

Assessment of Genetic Variation and Heritability for Morpho-agronomic Traits in Mungbean Germplasm under Cold Stress

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ABSTRACT: Cold stress during early stage of crop growth badly affects the survival of plants and drastically reduces the seed yield. Therefore, a set of 230 genotypes of mungbean were assessed for genetic variability, heritability, genetic advance for yield and related ancillary traits over two locations in winter season. The test germplasm lines revealed significant variability for all the traits. The estimates of PCV were higher than GCV for all characters under study and the deviation was comparatively more in case of single plant seed yield suggesting greater influence of G × E interaction. The broad sense heritability estimates were found higher in number of days to 50% flowering, plant height, 100-seed weight, pod length and seeds per pod. Higher estimates of heritability along with extremely high genetic advance was observed for number of clusters per plant indicating major role of additive gene action. Such component trait-specific selection would be rewarding for enhancement of yield potential under cold stress in the winter season.

Keywords: Genetic variability, heritability, genetic advance, seed yield, yield related traits, cold stress, mungbean

INTRODUCTION

Mungbean (*Vigna radiata* L. Wilczek) is considered as an important short duration tropical and subtropical pulse crop (Roychowdhury *et al.*, 2012). The crop is a native of India and Central Asia (Singh and Singh, 2021). It harbours higher amount of proteins (about 24%), minerals and vitamins. It is also chief source of essential amino acids particularly lysine, which is reported to be minimum in most of the cereals. Owing to short duration and photo-thermo insensitivity, mungbean is well fit to a variety of crop rotation and offers a scope to enhance soil fertility through symbiotic nitrogen fixation (Ali and Kumar 2006; Idress *et al.*, 2006). In India, mungbean occupies an area of 3.38 mill ha with an average productivity of 4.74 qt/ha and production of 1.61 million tonnes (IIPR Annual Report 2015-2016). Yield potential of mungbean is reported to be in the range of 2.5-3.0t/ha although, its average productivity is staggering low at 5.0qt/ha (Nair *et al.*, 2019 and Pratap *et al.*, 2021). Primarily due to low yield potential of the available varieties with indeterminate habit, flower and fruit drop, poor source-sink relationship, poor harvest index and lack of cold and moisture stress (Malla *et al.*, 2014). The main hindrance for breeding in the crop lies with narrow genetic variability and sensitivity to a variety of biotic and abiotic stresses. Low temperature

in the early growing season greatly affects mungbean cultivation and results a significant reduction in relative growth rate and seed yield (Chen *et al.*, 2017). In this context, assessment of genetic variation present in the primary gene pool seems to be the most important factor to explore elite germplasm with desirable traits. Fluctuations in environment is the major factor for appreciable G × E interaction that generally hinder proper assessment of yield. Assessment of genetic variability, heritability and genetic advance of the characters at least over two location can offer proper choice of base material and mode of selection for genetic improvement in the crop. The study of heritability coupled with genetic advance is more justifiable than the heritability alone. Hence, the information of variability (both genotypic and phenotypic level), heritability, genetic advance is beneficial during selection process in breeding programs. Keeping in view the above facts, the present investigation was undertaken to gauge the extent of genetic variability and other genetic parameters in set of 230 available mungbean germplasm lines under cold stress situation during winter season.

MATERIALS AND METHODS

The experimental materials (230 genotypes) including standard ruling varieties, important pre-released cultures were laid out in randomized block design

(RBD) in two replications. The trial was sown on 13th December 2018 at Bhubaneswar and 13th January 2020 at Jeypore location in Odisha to expose the crop to low temperature stress at the early growth stage (Fig. 1). Each genotype was represented by two rows with

spacing of 30cm×10cm. Fertilizers were applied @ 20:40:20 kg of N: P₂O₅: K₂O along with 3.0 ton FYM per hectare. Other standard cultural operations or practices were taken up as per normal package of practices.

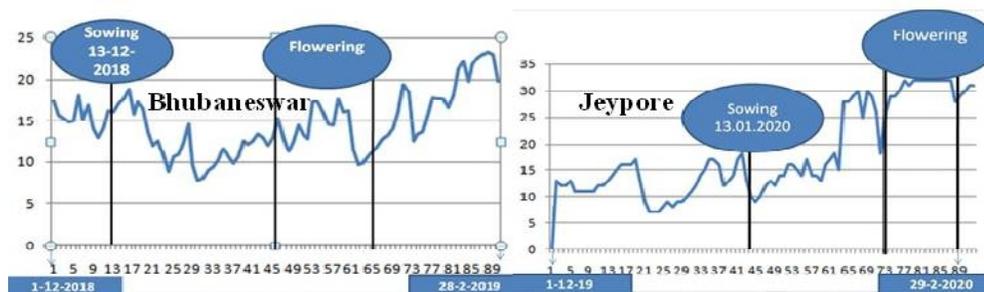


Fig. 1. Minimum temperature at sowing time at Bhubaneswar and Jeypore location.

