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## Assessment of genetic variation and heritability for morpho-agronomic traits in mungbean (*Vigna radiata* L.) genotypes under deficit moisture stress

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### Abstract

The present experiment comprised of fifty-five mungbean germplasm lines tested over two years to assess inter-relationship of agronomic traits including seed yield under deficit moisture stress. In stress condition heritability in broad sense ( $h^2$  in %) was the highest for seed yield per plant followed by no. of pods per plant. Seed yield/plant, no. of pods/plant showed the high genetic advance coupled with high heritability in deficit moisture stress. Resembling the action of additive gene in controlling these characters and selection would be rewarding for enhancement of yield. It was found that single plant yield/plant showed highly significant positive correlation with number of pods/plants, number of clusters per plant, no. of pods per cluster, no. of seeds per pod and plant height. However, path analysis revealed that pods/plant, hundred seed weight, no. of seeds per pod had the highest direct positive effect on single plant yield. Hence, for genetic improvement in the seed yield, direct selection of genotypes based on component traits exhibiting positive correlation and higher positive direct effect will be more effective and fruitful in mungbean under deficit moisture stress.

**Keywords:** Character association, path analysis, seed yield, yielded related traits, deficit moisture stress, mungbean

### Introduction

Mungbean (*Vigna radiata* L. wilczek,  $2n=22$ ) is the most important short duration pulse crop of India and Orissa in particular. It is also called greengram, golden gram or Mungdal. It is a self-pollinated legume. Mungbean is considered to be originated from *Vigna sablobata* in south Asia belongs to the family Fabaceae. It is one of the most important summer season pulse crops in India with high nutritional value, with short growing season. It is having high protein (ranging from 17.2-29.9% and average of 22.83%) with high digestibility, and it has low levels of oligosaccharides (Ihsan *et al.*, 2013)<sup>[14]</sup>. Abiotic stresses such as deficit moisture, salinity, drought, nutrient deficiency or toxicity, and flooding limit crop productivity world-wide. However, this situation becomes more problematic in developing countries leading to cause severe food insecurity for large population and poverty particularly in rural areas. Among these, drought affects more than 70 million ha. of rice growing land world-wide thereby resulting low outputs, poor human nutrition and reduced employment opportunities. The extent and rate of progress in improving deficit moisture stress tolerance in crops through conventional breeding is limited owing to its complex mechanism, time consumable selection of tolerant plants and expensive cost involved.

In this context, assessment of existing genetic variation especially in the primary gene pool seems to be the most crucial factor to explore elite germplasm with desirable traits. Fluctuations in environment is the major factor for appreciable G x E interaction that generally hinder proper assessment of yield. Estimation of genetic variability, heritability and genetic advance of the characters at least over two years can offer proper choice of base material and mode of selection for genetic improvement in the crop. The estimation of heritability along with genetic advance is more applicable than the heritability value alone. Hence, the information of variability and heritability coupled with genetic advance is beneficial during selection process in breeding programs. Hence, an attempt was undertaken to gauge the extent of genetic variability and above other genetic parameters in set of 55 available mungbean germplasm lines under deficit moisture stress.

## Materials and Methods

The experiment was laid out in randomized block design (RBD) in two replications with 55 genotypes including standard ruling varieties, important pre-released cultures and popularly adapted local land races. The deficit moisture stress condition induced by withholding the irrigation for 15 days prior to the flowering. The trial was sown on 13<sup>th</sup> February of 2019-20 and 2020-21 at EB-II section of Ouat Bhubaneswar. Each genotype was represented by two rows with spacing of 30cm×10cm. Fertilizers were applied @ 20:40:20 kg of N: P<sub>2</sub>O<sub>5</sub>: K<sub>2</sub>O along with 300 cft. of farmyard manure (FYM) per hectare. Half of nitrogenous and whole of phosphatic and potassic fertilizers were applied in lines as basal at the time of sowing. The rest amount of nitrogen was applied after 25 days of sowing as top dressing. Weeding was done before top dressing of nitrogenous fertilizer. Other management practices were followed as per recommended package of practices.

