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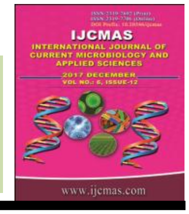

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Genetic Variability, Heritability and Genetic Advance in F_3 Progenies of Mungbean [*Vigna radiata* (L.) Wilczek]

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A B S T R A C T

The present study was conducted to assess the genetic variability, heritability and genetic advance in four F_3 populations for 11 quantitative traits including seed yield per plant. The material comprised of four F_3 generations derived from crosses *viz*., Meha x Pusa Vishal, Meha x GJM-1006, Meha x GM-4 and Meha x GJM-1008 comprising of 23, 20, 22 and 15 progenies, respectively. These progenies were laid out in separate Randomized Block Design trials with 3 replications along with respective parents, population size being 20 plants per progeny per row. Low to moderate GCV and PCV values were observed for days to 50 % flowering, days to maturity, plant height, primary branches per plant, seeds per pod and 100 seed weight indicated limited scope for improvement of these traits. While, GCV and PCV estimates were moderate to high for pods per plant, seed yield per plant, clusters per plant, straw yield per plant and harvest index suggesting that there is greater scope for improvement of these characters. High heritability estimates coupled with high genetic advance were observed for pods per plant, clusters per plant, seed yield per plant, straw yield per plant and harvest index coupled with high genetic advance as per cent mean suggested the importance of additive genetic variance for these traits. Hence, priority should be given to these traits in selection to obtain better gains. The F_3 population of crosses *viz.*, Meha x 1006 and Meha x GJM-1008 needs to be handled under different selection schemes for improving productivity as they depicted high heritability along with high genetic advance as per cent mean for most of the traits.

Introduction

Mungbean [*Vigna radiata* (L.)Wilczek] is 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 is known by various names in India as mung, moong, but the name greengram is more common (Chatterjee and Randhawa, 1952). Mungbean is a self-pollinating diploid plant with 2n = 2x = 22 chromosomes and a genome size of 579 Mb (Parida *et al.*, 1990). Mungbean is an excellent source of high quality protein in the form of split pulse and fresh sprouts. Mungbean seeds are rich in protein, easily digestible and lack flatulence which makes it important component of balance diet. Seeds are also very good source of minerals (calcium, iron, zinc, potassium and phosphorus), vitamins (folate and vitamin K) and dietary fibers (Keatinge *et al.*, 2011).

Ascorbic acid is synthesized in sprouted seeds of mungbean with increment in riboflavin and thiamine. The protein is rich in lysine, an amino acid that is deficient in cereals. Mungbean is grown in all seasons in India, however, summer cultivation during February to June is the most suitable growing period when there is a plenty of sunshine, high temperature and low humidity that keep insects and disease infestations at their lowest. Being a leguminous crop, it has the capacity to fix atmospheric nitrogen through symbiotic nitrogen fixation and is also used as a green manure crop. It is a short duration crop and therefore widely used as intercropor in rotation to improve nitrogen status of soil to break disease/ pest cycles.

Being highly self-pollinated crop, natural variability for yield and yield related traits is very narrow in mungbean making selection ineffective. 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 in order to choose best genotypes for improvement (Degafa *et al.*, 2014). Estimates of genetic parameters provide an indication of the relative importance of the various types of gene effects affecting the total variation of a plant character. Therefore, the present study was conducted to assess genetic variability, heritability and genetic advance among F_3progenies of four different crosses, separately.

Materials and Methods

The present investigation was carried out during summer, 2015 at College Farm, N. M. College of Agriculture, Navsari Agricultural University, Navsari. Experimental material comprised of 23, 20, 22 and 15F_3 progenies of the crosses Meha x Pusa Vishal, Meha x GJM-1006, Meha x GM-4 and Meha x GJM-1008, respectively. These F_3progenies were laid out in Randomized Block Design along with respective parents adopting three replications. Meha was kept as common parent with a view to transfer mosaic resistance and suitability for summer season. Each row comprised of 20 plants with 60 cm x 15 cm inter and intra row spacing. Each progeny / parental row consisted of 20 plants and observations were recorded from 10 randomly selected plants.

The data collected for each quantitative trait mentioned above were subjected to genetic variability analysis. Phenotypic, genotypic and environmental variances and coefficient of variation were estimated according to the methods suggested by Burton and Devane (1953), whereas estimation of heritability and expected genetic advance were computed using the formula according to Allard (1960) and Jonson *et al.,* (1955), respectively. Estimates of GCV, PCV, heritability and genetic advance as per cent mean were categorized as low, moderate and high by following Shivasubramanian and Menon (1973), Robinson *et al.,* (1951) and Johnson *et al.,* (1955), respectively.

