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Estimation of Genetic Variability in F₄ Progenies of Green Gram (*Vigna radiata* (L.) R. Wilczek) for Yield and Component Traits

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A B S T R A C T

The present study was conducted to assess variability paramters for ten quantitative characters including seed yield per plant in mung bean utilizing thirty progenies of F₄ population derived from two crosses *viz*., Meha x GJM-1006 (17 progenies) and Meha x GJM-1008 (13 progenies). Randomized Block Design with three replications was used and each genotype was planted on a spacing of 60 cm x 15 cm. Observations were recorded from 10 randomly selected plants. F₄ progenies of Meha x GJM-1006 had highest genotypic variance for days to maturity, pods per plant and seed yield per plant, while progenies of Meha x GJM-1008 depicted highest genotypic variance for days to 50% flowering, plant height, primary branches per plant, seeds per plant, clusters per plant, harvest index and 100 seed weight. Most of the traits showed moderate to high heritability as well as genetic advance as per cent mean. High heritability values of more than 65 per cent have been observed for plant height in the cross Meha x GJM-1006 and days to 50% flowering in Meha x GJM 1008. Higher genetic advance as per cent mean was observed for pods per plant and seed yield per plant, and low genetic advance as per cent mean for days to 50% flowering, days to maturity, primary branches per plant, seeds per pod and 100 seed weight. The present findings could be useful for establishing selection for improvement of high seed yield in the mung bean breeding program.

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek] is an ancient and well known pulse crop of Asian countries. It is one of the thirteen food legumes grown in India and third most important pulse crop of India after chickpea and pigeonpea.

It contains protein (24.0 %), carbohydrate (56.7 %), fat (1.3 %), fibre (4.1 %) and mineral like calcium 124mg/l00g of edible portion. It is drought tolerant and has high adaptation ability for poor characterized soils. Mungbean is an excellent source of high quality protein in the form of dry edible seeds and fresh sprouts. The seeds have high (28%) protein which is two times more of wheat and three time of rice.

A plant breeding programme can be divided into three stages *viz.,* building up a gene pool of variable germplasm, selection of individuals from the gene pool and utilization of selected individuals to evolve a superior variety (Kempthorne, 1957). The quantitative measurement of individual character provides the basis for interpreting analysis of variance.

The available variability in a population can be partitioned into heritable and non-heritable parts with the aid of genetic parameters such as genetic coefficient of variation, heritability and genetic advance (Miller *et al.,* 1958). Yield is a complex character governed by quantitative components traits and the environments where it is grown. Thus, selection for seed yield becomes difficult unless the associations between the yield contributing characters are known. Measurement of correlation helps to identify the relative contribution of component characters towards yield (Panse, 1957). Phenotypic correlation reflects the observed relationship, while genotypic correlations underline the true relationship among the characters. Estimates of correlation coefficient are useful in determining yield component which can be used for genetic improvement of yield. Indirect selection through component characters with high heritability is advantageous for polygenic character like yield.

Heritability and genetic advance are important selection parameters. Heritability specifies the proportion of the genotypic variance to the total variance. It is a good index of the transmission of characters from parents to the offspring (Falconer, 1960). Genetic advance is the difference between the mean genotypic value of the selected lines and the mean genotypic value of the base population.

Materials and Methods

The present experiment is comprised of two F_4 generations (total 30 F_4 progenies) derived from the crosses Meha x GJM-1006 and Meha x GJM-1008 evaluated in Randomized Block Design with three replications of spacing 60 cm x 15 cm with 20 plants per progeny. Meha was kept as common parent because of its mosaic resistance and suitability for summer cultivation. Observations were recorded from 10 randomly selected plants. The experiment was carried during summer, 2016 at College Farm, N. M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat. Observations on ten quantitative characters *viz.*, days to 50% flowering, plant height, primary branches per plant, days to maturity, clusters per plant, pods per plant, seeds per pod, 100 seed weight, seed yield per plant and harvest index were recorded from parents and F_4 progenies.