A sample size of five random plants of each genotype per replication were used for the collection of data on 8 quantitative traits including single plant seed yield. The replication mean values of each character was considered for analysis of variance (Singh and Choudhury 1985) and the data were further analyzed for study of genetic variability as suggested by Burton (1952). Estimates of heritability (h_b^2) and genetic advance for each quantitative trait were calculated following the standard statistical procedure of Burton and Devane (1953) and Johnson *et al.*, (1955) respectively.

RESULTS AND DISCUSSION

A. Analysis of variance

The presence of natural variability among the genotypes was apparent from the broad range for each of the traits under study. Genotypic difference among these genotypes was found to be statistically significant at 1% level for all agro-morphological traits suggesting presence of substantial variability among the genotypes under investigation which will be much beneficial for the selection of breeding materials. Similar wide range of variations with different set of collections for different traits in mungbean has been reported by Khajudpam and Tantasawat (2011), Patel *et al.*, (2012); Raturi *et al.*, (2014); Pinchhyo *et al.*, (2016). Wide range of variation revealed in different traits in the present study envisaged their diverse origin. Clusters number per plant and seeds per pod followed by pod number per plant revealed wider range than other agronomic traits which indicated greater scope for enhancing seed yield through selection pressure on above component traits.

B. Phenotypic and Genotypic Coefficient of Variation

The ultimate desirable outcome of selection in a crop depends upon the genetic variation present within the population and/or among genotypes subjected to selection. In the present study, estimates of phenotypic co-efficient of variability (PCV) exceeded the genotypic co-efficient of variability (GCV) for all agro-morphological traits under study indicating appreciable environmental influence. This result was in conformity with the findings of Rahim *et al.*, (2010); Kumar *et al.*,

(2010a); Degefa *et al.*, (2014). Higher estimates of GCV and PCV were observed for seed yield/plant as also reported earlier by Kumar *et al.*, (2010b); Rahim *et al.*, (2010), Khajudpam and Tantasawat (2011) and Patel *et al.*, (2014). Considering pooled data, seed yield/plant, cluster number per plant and pods/plant had shown appreciably higher difference between GCV and PCV, which further indicated trait-specific environmental effect. Therefore much care should be taken up while selecting these characters.

Although range- a parameter of central tendency, can focus existence of variability but coefficient of variation is considered as a reliable parameter at its estimate is independent of the unit of measurement. As per Sivasubramanian and Menon (1973), estimates of PCV and GCV exceeding 20% are considered high, values less than 10% are low and values between 10% and 20% as medium. High values of PCV and GCV in case of cluster number per plant and seed yield indicate the presence of substantial variability, and selection might be effective for the said characters. While, Degefa *et al.*, (2014) reported higher variability (GCV and PCV) for ancillary traits e.g., pods per plant, seeds per plant, number of primary branches and harvest index.

C. Heritability and genetic advance

Heritability estimate of each character reflect an idea that how much proportion of the phenotypic variation can heritable and realized in the follow-up generation. While, the genetic advance reflects the extent of genetic improvement achieved in the selected population over the base population for the trait concerned. In other words, genetic advance is the measure of the expected genetic gain obtainable through selection. Therefore, genetic advance are often used to evaluate the selection efficiency realized in different breeding schemes. Heritability in conjunction with genetic advance can provide more reliable information than the study of heritability alone (Johnson *et al.*, 1955).

Besides, genotypic coefficient of variation (GCV) coupled with heritability estimate would reflect the precise amount of genetic advance expected to be realized through selection (Burton and Devane, 1953). Heritability estimates is the proportion of heritable

variability out of the total variation present in the population. The estimate of heritability exceeding 60% is considered high, while those between 30 to 60% are moderate and estimates less than 30% are low (Jhonson *et al.*, 1955). Traits with high heritability estimate are conceptually considered to have high additive effect (fixable component of variation) and less influence by the environment.

In the present study, heritability in broad sense (h_b^2) was computed considering pooled data over two locations. High heritability was recorded for days to 50% flowering, plant height, cluster number/plant,

seeds/pod and 100- seed weight, but moderately higher heritability was shown to be associated with pods/plant and single plant seed yield. This confirms the findings of Khajupdam and Tantasawat (2011) for pod length, Zaid *et al.*, (2012) for plant height, Hozayn *et al.*, (2013) for number of plants and seed yield, and Raturi *et al.*, (2015) for days to 50% flowering. While, Manivelan *et al.*, (2019) revealed the highest heritability for plant height followed by seed yield per plant, number of pods per plant, number of branches per plant, number of clusters per plant and hundred seed weight (g).

Table 1: Pooled Analysis of variance for eight morphological traits among 230 genotypes of mungbean.