Results and Discussion

Analysis of variance (ANOVA) revealed significant differences among the F_3 progenies for all the characters under study indicating presence of ample amount of variability (Table 1). 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 population, Meha x Pusa Vishal exhibited highest variance for pods per plant, Meha x GJM-1006 manifested highest mean square for plant height, primary branches per plant, seeds per pod, 100 seed weight, seed yield per plant and clusters per plant, Meha x GM-4 did not depict highest variance for any of the trait while Meha x GJM-1008 expressed higher variance for days to 50 % flowering, days to maturity, straw yield per plant and harvest index. The higher variances for most of the traits in F_3 generations indicated the presence of sufficient amount of variability. This population can be further advanced and explored for improvement of above mentioned traits.

Coefficient of variation is reliable as it is independent of unit of measurement. The extent of variability as measured by PCV and GCV also gives information regarding the relative amount of variation in the population. Considering F_3 progenies under study, the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values were low to moderate for days to 50 % flowering, days to maturity, plant height, primary branches per plant, seeds per pod and 100 seed weight.

The GCV and PCV estimates were moderate to high for pods per plant, seed yield per plant, clusters per plant, straw yield per plant and harvest index. The results revealed that GCV was close to that of PCV for almost all the characters indicating that phenotypic variability was due to genetic differences and less environmental influence (Table 2).

The progenies of all four crosses had higher GCV and PCV for seed yield per plant, straw yield per plant and harvest index. F_3 populations of all four crosses exhibited higher values of GCV and PCV for seed yield per plant, straw yield per plant and harvest index indicating that there is greater scope for improvement by applying selection on these characters in desirable direction. Among four F_3 population, the cross Meha x GJM-1006 showed highest value of GCV and PCV for plant height, primary branches per plant, seed yield per plant and clusters per plant; Meha x Pusa Vishal for pods per plant and seeds per pods while the cross Meha x GJM-1008 registered highest value for days to 50% flowering, days to maturity, 100 seed weight, straw yield per plant and harvest index. Similar results were reported by Pandiyan *et al.,* (2006), Rao *et al.,* (2006), Singh *et al.,* (2009), Tabasum *et al.,* (2010), Reddy *et al.,* (2011), Prakash and Shekhawat (2012), Gadakh *et al.,* (2013), Prasanna *et al.,* (2013), Ahmad *et al.,* (2014), Ahmad *et al.,* (2015), Muralidhara *et al.,* (2015) and Vir and Singh (2016).

Low GCV and PCV values were observed for days to 50% flowering, days to maturity and seeds per pod indicating a narrow range of variability for these characters and restricting the scope of selection. Low to moderate GCV and PCV values were observed for plant height, primary branches per plant and 100 seed weight. While, pods per plant and clusters per plant depicted moderate GCV and PCV values. Low to moderate GCV and PCV values indicated presence of narrow spectrum of variability and influence of the environment rendering limited scope for improvement by selection.

The results revealed that genotypic coefficient of variation was close to that of phenotypic variation for all the characters studied indicating that phenotypic variability was largely due to genetic differences and less environmental influence.

Similar trend was observed 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) and Vir and Singh (2016).

Table.1 ANOVA for various characters in F_3 progenies of four crosses in mungbean

