 with an overall mean of 9.88 (Table 3). The analysis of variance results for pods per plant showed that there were significant variations observed among the genotypes for the number of pods per plant (Table 2) and ranged from 9.0 to 46.0 with an overall mean of 19.52 (Table 3). The analysis of variance results depicted that there were significant differences observed among the genotypes for the number of seeds per pod (Table 2) and ranged from 4.0 to 13.0 with the mean value of 9.53 (Table 3). This finding is in agreement with the report of Ahmad *et al*. (2012), who observed a sufficient amount of variability for seeds per pod with the mean value for seeds per pod ranged from 5.18 to 10.85 on mung bean genotypes. As shown in (Table 2), the analysis of variance results depicted that there were significant differences observed among the genotypes for seed yield per hectare. As indicated in Table 3, the values for seed yield per hectare ranged from 0.81 to 1.81 (t ha^{-1}) with a mean of 1.24 (t ha^{-1}). From these results, it was suggested that there was a wide range of variability among mung bean genotypes for seed yield and yield-related traits.

Table 2. Analysis of variance for 17 quantitative traits studied on mung bean at Jinka, in 2018.

Traits	Mean Square of Replication (DF=1)	Mean Square of Genotype (DF=59)	Mean Square of Blocks Within Rep (DF=10)	Mean Square of Error (DF=49)	LSD (5%)	CV (%)
DTF	67.500**	9.915*	24.296***	6.217	5.007	5.98
DTM	25.208ns	18.194*	69.042***	11.058	6.679	3.66
PTL	0.012ns	2.867*	1.777ns	1.671	2.596	15.48
TLL	8.154*	2.961*	3.411*	1.568	2.515	21.30
TLW	1.666ns	3.367**	2.128ns	1.564	2.512	12.17
PDCL	0.200ns	3.814***	1.366ns	0.891	2.347	11.30
PHT	11.163ns	127.264***	44.957ns	32.373	11.428	15.21
BRN	0.033ns	0.745***	2.015***	0.276	1.056	17.34
PODL	2.760ns	4.727*	2.650ns	1.580	3.269	12.72
PPC	7.500*	1.632*	1.200ns	0.389	2.200	15.03
PPP	163.33ns	60.237*	41.37ns	38.167	12.40	31.65
SPP	1.220ns	4.621***	2.045ns	1.719	2.634	13.76
SYPP	0.0029ns	0.3050**	6.0788***	0.1400	0.7515	9.42
HSW	5.663***	1.661***	7.017***	0.424	1.308	12.17
SYLD	572683***	49792***	260218***	14178	239.159	9.60
BM	12580601***	458227***	3111440***	184920	863.727	9.89
HI	0.0037***	0.00057***	0.00258***	0.0002	0.0289	4.88

LSD=least significance difference, CV = coefficient of variation (%), DF= degree of freedom, DTF=days to flowering, DM= days to maturity, PTL = petiole length (cm), TLL = terminal leaf length (cm), TLW = terminal leaf width (cm), PDL = peduncle length (cm), PHT= plant height (cm), BRN=number of primary branches per plant, PODL = pod length (cm), PPC=number of pods per cluster, PPP=number of pods per plant, SPP= number of seeds per pod, SYPP= seed yield per plant (g), HSW= hundred seed weight (g), SYLD= seed yield (kg ha^{-1}), BM= biomass yield (kg ha^{-1}), HI=harvest index.