Sr. No.	Character	Source	D.F.	S.S	M.SS
1.	Days to 50% flowering	Replication	1	26.452	26.452
		Factor A	1	29,549.778	29,549.778**
		Factor B	229	4,095.830	17.886**
		Intraction A × B	229	2,552.222	11.145**
		Error	459	2,030.548	4.424
		Total	919	38,254.830	
2.	Plant Height (cm)	Replication	1	787.282	787.282
		Factor A	1	20,493.101	20,493.101**
		Factor B	229	10,364.075	45.258**
		Intraction A × B	229	10,550.276	46.071**
		Error	459	11,237.325	24.482
		Total	919	53,432.058	
3.	No. of cluster/Plant	Replication	1	0.007	
		Factor A	1	403.008	403.008**
		Factor B	229	432.593	1.889**
		Intraction A × B	229	410.824	1.794**
		Error	459	387.324	0.844
		Total	919	1,633.755	
4.	No. of pods/plant	Replication	1	547.029	547.029
		Factor A	1	12,313.485	12,313.485**
		Factor B	229	1,498.387	6.543**
		Intraction A × B	229	1,623.197	7.088**
		Error	459	1,903.405	4.147
		Total	919	17,885.503	
5.	Pod length (cm)	Replication	1	16.579	16.579
		Factor A	1	95.061	95.061**
		Factor B	229	217.937	0.952**
		Intraction A × B	229	163.482	0.714**
		Error	459	163.626	0.356
		Total	919	656.687	
6.	No. of seeds per pod	Replication	1	0.692	0.692
		Factor A	1	1,541.535	1,541.535**
		Factor B	229	761.464	3.325**
		Intraction A × B	229	798.455	3.487**
		Error	459	650.956	1.418
		Total	919	3,753.102	
7.	100 Seed weight(gm)	Replication	1	9.035	9.035
		Factor A	1	104.944	104.944**
		Factor B	229	167.727	0.732**
		Intraction A × B	229	166.724	0.728**
		Error	459	119.782	0.261
		Total	919	568.213	
8.	Single plant Yield(gm)	Replication	1	70.255	70.255
		Factor A	1	1,398.890	1,398.890**
		Factor B	229	140.151	0.612**
		Intraction A × B	229	173.931	0.760**
		Error	459	276.577	0.603
		Total	919	2,059.805	

Genetic Advance expressed as percentage of mean (GA) or genetic gain under selection (5% selection intensity) were estimated for all the ten quantitative characters. Customarily, the value of genetic advance (as % mean) are classified as low (<10%), moderate (10–20%) and high (>20%) as per Johnson *et al.*, (1955). In the present study, higher magnitude of genetic advance can be expected for plant height, branch number/plant, cluster number/plant, pod number/plant, 100-seed weight and seed yield/plant. The results under this study corroborate the findings of Kumar *et al.*, (2010a) for hundred seed weight and Pinchhyo *et al.*, (2016) for seed yield/plant. In contrast, days to 50% flowering showed high heritability with low expected genetic advance which confirms the role of non-additive gene action (epistatic and/or dominance effects) in expression of the characters. Similar observations were reported by Degefa *et al.*, (2014) for days to 50% flowering, days to maturity and number of seeds/pod.

Cluster number/plant exhibited high heritability accompanied with extremely high genetic advance which envisaged higher proportion of fixable (additive gene action) component of genetic variation in controlling the trait. However, Manivelan *et al.*, (2019) have reported high heritability coupled with high genetic advance (GA) as percentage of mean for plant height. Hence, selection based on this component trait would be rewarding for enhancement of yield potential. Similar findings for yield/plant was also reported by Das *et al.*, (2010); Reddy *et al.*, (2011); Patel *et al.*, (2014); Raturi *et al.*, (2015); Sofia *et al.*, (2017); Ramakrishnan *et al.*, (2018); Mariyammal *et al.*, (2019). Thus, it is evident that the present set of materials retain an appreciable genetic variability for agro-morphological traits which can be harnessed for judicious selection of elite genotypes based on above genetic parameters for augmentation of productivity in mungbean.

Table 2: Estimates of variability parameters and expected genetic advance for 8 characters pooled over two locations (Bhubaneswar and Jeypore).

Sr.No.	Characters	Mean	Range	PCV%	GCV%	h ² (%)	GA % of population
1.	Days to 50% flowering	42.341	31.75-49.5	6.531	6.130	88.119	11.855
2.	Plant Height (cm)	32.195	19.975-46.3	14.953	14.146	89.498	27.569
3.	No of cluster/Plant	2.792	0.863-6.605	39.334	36.745	87.267	70.711
4.	No. of pods/plant	8.733	4.5-12.6	21.808	19.365	78.856	35.425
5.	Pod Length (cm)	6.189	4.7-8.55	10.711	10.019	87.500	19.307
6.	Seeds Per Pod	6.382	1.975-8.600	18.386	16.883	84.323	31.938
7.	100 Seed Weight (g)	3.131	1.978-4.48	16.397	15.173	85.633	28.924
8.	Single plant Yield(g)	2.028	0.752-3.689	29.109	25.514	76.827	46.068

FUTURE SCOPE

The present findings would be helpful for formulation of selection strategy for identification of parent materials in a set of germplasm lines as well as selection of elite plant types in mungbean breeding programme under cold stress.

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Conflict of Interest. The authors declare that there is no conflict of interests

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