Sr. No.	Character	Crosses	Mean squares		
			Replications	Progenies	Error
	Degree of freedom	C1	2	22	44
		C2	2	19	38
		C3	2	21	42
		C4	2	14	28
1.	Days to 50 % flowering	C1	46.22	8.41*	4.01
		C2	20.60	15.41*	4.71
		C3	11.56	5.95*	2.69
		C4	17.69	38.64*	8.74
2.	Days to maturity	C1	38.45	8.05*	4.49
		C2	2.92	16.82*	8.99
		C3	30.02	14.98*	7.71
		C4	46.87	27.70*	12.91
3.	Plant height (cm)	C1	113.57	61.97*	10.57
		C2	70.34	91.56*	18.24
		C3	18.75	39.73*	17.22
		C4	39.87	65.17*	11.86
4.	Primary branches per plant	C1	0.42	0.12*	0.06
		C2	2.44	0.93*	0.17
		C3	7.84	0.57*	0.27
		C4	0.34	0.26*	0.11
5.	Pods per plant	C1	107.26	679.83*	34.90
		C2	63.40	495.68*	19.33
		C3	25.00	377.39*	30.45
		C4	180.35	268.17*	35.02
6.	Seeds per pod	C1	5.49	1.15*	0.43
		C2	0.52	1.24*	0.08
		C3	0.28	0.95*	0.46
		C4	0.87	1.14*	0.37
7.	100 seed weight (g)	C1	0.45	0.32*	0.04
		C2	0.26	0.35*	0.09
		C3	0.02	0.25*	0.10
		C4	0.52	0.30*	0.08
8.	Seed yield per plant (g)	C1	5.05	41.47*	2.64
		C2	14.63	79.01*	4.79
		C3	4.87	41.08*	4.38
		C4	10.92	35.52*	4.57
9.	Clusters per plant	C1	11.56	20.02*	2.87
		C2	15.58	24.68*	2.42
		C3	17.57	7.29*	1.72
		C4	14.50	10.35*	1.12
10.	Straw yield per plant (g)	C1	52.06	4037.05*	38.43
		C2	41.12	3477.08*	19.06
		C3	9.74	5295.75*	18.54
		C4	35.88	7303.24*	140.78
11.	Harvest index (%)	C1	0.36	189.16*	5.42
		C2	35.37	287.40*	5.67
		C3	8.00	181.09*	3.19
		C4	5.95	400.63*	6.00

** and * indicates significance at 0.01 and 0.05 levels of probability
C1 –Mehax Pusa Vishal, C2 – Mehax GJM-1006, C3 – Mehax GM-4, C4 – Mehax GJM-1008

Table.2 Estimates of genetic variability parameters for eleven quantitative characters in F_3 progenies of four crosses in mungbean

Sr. No.	Character	Crosses	Range	σ^2g	σ^2p	GCV (%)	PCV (%)	h^2 (b) (%)	GAM (%)
1.	Days to 50 % flowering	C1	35.33-42	1.47	5.47	3.16	6.10	26.82	3.37
		C2	35.33-43.67	3.57	8.27	4.84	7.37	43.14	6.54
		C3	35-40	1.09	3.78	2.84	5.28	28.83	3.13
		C4	35-45.67	9.97	18.70	8.01	10.97	53.29	12.04
2.	Days to maturity	C1	73.67-79.67	1.19	5.68	1.41	3.09	20.87	1.32
		C2	69.33-77.67	2.61	11.60	2.19	4.61	22.52	2.13
		C3	68.33-76.33	2.42	10.13	2.17	4.43	23.89	1.52
		C4	68.67-79	4.93	17.84	2.97	5.64	27.63	3.21
3.	Plant height (cm)	C1	43.75-64.28	17.13	27.70	7.90	10.04	61.86	12.79
		C2	35.33-57.27	24.44	42.68	9.81	12.96	57.27	15.28
		C3	39.33-52.80	7.50	24.72	6.05	10.97	30.35	6.86
		C4	38.74-53.47	17.77	29.63	9.26	11.96	59.97	14.77
4.	Primary branches per plant	C1	5.17-6.03	0.02	0.08	2.52	5.19	23.53	2.51
		C2	4.23-6.33	0.25	0.43	9.57	12.39	59.65	15.23
		C3	4.07-6.00	0.10	0.37	6.36	12.10	27.60	6.87
		C4	4.87-6.07	0.05	0.16	4.15	7.35	31.83	4.82
5.	Pods per plant	C1	35.26-96.57	214.98	249.87	20.65	22.26	86.03	39.44
		C2	37.91-90.14	158.78	178.12	17.79	18.84	89.15	34.60
		C3	38.45-78.64	115.65	146.10	18.05	20.28	79.16	33.07
		C4	39.47-69.71	77.72	112.73	16.21	19.53	68.94	27.73

σ^2g = Genotypic variance, σ^2p = 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
C1 – Meha x Pusa Vishal, C2 – Meha x GJM-1006, C3 – Meha x GM-4, C4 – Meha x GJM-1008