Estimations of Genetic Parameters

Estimates of variance components

Genetic parameters such as genotypic variance, phenotypic variance, genotypic and phenotypic coefficients of variation (GCV and PCV %), heritability, and genetic advance are presented in Table 3. The GCV and PCV values for days to flowering (3.26% and 6.82%), days to maturity (2.08% and 4.20%), petiole length (9.28% and 18.04%), terminal leaf length (14.2% and 25.57%), terminal leaf width (9.23% and 15.29%), peduncle length (13.2% and 19.27%), plant height (18.41% and 23.88%), the number of primary branches per plant (15.83% and 23.57%), pod length (10.32% and 19.44%), the number of pods per cluster (11.3% and 28.71%), number of pods per plant (17.02% and 35.93%), the number of seeds per pod (12.64% and 18.68), seed yield per plant (10.08% and 13.56%), 100-seed weight (14.72% and 19.06%), and harvest index (48.77% and 59.73%). Similar results were reported by Garg *et al.* (2017) for the number of pods per plant, biological yield, harvest index, and seed yield per plant; by Rao *et al.* (2006) for pods per plant, seed yield per plant, and biological yield; by Pandey *et al.* (2007) for harvest index and seed yield per plant; by Kumhar and Chaudhary (2007) for seed yield per plant; and Makeen *et al.* (2007) and Anand *et al.* (2016) for the number of pods per plant and seed yield; by Mehandi *et al.* (2013) for the number of clusters per plant and plant height; Hozayn *et al.* (2013) for plant height and 100-seed weight; Jyothsna and Anuradha (2013) for pod length; Swathi (2013) for the number of clusters per plant; Garg *et al.* (2017) for plant height, the number of branches per plant and 100-seed weight, thus offering the moderate scope for further improvement of these traits through simple selection. Therefore, the study of GCV and PCV in mung bean genotypes showed variability for almost all the studied traits (Table 4), indicating the existence of wider genetic variation among the genotypes, and these results were strongly supported by the previous works on snake gourd (Rana and Pandit, 2011; Deepa and Mariappan, 2013; Ahsan *et al.*, 2014; Khan *et al.*, 2016).

The PCV and GCV values were considered as low (0 to 10%), moderate (10 to 20%), and high with the value greater than 20% (Sivasubramaniah and Madhavamenon, 1973; Deshmukh *et al.*, 1986). In this study, the result of variance components, genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV) of the traits exhibited that the magnitude of GCV and PCV was maximum for harvest index (48.77% and 59.73%), while moderate estimates of GCV and PCV were observed for traits such as hundred seed weight (14.7% and 19.0%), the number of seeds per pod (12.6% and 18.6%), pod length (10.3% and 19.4%), seed yield per plant (10.08% and 13.5%) and peduncle length (13.23% and 19.2%). This finding is in agreement with the work of Sharma *et al*. (2018) reported moderate estimates GCV and PCV for most of the studied traits on mung bean genotypes. In the present study, moderate GCV and highest PCV values of (14.23%, 25.5%), (18.41%, 23.8%), (15.83%, 23.5%), (11.30%, 28.7%) and (17.02%, 35.9%) were noted for terminal leaf length, plant height, the number of primary branches per plant, the number of pods per cluster and the number of pods per plant, respectively (Table 3).

However, low GCV and moderate PCV estimates were observed for petiole length (9.28% and 18.0%) and terminal leaf width (9.23% and 15.2%), indicating that the presence of a narrow spectrum of variability for these traits and the existence of a high environment influence leading to the limited scope for improvement by simple phenotypic selection alone. In this line Shiv *et al*. (2017) reported low to moderate GCV and PCV values for plant height, primary branches per plant, and hundred seed weight. The result also depicted that the lowest GCV and PCV estimates (3.26% and 6.82%), (2.08% and 4.20%), (0.34% and 0.45%), and (0.08% and 0.13%), were recorded for days to flowering, days to maturity, seed yield per hectare and biomass yield per hectare, respectively (Table 3). Sharma *et al*. (2018) similarly observed low estimates of GCV and PCV for the number of seeds per pod (7.87% and 9.05%), days to maturity (6.11% and 6.20%), days to 50% flowering (6.03% and 6.11%), pod length (3.52% and 6.83%). Likewise; Mehandi *et al*. (2013) reported low estimates of GCV and PCV for days to 50% flowering, days to maturity, and pod length; Garg *et al.* (2017) for days to 50% flowering and days to maturity; Jyothsna and Anuradha (2013) also reported low estimates of GCV and PCV for days to flowering, and Swathi (2013) for relative water content. Also, Makeen *et al.* (2007), Nan and Anuradha (2013), and Kumhar and Choudhary (2007) reported low GCV and PCV values for most of the studied traits on mung bean. Therefore, offering little scope for further improvement of these traits through simple selection, but it rather indicated that there is considerable possibility of further improvement through crossing followed by appropriate selection for these characters.