Five randomly selected plants of each genotype per replication were used for the collection of data on 10 traits including single plant seed yield. The replication mean values of each character was considered for analysis of variance (Singh and Choudhury 1985) [37] and the data were further analyzed for study of genetic variability as suggested by Burton (1952) at both phenotypic and genotypic level.

Heritability and estimate of genetic advance for each quantitative trait were calculated following the standard statistical procedure of Johnson *et al.* (1955) [14] respectively.

## Results and Discussion

The wide range for each of the studied variables suggested that there was some natural variability among the genotypes. For all of the features, the genotypic difference between these genotypes was determined to be statistically significant at the 1% level, indicating the presence of significant variability in the material under study (Table :1), which will be very helpful for the selection of breeding material. Greengram researchers Das *et al.* (2010) [7], Khajudpam and Tantasawat (2011) [16], Reddy *et al.* (2011) [33], Patel *et al.* (2012) [24], Raturi *et al.* (2014) [32] and Vir and Singh (2016) [40] have all reported on a similar large range of variability with different sets of collections for different features. Because of their varied ancestry and local adaptability, the features in the current study showed a wide range of variation. For the success of any breeding programme depends on the spectrum of genetic variability present in the germplasm. All the characters showed significant results at 1% level of significance among all genotypes it suggests the presence of substantial variability.

**Table 1:** Analysis of variance for the 10 traits pooled over two years for the 55 germplasm under drought condition

Sr. No.	Character	Source	DF	S.S	M.S.S
1.	Days to 50% flowering	Replicate	1	0.409	0.409
		Environments	1	0.458	0.458**
		Interactions	1	4.290	4.290
		Overall, Sum	3	5.156	1.719
		Treatments	54	331.839	6.145
		Error	162	799.804	4.937
2.	Days to maturity	Replicate	1	1.364	1.364
		Environments	1	282.616	282.616**
		Interactions	1	3.328	3.328
		Overall, Sum	3	287.307	95.769**
		Treatments	54	320.202	5.930**
		Error	162	651.342	4.021
3.	Plant Height (cm)	Replicate	1	3.063	3.063
		Environments	1	1203.416	1203.416**
		Interactions	1	1.590	1.590**
		Overall, Sum	3	1208.068	402.689
		Treatments	54	1814.083	33.594**
		Error	162	1876.655	11.584
4.	No. of cluster/Plant	Replicate	1	0.113	0.113
		Environments	1	0.444301	0.444
		Interactions	1	0.258	0.258
		Overall, Sum	3	0.815	0.272
		Treatments	54	57.706	1.069**
		Error	162	30.081	0.186
5.	No. of Pods/clster	Replicate	1	0.003	0.003
		Environments	1	0.558	0.558**
		Interactions	1	0.008	0.008
		Overall Sum	3	0.568	0.189*
		Treatments	54	9.521	0.176**
		Error	162	10.679	0.066
6.	No. of pods/plant	Replicate	1	21.311	21.311
		Environments	1	0.256	0.256**
		Interactions	1	1.401	1.401**
		Overall, Sum	3	22.968	7.656
		Treatments	54	478.570	8.862**
		Error	162	173.587	1.072
7.	Pod length (cm)	Replicate	1	0.590	0.590

		Environments	1	1.051	1.051**
		Interactions	1	0.011	0.011
		Overall, Sum	3	1.653	0.551*
		Treatments	54	26.847	0.497**
		Error	162	28.454	0.176
8.	No. of seeds per pod	Replicate	1	2.478	2.478
		Environments	1	0.739	0.739**
		Interactions	1	0.628	0.628
		Overall, Sum	3	3.845	1.282**
		Treatments	54	48.067	0.890**
		Error	162	63.486	0.392
9.	100 Seed weight (gm)	Replications	1	2.332	2.332
		Environments	1	0.001	0.001*
		Interactions	1	0.000	0.000
		Overall, Sum	3	2.334	0.778*
		Treatments	54	12.933	0.239**
		Error	162	16.965	0.105
10.	Single plant Yield (gm)	Replicate	1	0.067	0.067
		Environments	1	0.006	0.006**
		Interactions	1	0.003	0.003
		Overall, Sum	3	0.076	0.025**
		Treatments	54	31.015	0.574**
		Error	162	3.125	0.019