The data recorded for all the characters were subjected family-wise to analysis of variance with the formula suggested by Panse and Sukhatme (1978). The genotypic, phenotypic and environmental components were estimated as explained by Johnson *et al.,* (1955). The coefficients of phenotypic and genotypic variations were calculated by the formula suggested by Burton (1953), while GCV and PCV were categorized as low, moderate and high following Shivasubramanian and Menon (1973). Heritability in broad sense was calculated by using the formula proposed by Allard (1960) and it was categorized as demonstrated by Robinson *et al.,* (1949). Expected genetic advance was calculated by using the methodology suggested by Allard (1960) at 5 per cent selection intensity using the constant 'K' as 2.06. The expected genetic advance as expressed in per cent of mean was calculated by the method suggested by Johnson *et al.,* (1955) and it was categorized as suggested by Johnson *et al.,* (1955).

Results and Discussion

Success of any plant breeding programme depends on the extent of variability present in a crop. The presence of genetic variability for economic traits is a key factor for improving

the locally adapted varieties with regard to specific traits. Variability can be created by hybridization and needs to be assessed. This variability generated is a pre-requisite for any breeding programme aimed at improving the yield and other characters. Thus, it is necessary to have information on both genotypic and phenotypic coefficients of variation to have an insight about heritability of the trait. The information on phenotypic coefficient of variation and heritability will be handy for prediction of the possible genetic advance when selection is applied for a given trait(s). The genetic parameters such as genotypic coefficient of variability and genetic advance help to split the total variability into heritable and non-heritable components.

The present investigation was carried out on F_4 populations (total 30 progenies) of green gram, assessed for the genetic variability generated by hybridization, segregation and recombination. Highest mean value was depicted by F_4 population of Meha x GJM-1006 for days to 50% flowering, days to maturity, plant height, pods per plant, seed yield per plant, clusters per plant, harvest index and seeds per pod. F_4 Progenies of Meha x GJM-1008 showed highest mean for primary branches per plant and 100 seed weight. Hence, in the present study, wide range has been observed for almost all characters suggesting that it is possible to increase the pods per plant and seed yield per plant by exercising selection in the segregating generations.

Analysis of variance indicated large differences in the variances for most of the characters under study among different progenies pertaining to the cross. Among the segregating populations, the F_4 population of Meha x GJM-1006 (Table 1) exhibited highest variance for days to maturity, pods per plant and seed yield per plant. The F_4 population of Meha x GJM-1008 (Table 2)

expressed higher variance for days to 50 % flowering, plant height, primary branches per plant, seeds per pod, 100 seed weight, clusters per plant and harvest index. The higher variances for most of the traits in these F_4 generations indicated the presence of sufficient amount of variability which had been generated in segregating populations. This population can be further advanced and explored for improvement of mentioned traits.

Considering all F_4 progenies under study, the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values (Tables 1 and 2) were low for days to 50 % flowering, days to maturity, seeds per pod and 100 seed weight. Similar results were reported by Parameswarappa (2005), Sadiq *et al.,* (2005), Makeen *et al.,* (2007), Pandey *et al.,* (2007), Singh *et al.,* (2009[a]), Das *et al.,* (2010), Kumar *et al.,* (2010[a]), Kumar *et al.,* (2010[b]), Khajudparn and Tantasawat (2011), Prakash and Shekhawat (2012), Singh *et al.,* (2012), Srivastava and Singh (2012), Gadakh *et al.,* (2013), Ahmad *et al.,* (2014), Alom *et al.,* (2014), Kumar and Katiyar (2015), Payasi *et al.,* (2015), Ahmad *et al.,* (2015), Das and Baru (2015), Jangra *et al.,* (2015), Raselmiah *et al.,* (2016) and Usharani *et al.,* (2016).

Low to moderate PCV and GCV were observed in plant height and primary branches per plant. Low to moderate GCV and PCV values indicated the influence of the environment and limited scope for improvement by selection on these traits. The GCV and PCV estimates were moderate to high for clusters per plant and harvest index.

Pods per plant and seed yield per plant showed higher PCV and GCV values in both the segregating population. The PCV and GCV estimates exhibited wide variation for most of the characters in the two segregating populations. The progenies of the two crosses had higher GCV and PCV for pods per plant, seed yield per plant and clusters per plant.