In the present investigation, the PCV values of all traits were higher than GCV values, indicating that the greater influence of the environment on these traits. This finding is in harmony with the previous reports on mung bean genotypes (Sadiq *et al*., 2005; Siddique *et al*., 2006; Makeen *et al*., 2007; Tabasum *et al*., 2010; Sheetal *et al*., 2014; Jangra and Yadav, 2015; Abbas *et al*., 2018; Sandhiya and Saravanan, 2018). Likewise, Jagdhane *et al*. (2017) reported that the magnitude of PCV was higher than GCV for the number of clusters per plant (32.51%, 31.33%) followed by the number of primary branches per plant (32.95%, 30.58%), the number of pods per plant (24.07%, 20.07%), plant height (12.10%, 12.74%), harvest index (11.89%, 13.09), seed yield per plant (10.16%, 11.49%), and seeds per pod (8.33%, 12.44%) on 20 mung bean genotypes.

The estimates for GCV ranged from 0.08% for biomass yield per hectare to 48.77% for harvest index. The values for PCV ranged from 0.13% for biomass yield per hectare to 59.73% for harvest index (Table 3). This finding is in line with the report of Jangra and Yadav (2015) who observed wide differences between phenotypic (PCV) and genotypic (GCV) coefficient of variance in traits like days to maturity and the number of branches per plant, signifying that their susceptibility to environmental fluctuations than other characters with narrow differences. Generally, high genetic variability was observed among the mung bean genotypes for all the studied traits. The observed variability was the sum of variation arising due to the genotypic and environmental effects. As a result, knowledge of the nature and magnitude of genetic variations contributing to the genetic gain under selection is essential.

The maximum values for the difference between GCV and PCV were recorded for pods per plant (17.02 to 35.94%) followed by pods per cluster (11.30 to 28.7%), indicating that the expressions of these traits were relatively more influenced by the environments. However, the minimum differences between GCV and PCV estimates were noted for harvest index (48.77 to 59.7%) followed by biomass yield per hectare (0.08 to 0.13%), indicating that these traits had low environmental influence and had a reasonable effect on genotypic factors or fixable genes on the expression of these traits. This result agreed with the previous reports by Pandiyan *et al.*, (2006), Prakash (2006), Rao *et al.* (2006), Singh *et al.* (2009), Kumar *et al.* (2010), Suresh *et al.* (2010), Tabasum *et al.* (2010), Reddy *et al.* (2011), Prakash and Shekhawat (2012), Gadakh *et al.* (2013), Prasanna *et al.* (2013), Ahmad *et al.* (2014), Javed *et al.* (2014), Ahmad *et al.* (2015), Das and Barua (2015), Muralidhara *et al.* (2015), Vir and Singh (2016), and Shiv *et al.* (2017) who reported that a narrow gap between GCV and PCV, indicating a narrow range of environmental influence on the studied traits. Generally, the existence of narrow gaps between the genotypic coefficients of variation and that of the phenotypic variation for some of the studied traits indicated that phenotypic variability was largely due to genetic differences and less environmental influence. In general, phenotypic and genotypic coefficients of variations suggested that there are good opportunities for the improvement of mung bean through direct selection. Therefore, selection based on the phenotype alone can be effective for the improvement of these traits.

Estimates of heritability and genetic advance

The results of broad-sense heritability (H^2) and genetic advance for various traits of mung bean genotypes are presented in Table 3. Estimates of heritability ranged from (15.49%) for the number of pods per cluster to (66.67%) for harvest index (Table 3). Heritability values are used to predict the expected progress to be achieved through the process of selection. As reported by Dabholkar (1992), heritability is generally classified as low (<10%), moderate (10-30%), and high (>30%). Higher magnitudes of heritability were observed for harvest index (66.67%), hundred seed weight (59.62%), plant height (59.45), seed yield per hectare (55.94%), seed yield per plant (55.17%), peduncle length (47.1%), for the number of seeds per pod (45.74%), for the number of primary branches per plant (45.1%), and biomass yield per hectare (42.49%). Abbas *et al.* (2018) correspondingly reported higher magnitudes of heritability were observed for the hundred seed weight (97%), plant height (94%), biological yield (89%), pods per plant (83%), harvest index (85%), and seed yield (84%) on mung bean genotypes and which agrees with the earlier reports of (Rohman and Hussain, 2003; Siddique *et al.*, 2006; Idrees *et al.*, 2006) on mung bean.