### Genetic variability, heritability and genetic advance

The effectiveness of selection within a population on a crop is impacted by genetic heterogeneity. There is no need for selection if there is no variance. The success of any breeding programme depends on the spectrum of variability present in the germ plasm. Plant breeding is an exercise in the management of the variability (Hutchinson, 1958) [2]. However, because the coefficient of variation is independent on the unit of measurement, range can only provide an approximate idea of the variability. PCV and GCV values between 10% and 20% were regarded by Sivasubramanian and Menon (1973) [36] as medium, values between 10% and 20% as low, and values greater than 20% as high. High PCV and GCV values indicate that any character has high variability, indicating that selection based on that feature may be successful.

Higher PCV estimations than GCV for all the characters under examination in the current study suggest that these characters may have been affected by their environment. Similar findings were earlier reported in greengram by Gadakh *et al.* (2013) [4] and Defega *et al.* (2014) [10]. In stress conditions Estimates of PCV and GCV were higher for seed yield per plant and no. of pods/plant, Similar results were reported by Garg *et al.* (2017) [11] for the number of pods per plant and seed yield per plant; by Rao *et al.* (2006) [32] for pods per plant, seed yield per plant. Plant height and hundred seed weight have the highest difference in the PCV and GCV. which indicated appreciable environmental effect on the trait. So much care should be taken up while selecting these characters. These important agronomic traits also exhibited higher GCV and PCV values than rest of the traits indicating further scope for genetic improvement in mungbean. This has been earlier reported by Rahim *et al.* (2010) [30], Khajudpam and Tantasawat (2011) [16], Kumar *et al.* (2010<sup>b</sup>) [19] and Patel *et al.* (2014) [25]. For seed yield per plant, Kumhar and Chaudhary (2007) [18] and Makeen *et al.* (2007) [19] for the number of pods per plant and plant height, Mehandi *et al.* (2013) [21]; and for the plant height and the number of branches per plant. In line of this, the analysis of PCV and GCV in mung bean genotypes revealed variance for nearly all

of the variables tested, indicating the presence of more genetic diversity among the genotypes. Overall, the coefficients of phenotypic and genotypic variation indicated that there are considerable potential for the scope of mung bean improvement by direct selection. Therefore, enhancement of these features can be achieved by selection based solely on phenotype.

### Heritability

Genotypic coefficient of variation (GCV) along with heritability estimate would give the proper accuracy of the amount of advance to be expected from selection (Burton and Devane, 1953) [1]. Thus, heritability estimates could be more useful in assessing the heritable portion of the total variation present in the population. According to Jhonson *et al.* (1955) [14] heritability estimates greater than 60% were high, estimates ranging between 30 to 60% were moderate and estimates less than 30% were low. Any quantitative trait with a high heritability estimate suggests that environmental influences contribute to phenotypes in a relatively small amount, therefore selection for such a trait may be simpler owing to the large additive effect. Higher heritability estimates were more impacted by fixable variables since they were less influenced by the environment.

In the present study, heritability in broad sense ( $h^2$ ) was assessed for all the quantitative traits studied. In stress condition heritability in broad sense ( $h^2$  in %) was the highest for seed yield per plant (87.8%) followed by no. of pods per plant (64.5%) (Table:2). Similar results were also reported by Hozyan *et al.* (2013) [11] for plant number and seed yield, Khajudpam and Tantasawat (2011) [16] for pod length, Zaid *et al.* (2012) for plant height, and Raturi *et al.* (2015) [33] for days to 50% flowering. Abbas *et al.* (2018) 100-seed weight (97%) and seed yield(84%) on mungbean genotypes and which agrees with the earlier reports of Idrees *et al.*, 2006 [12].