Table.1 Estimation of analysis of variance and genetic variability parameters for ten quantitative characters in F_4 generation of cross Meha x GJM-1006 in mung bean

Characters	Mean square			Range	$\sigma^2 g$	$\sigma^2 p$	GCV (%)	PCV (%)	$h^2_{(b)}$	GAM
	Replication	Progenies	Error							
Days to 50% flowering	43.61	6.00*	3.00	42.67-48.67	0.99	4.00	2.16	4.32	24.95	2.22
Days to maturity	31.90	30.65**	5.03	68.33-80.67	8.54	13.57	4.06	5.12	62.95	6.63
Plant height (cm)	254.46	85.72**	8.31	43.23-59.69	25.80	34.11	10.25	11.79	75.64	18.37
Primary branches per plant	33.92	1.42*	0.69	6.33-9.47	0.25	0.93	6.66	12.95	26.44	7.05
Pods per plant	1322.27	868.52**	155.85	39.13-106.53	237.55	393.41	25.37	32.64	60.38	40.61
Seeds per pod	3.97	0.42 NS	0.23	8.78-10.02	0.06	0.29	2.69	5.70	22.26	2.61
100 seed weight (g)	0.16	0.12 NS	0.07	3.58-4.32	0.02	0.09	3.27	7.51	18.57	2.87
Seed yield per plant (g)	74.90	64.75**	13.38	9.21-26.48	17.12	30.51	23.95	31.97	56.19	36.96
Clusters per plant	71.94	14.16*	5.12	8.83-18.6	3.01	8.13	14.53	23.88	40.69	18.21
Harvest index (%)	135.05	42.65*	16.69	37.04-49.89	8.65	25.34	7.05	12.06	34.15	8.48

** - Significant at 1.0 per cent level of probability, * - Significant at 5.0 per cent level of probability, NS- Non-Significant.

$\sigma^2 g$ = Genotypic variance, $\sigma^2 p$ = Phenotypic variance, GCV = Genotypic Coefficient of variance, PCV = Phenotypic Coefficient of variance, $h^2_{(b)}$ = Heritability (Broad sense), GAM = Genetic advance as per cent mean.

Table.2 Estimation of analysis of variance and genetic variability parameters for ten quantitative characters in F_4 generation of cross Meha x GJM-1008 in mung bean

Characters	Mean square			Range	$\sigma^2 g$	$\sigma^2 p$	GCV (%)	PCV (%)	$h^2_{(b)}$	GAM
	Replication	Progenies	Error							
Days to 50% flowering	23.72	17.47**	2.69	40.67-48.67	4.93	7.62	4.94	6.15	65.68	8.19
Days to maturity	2.33	16.27*	4.33	67.33-74.33	3.98	8.31	2.82	4.08	47.87	4.02
Plant height (cm)	29.35	86.21**	18.20	35.96-52.46	22.67	40.87	9.97	13.79	55.47	15.75
Primary branches per plant	7.67	2.54 NS	1.30	6.33-9.13	0.42	1.71	8.19	16.65	24.23	8.31
Pods per plant	386.31	631.22**	129.41	25.17-74.67	167.27	296.68	23.61	31.45	56.38	36.52
Seeds per pod	3.81	1.26**	0.24	7.78-10.42	0.34	0.58	6.31	8.28	58.08	9.91
100 seed weight (g)	0.23	0.19*	0.04	3.77-4.53	0.05	0.09	5.34	7.40	52.07	7.94
Seed yield per plant (g)	27.49	43.30*	11.30	7.40-20.76	10.66	21.97	21.41	30.73	48.55	30.74
Clusters per plant	20.23	19.45*	5.56	6.80-14.47	4.63	10.19	18.87	27.99	45.45	26.21
Harvest index (%)	48.12	45.73*	12.16	33.26-45.57	11.18	23.35	8.22	11.87	47.92	11.72

** - Significant at 1.0 per cent level of probability, * - Significant at 5.0 per cent level of probability, NS- Non-Significant.

$\sigma^2 g$ = Genotypic variance, $\sigma^2 p$ = Phenotypic variance, GCV = Genotypic Coefficient of variance, PCV = Phenotypic Coefficient of variance, $h^2_{(b)}$ = Heritability (Broad sense), GAM = Genetic advance as per cent mean.