In the present study, heritability estimates of greater than 30% were recorded for terminal leaf width, peduncle length, plant height, number of primary branches per plant, seeds per pod, seed yield per plant, hundred seed weight, seed yield per hectare, biomass yield and harvest index. Therefore, these highly heritable traits are expected to remain stable under different environments, as the environment is less influential and could easily be improved through selection pressure. High heritability estimates indicated the variability observed was mainly under genetic control with less environmental influence on the traits. A similar result reported by Singh *et al.* (2014), indicated that there were high heritability values observed for the studied traits, indicating that the variation arises due to additive genetic effect. This is inline with the previous studies on mung bean (Kapoor *et al.*, 2005; Sadiq *et al.*, 2005; Gul *et al.*, 2007; Ahmad *et al.*, 2012; Perera *et al.*, 2017), on black gram (Veerasmani *et al.*, 2005), on chickpea (Arshad *et al.*, 2002; Khan *et al.*, 2005), and on lentil (Neha *et al.*, 2005; Hakim *et al.*, 2006). In general, traits having high heritability estimates were mainly controlled by additive types of genes while those traits with low heritability indicate those characters are highly influenced by environmental effects and governed by the non-additive types of genes.

Though the estimates of high heritability alone will not ensure the amount of gain through selection, rather a heritability estimate with GAM considered together can help to conclude the nature of gene action governing particular traits. Johnson *et al*. (1955) indicated that the estimates of heritability alone fail to indicate the response to selection. As suggested by Johnson *et al.* (1955), GMA percent was considered as low (<10%), moderate (10-20%), and high (>20%). The estimate of genetic advance as percent of the mean (GMA) at 5% selection intensity ranged from 0.11% (biomass yield per hectare) to 82.14% (harvest index). Heritability alone does not provide a true indication of the genetic potentiality of the genotypes due to interaction between genotype and environment. The selection of traits based on heritability and genetic advance as percent of mean is of great importance to the breeder for making criteria for improvement in a complex character. High genetic advance coupled with high heritability was observed for plant height (29.28% and 59.45%), the number of primary branches per plant (21.93% and 45.1%), hundred seed weight (23.44% and 59.6%), and harvest index (82.14% and 66.67%). Dhunde *et al*. (2021) similarly observed high heritability estimates (52.9%) coupled with high genetic advance as percent of the mean (20.074%) for the trait plant height on thirty-five mung bean genotypes, indicating the impact of additive gene expression and which coincides with the earlier reports by (Jagdhane *et al*., 2017; Shiv *et al*., 2017; Ramakrishnan *et al*., 2018) for the number of primary branches per plant and pods per plant on mung bean. Similarly, Garg *et al*. (2017) observed high heritability and high genetic advance for plant height, number of branches per plant, pod length, number of seeds per pod, hundred seed weight, and number of pods per plant, biological yield, seed yield, harvest index. Similar results reported by Hemavathy *et al.,* (2015) , Pandey *et al.* (2007), Itefa *et al.* (2014), Rao *et al.* (2007), Hari *et al.* (2017) Godakh *et al.* (2013) and Jagdhane *et al*. (2017) for different traits for plant height, seed yield per plant, number of pods per plantight, seed yield per plant and harvest index, and biological yield per plant. Also, Jagdhane *et al*. (2017) reported that high heritability (99.00%) coupled with high genetic advance was observed in the biological yield of 20 mung bean genotypes.