### Genetic advance

Genotypic and phenotypic coefficients of variation along with heritability plus genetic advance are very essential to improve traits of interest. Genetic Advance expressed as percentage of

mean (GA) or genetic gain under selection (5% selection intensity) were estimated for all the ten quantitative characters. According to Johnson *et al.* (1955)<sup>[14]</sup>, the value of genetic advance as per cent of mean were categorized as low (<10%), moderate (10–20%) and high (>20%).

In deficit moisture stress condition seed yield per plant (36.9%), no. of pods/plant(25.12%), no. of clusters(20.30%) (Table:2), showed high (>20%) values of expected genetic advance. The results were in agreement with the findings of Kumar *et al.* (2010<sup>a</sup>)<sup>[17]</sup> for hundred seed weight and Pinchhyo *et al.* (2016)<sup>[27]</sup> for seed yield/plant.

The heritability coupled with genetic advance could be more useful in selecting any genotype (Johnson *et al.*, 1955)<sup>[14]</sup>. High heritability and high genetic advance as a percentage of mean were found in the current study for some traits, which suggests that additive gene action predominates with little environmental influence in the determination of these traits. As a result, simple selection would be more effective for the improvement of these characters.

Seed yield/plant, No. of pods/plant showed the high genetic advance coupled with high heritability in deficit moisture stress. Resembling the action of additive gene in controlling these characters and selection would be rewarding for

enhancement of yield. Evidently, high heritability coupled with high genetic advance suggesting the role of additive gene action for yield/plant was reported by Agarwal *et al.* (2001)<sup>[6]</sup>, Das *et al.* (2010)<sup>[7]</sup>, Reddy *et al.* (2011)<sup>[33]</sup>, Narasimhulu *et al.* (2013)<sup>[22]</sup>, Patel *et al.* (2014)<sup>[25]</sup>, Raturiet *et al.* (2015)<sup>[33]</sup>, Payasi *et al.* (2015)<sup>[26]</sup>, Sultana (2015)<sup>[38]</sup>, Sofia *et al.* (2017)<sup>[37]</sup>, Ramakrishnan *et al.* (2018)<sup>[29]</sup>, Sandhiya and Saravanan (2018)<sup>[34]</sup> and Mariyammal *et al.* (2019)<sup>[20]</sup>. Singh *et al.* (2009) stated that high heritability coupled with high genetic advance is an indicator of a higher proportion of the additive genetic variance and consequently more genetic gain is expected from the selection. In stress condition low heritability coupled with low genetic advance for the characters days to 50% flowering, days to maturity, Plant height, no. of pods per cluster, Pod length, seeds per pod and hundred seed weight. Similar results with low heritability coupled with low genetic advances as a percent of mean for days to maturity was noted on 80 mungbean genotypes (Sultana, 2015)<sup>[38]</sup>. Thus, it is stating that the present set of genotypes retain an appreciable genetic variability for agro morphological traits which can be used for the 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 10 characters pooled over two years

S. No.	Character	Range	Mean	SE	CD (5%)	PCV	GCV	H <sup>2</sup>	GA % of population mean
1	Days to 50% flowering	27.45-32.89	29.99	1.11	2.23	7.63	1.83	0.06	0.91
2	Days to maturity	43.00-48.25	45.93	1.00	2.79	4.62	1.50	0.11	1.01
3	Plant height	24.10-37.80	28.22	1.70	4.75	14.65	8.31	0.32	9.72
4	No. of clusters/plant	2.30-4.88	3.51	0.22	0.60	18.14	13.37	0.54	20.30
5	No. of pods/ cluster	2.11-3.28	2.62	0.13	0.36	11.69	6.35	0.30	7.11
6	No. of pods/plant	5.44-12.51	9.19	0.52	1.44	18.90	15.18	0.65	25.12
7	Pod length	4.18-6.10	5.19	0.21	0.59	9.76	5.47	0.31	6.31
8	Seeds per pod	7.43-9.45	8.35	0.31	0.87	8.61	4.23	0.24	4.28
9	Hundred seed weight	1.81-3.04	2.47	0.16	0.45	15.04	7.42	0.24	7.54
10	Seed yield per plant	0.93-2.65	1.95	0.07	0.19	20.40	19.12	0.88	36.90

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