F$_4$ progenies of a cross Meha x GJM-1006 exhibited the higher values of GCV and PCV for pods per plant, seed yield per plant and clusters per plant indicating that there is greater scope for improvement by applying selection on these characters in desirable direction and also greater diversity among the progenies for these characters. Similar findings were also observed by Kumar *et al.,* (2005), Parameswarappa (2005), Sadiq *et al.,* (2005), Lavanya (2006), Makeen *et al.,* (2007), Rahim *et al.,* (2010), Suresh *et al.,* (2010), Khajudparn and Tantasawat (2011), Reddy *et al.,* (2011), Narasimhulu *et al.,* (2013), Prasanna *et al.,* (2013), Javed *et al.,* (2014), Das and Baru (2015), Rathor *et al.,* (2015), More *et al.,* (2016), Usharani *et al.,* (2016), Vir and Singh (2016) and Raselmiah *et al.,* (2016). The results revealed that genotypic coefficient of variation was close to that of phenotypic variation for primary branches per plant, seed yield per plant and clusters per plant indicating that phenotypic coefficient of variation was largely due to genetic differences and less environmental influence for these traits.

Most of the characters exhibited moderate to high heritability in almost all the traits in two segregating populations. High heritability values of more than 65 per cent have been observed for plant height in the cross Meha x GJM-1006 (Table 1) and days to 50% flowering in Meha x GJM 1008 (Table 2). Similar results were obtained by Kumar *et al.,* (2005), Sadiq *et al.,* (2005), Lavanya (2006), Pandiyan *et al.,* (2006), Prakash *et al.,* (2006), Das *et al.,* (2010), Rahim *et al.,* (2010), Suresh *et al.,* (2010), Tabasum *et al.,* (2010), Kumar *et al.,* (2010[b]), Srivastava and Singh (2012), Gadakh *et al.,* (2013), Narasimhulu *et al.,* (2013), Kumar *et al.,* (2013), Prasanna *et al.,* (2013), Javed *et al.,* (2014), Ahmad *et al.,* (2014), Bisht *et al.,* (2014), Degefa *et al.,* (2014), Rathore *et al.,* (2014), Sahu *et al.,* (2014), Ahmad *et al.,* (2015), Muralidhara *et*

al., (2015), Raturi *et al.,* (2015), Jangra *et al.,* (2015), More *et al.,* (2016), Usharani *et al.,* (2016), Sohel *et al.,* (2016) and Raselmiah *et al.,* (2016). Comparison of genetic advance as per cent mean value of all the populations revealed higher genetic advance as per cent mean value for pods per plant and seed yield per plant, and low genetic advance as per cent mean (GAM) value for days to 50% flowering, days to maturity, primary branches per plant, seeds per pod and 100 seed weight. The genetic advance was moderate to high for the traits plant height, cluster per plant and harvest index, in almost both the populations. These results are also in agreement with the findings of Kumar *et al.,* (2005), Sadiq *et al.,* (2005), Lavanya (2006), Makeen *et al.,* (2007), Pandey *et al.,* (2007), Kumar *et al.,* (2010[a]), Khajudparn and Tantasawat (2011), Singh *et al.,* (2012), Srivastava and Singh (2012), Kumar *et al.,* (2013), Narasimhulu *et al.,* (2013), Bisht *et al.,* (2014), Rathore *et al.,* (2014), Alom *et al.,* (2014), Ahmad *et al.,* (2014), Degefa *et al.,* (2014), Kumar and Katiyar (2015), Jangra *et al.,* (2015), Kumar *et al.,* (2015), Sohel *et al.,* (2016), More *et al.,* (2016), Usharani *et al.,* (2016) and Vir and Singh (2016). The moderate to high heritability coupled with moderate to high GAM estimates for these traits suggested the importance of additive genetic variance for these traits and effectiveness of simple selection. The heritability estimates of pods per plant, clusters per plant and seed yield per plant were high with high genetic advance as per cent mean compared to other traits, hence, priority should be given to these traits in formulating selection strategies on the basis of these characters to realize better gains by selection.

The results of the present experiment indicated that the variability for yield related traits can be generated by hybridization involving carefully selected parents. In the present study, hybridized populations

involving three genotypes, Meha used as female parent and GJM-1006 and GJM-1008 used as male parents resulted in increased variability, heritability and genetic advance as per cent mean (GAM) values. The F_4 populations of crosses *viz.,* Meha x 1006 and Meha x GJM-1008 are need to be handled under different selection schemes for improving productivity as they depicted moderate to high heritability along with moderate to high genetic advance as per cent mean for most of the trait.

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