High heritability values coupled with high genetic advance as a percent of mean were reported by Ahmad *et al.* (2012) for hundred seed weight, pod length, and pods per plant; by Yusufzai *et al.* (2017) for the number of pods per plant, which coincides with the report by Itefa *et al.* (2014) for seed yield per hectare and pods per plant on mung bean genotypes. Similar results were obtained on black gram genotypes (Sharma *et al.,* 2006; Konda *et al.,* 2009; Balachandran *et al.,* 2010). Likewise, various authors (Nehru *et al.,* 2009; Idahosa *et al.,* 2010; Manggoel *et al.,* 2012; Ajayi *et al.,* 2014) reported high heritability coupled with high GAM for hundred seed weight on cowpea genotypes, indicating that the possibility of direct selection. Similarly, high heritability with a high genetic advance in percent of mean was observed on soybean genotypes (Jain and Ramgiry, 2000; Mehetre *et al*., 2000; Agarwal *et al*., 2001). Likewise, Ansari *et al.* (2004) reported that a high heritability estimate observed on bread wheat genotypes reflects the large heritable variance which may offer the possibility of improvement through direct selection.

In the present study, high heritability along with high genetic advance as percent of mean was observed for some of the traits, indicating the preponderance of additive gene action with low environmental influence for the determination of these traits, and hence simple selection would be more effective for the improvement of these characters. This result is in line with various reports that high heritability estimates along with high genetic advance as a percent of the mean for some of the studied traits on mung bean genotypes (Jain and Ramgiry, 2000; Mehetre *et al*., 2000; Agarwal *et al*., 2001; Sultana, 2015), indicating that the traits were controlled by additive genes and direct selection of these characters would be effective. Singh and Rai (1981) suggested that high heritability coupled with high genetic advance is an indicator of a greater proportion of the additive genetic variance and consequently a high genetic gain is expected from the selection. Therefore, the selection of these traits would offer the opportunity for the improvement of seed yield in mung bean. On the contrary, low heritability coupled with low genetic advances as a percent of mean for days to maturity was noted on mung bean genotypes (Sultana, 2015), which coincides with the work of Nehru *et al.* (1999) who observed low heritability coupled with low genetic advance as a percent of the mean. Low heritability for seed yield was reported by Tickoo and Jain (1988) on mung bean.

High heritability and moderate genetic advance as a percent of mean have been observed for terminal leaf length, terminal leaf width, and peduncle length, the number of seeds per pod, and seed yield per plant indicating equal importance of additive and non-additive gene actions. Therefore, this signifying that selection for the traits could be effective for mung bean improvements since the expression of the trait is governed by additive genes and is less influenced by environmental factors. There is an influence of fixable additive gene effects on the inheritance of these traits, and therefore, selection for these traits might lead to fast-track genetic improvement. This finding is in agreement with the work of Singh *et al.* (2009) in green gram genotypes, who reported that high heritability and moderate genetic advance as a percent of mean for days to 50% flowering and days to maturity on mung bean. Similar observations were reported (Idahosa *et al*., 2010; Ajayi *et al.*, 2014) on cowpea and Nehru *et al.* (1999) on soybean genotypes.

Moderate heritability coupled with moderate GAM was observed for the number of pods per plant, indicating that traits might be governed by nonadditive gene action and such traits could not be improved through simple or direct selection. Moderate heritability coupled with low GAM was observed for days to flowering, days to maturity, petiole length, and pods per cluster, signifying that the type of gene action that governs the expression of these traits is non-additive gene action, and also the environment had negatively influenced the expression of the traits. This finding is in line with Dhunde *et al.* (2021) reported moderate heritability coupled with low genetic advance as percent mean for some of the studied traits on thirty-five mung bean genotypes. Similar results were reported in mung bean (Tabasum *et al.,* 2010; Himabindu and RoopaLavanya, 2017; Shiv *et al.*, 2017). In this study high heritability and low GAM estimates were observed for seed yield per hectare and biomass yield per hectare. This finding is in agreement with the report of (Rao *et al.,* 2006; Makeen *et al.*, 2007) on mung bean.

Table 3. Estimates of mean, range, variance components, coefficients of variability, heritability, and genetic advance of the 17 quantitative traits of mung bean at Jinka, in 2018.