Table.2 Conti…

Sr. No.	Character	Crosses	Range	σ^2g	σ^2p	GCV (%)	PCV (%)	h^2 (b) (%)	GAM (%)
6.	Seeds per pod	C1	7.47-9.87	0.24	0.67	5.52	9.26	35.51	6.77
		C2	7.40-9.67	0.39	0.46	6.82	7.47	83.30	12.82
		C3	8.23-10.37	0.16	0.62	4.31	8.44	26.07	4.53
		C4	8.07-10.37	0.26	0.63	5.57	8.66	41.37	7.38
7.	100 seed weight (g)	C1	2.93-4.32	0.09	0.14	7.96	9.74	66.84	13.41
		C2	3.09-4.54	0.09	0.17	7.52	10.72	49.20	10.86
		C3	3.48-4.46	0.05	0.15	5.37	9.54	31.70	6.23
		C4	2.89-4.06	0.07	0.15	7.48	10.94	46.70	10.52
8.	Seed yield per plant (g)	C1	12-26.22	12.94	15.59	20.90	22.93	83.04	39.23
		C2	11.12-32.72	24.74	29.53	24.96	27.27	83.78	47.06
		C3	14.52-27.16	12.24	16.61	17.58	20.49	73.66	31.09
		C4	13.16-25.77	10.32	14.89	18.89	22.69	69.30	32.38
9.	Clusters per plant	C1	9.47-19.93	5.72	8.59	15.78	19.35	66.56	26.52
		C2	11.08-20.73	7.42	9.84	17.19	19.80	75.41	30.75
		C3	10.10-16.60	1.86	3.58	10.70	14.86	51.87	15.88
		C4	9.99-15.62	3.08	4.20	14.32	16.73	73.29	25.25
10.	Straw yield per plant (g)	C1	35-142.11	1332.87	1371.30	43.38	44.00	97.20	88.09
		C2	29.35-139.57	1152.67	1171.73	42.44	42.79	98.37	86.72
		C3	41.86-163.77	1759.07	1777.61	39.16	39.37	98.96	80.25
		C4	18.75-155.50	2387.49	2528.27	54.17	55.75	94.43	108.44
11.	Harvest index (%)	C1	10.32-40.37	61.25	66.67	39.80	41.53	91.87	78.59
		C2	9.60-44.04	93.91	99.58	43.09	44.37	94.30	86.19
		C3	8.35-34.13	59.30	62.49	42.70	43.83	94.90	85.68
		C4	9.82-41.91	131.54	137.54	55.90	57.16	95.64	112.62

σ^2g = Genotypic variance, σ^2p = 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
C1 – Meha x Pusa Vishal, C2 – Meha x GJM-1006, C3 – Meha x GM-4, C4 – Meha x GJM-1008

Broad sense heritability discriminates variation into heritable and non-heritable components hence reliable over coefficients of variation. Moderate to high heritability exhibited in almost all the traits in segregating population except for days to maturity. High heritability values of more than 85 per cent have been observed for pods per plant, straw yield per plant and harvest index in the cross Meha x Pusa Vishal and Meha x GJM-1006 while for straw yield per plant and harvest index in Meha x GM-4 and Meha x GJM-1008.

Moderate to high heritability estimates were observed for all the characters in majority of the segregating population. Their results are in agreement with previously reported by Singh *et al.,* (2009), Suresh *et al.,* (2010) and Narsimhulu *et al.,* (2013) for pods per plant and harvest index and Parmeswarappa *et al.,* (2005), Pandiyan *et al.,* (2006), Das *et al.,* (2010), Tabasum *et al.,* (2010), Prakash and Sekhawat (2012), Ahmad *et al.,* (2014), Javed *et al.,* (2014), Das and Barua (2015) and Muralidhara *et al.,* (2015) for pods per plant and Kumar *et al.,* (2010), Gadakh *et al.,* (2013) and Dagefa *et al.,* (2014) for harvest index.

Heritability and genetic advance used in conjunction for efficient prediction of response due to selection. Comparison of genetic advance as per cent mean value of all the population revealed higher genetic advance as per cent mean for pods per plant, clusters per plant except Meha x GM-4, seed yield per plant, straw yield per plant and harvest index and low to moderate genetic advance as per cent mean value for plant height and 100 seed weight. Heritability estimates of pods per plant, clusters per plant, seed yield per plant, straw yield per plant and harvest index were high coupled with high genetic advance as per cent mean compared to other traits indicating presence of additive gene action, hence, priority should be given to these traits while formulating selection strategies to realize better gains.

In the present investigation, hybridization involving five genotypes, Meha used as female parent and Pusa Vishal, GJM-1006, GM-4, GJM-1008 used as male parents resulted in increased variability, heritability and genetic advance. The F_3 population of crosses *viz.,* Meha x 1006 and Meha x GJM-1008 needs to be handled under different selection schemes for improving productivity as they depicted high heritability along with high genetic advance as per cent mean for most of the traits. There is need to study the comparative performance of the progenies by carrying out inter-mating within and between population and some sort of biparental mating involving the population *viz.,* Meha x GJM-1006 and Meha x GJM-1008.

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