Traits	Mean ± SE	Range	σ^2_g	σ^2_e	σ^2_{ph}	GCV	PCV	H^2b	GA	GAM
DTF	41.68±0.28	30-47	1.85	6.22	8.07	3.26	6.82	22.92	1.34	3.22
DTM	90.98±0.39	75-97	3.57	11.06	14.63	2.08	4.20	24.40	1.93	2.12
PTL	8.35±0.14	4.6-13	0.60	1.67	2.27	9.28	18.04	26.43	0.82	9.84
TLL	5.88±0.15	3.2-9.8	0.70	1.57	2.26	14.23	25.57	30.97	0.96	16.34
TLW	10.28±0.14	6.2-15.0	0.90	1.56	2.47	9.23	15.29	36.44	1.18	11.49
PDL	8.35±0.14	4.6-13.0	1.22	1.37	2.59	13.23	19.27	47.10	1.56	18.73
PHT	37.42±0.81	18.4-78.2	47.45	32.37	79.82	18.41	23.88	59.45	10.96	29.28
BRN	3.03±0.0691	2.0-3.0	0.23	0.28	0.51	15.83	23.57	45.10	0.66	21.93
PODL	9.88±0.17	5.0-13.6	1.04	2.65	3.69	10.32	19.44	28.18	1.12	11.30
PPC	4.15±0.101	2.0-5.0	0.22	1.20	1.42	11.30	28.71	15.49	0.38	9.18
PPP	19.52±0.651	9.0-46.0	11.04	38.17	49.20	17.02	35.93	22.44	3.25	16.63
SPP	9.53±0.161	4.0-13.0	1.45	1.72	3.17	12.64	18.68	45.74	1.68	17.63
SYPP	3.97±0.06	2.42-5.42	0.16	0.13	0.29	10.08	13.56	55.17	0.61	15.44
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SYLD	1.24±0.026	0.81- 1.81	17.81	14.17	31.84	0.34	0.45	55.94	6.51	0.52
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
HI	0.29±0.005	0.14-0.31	0.02	0.01	0.03	48.77	59.73	66.67	0.24	82.14

DTF=days to flowering, DM= days to maturity, PTL = petiole length (cm), TLL = terminal leaf length (cm), TLW = terminal leaf width (cm), PDL = peduncle length (cm), PHT= plant height (cm), BRN=number of primary branches per plant, PODL = pod length (cm), PPC=number of pods per cluster, PPP=number of pods per plant, SPP= number of seeds per pod, SYPP= seed yield per plant (g), HSW= hundred seed weight (g), SYLD= seed yield (t ha^{-1}), BM= biomass yield (t ha^{-1}), HI=harvest index.

Conclusions

There were significant variations observed among the mung bean genotypes for most of the studied traits. Harvest index was found to be with high estimates of GCV and PCV which indicated the presence of enough variation among the genotypes for this trait. The estimates of variances due to genotypic, phenotypic, and environmental effects for the seventeen characters of mung bean showed wide variation among different traits. A wide range of phenotypic variability was observed among all the traits studied. Maximum genotypic and phenotypic variances (GCV and PCV) was recorded for harvest index (48.77% and 59.73%), whereas lowest for biomass yield per hectare (0.08% and 0.13%) followed by seed yield per hectare (0.34% and 0.45%). Therefore, there is a chance for selection for the majority of the traits in the genotypes. The phenotypic coefficients of variability had higher values as compared to their corresponding genotypic coefficients for all traits, indicating that the environment had a significant role in the expression of traits, which makes the selection for such traits based on the phenotypic variance alone is often misleading.

High estimates of heritability coupled with high genetic advance as a percent of mean were recorded for plant height, the number of primary branches per plant, a hundred seed weight, and harvest index. Therefore, the presence of high heritability values coupled with high genetic advance as a percent of the mean for these traits suggested that the preponderance of additive gene action with low environmental influence and the improvement of these characters and could be effective through direct phenotypic selection. Thus, this is an opportunity for the improvement of mung bean genotypes. Terminal leaf length, terminal leaf width, peduncle length, plant height, number of primary branches per plant, seed yield per plant, hundred seed weight, seed yield per hectare, biomass yield per hectare, and harvest index showed high heritability values which are believed to be governed by additive gene actions and selection for their improvement could be effective. High heritability coupled with high genetic advance as percent of the mean are attributed to additive gene effect was observed for plant height, hundred seed weight, and harvest index. Hence, high heritability coupled with moderate genetic advance estimates for terminal leaf length, terminal leaf width, peduncle length, the number of seeds per pod, and seed yield per plant and seed yield per hectare.

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