Available online at www.ijpab.com

DOI: http://dx.doi.org/10.18782/2320-7051.2461

ISSN: 2320 – 7051

Int. J. Pure App. Biosci. **5 (2):** 532-535 (2017)

Research Article

International Journal of Pure & Applied Bioscience

OPEN ACCESS

Genetic Variability, Heritability and Genetic Advance for Seed Yield and Its Components in F_2 Generations of Mungbean (*Vigna radiata* (L.) R. Wilczek)

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Received: 15.01.2017 | Revised: 27.01.2017 | Accepted: 28.01.2017

ABSTRACT

In the present investigation, 26 F_2s of mungbean were used for variability, heritability and genetic advance for 10 traits. Analysis of variance revealed highly significant difference among all the characters suggesting sufficient amount of variability. The high genotypic coefficients of variation were observed only for seed yield per plant. High estimates of heritability was observed for days to flowering, seed yield per plant, days to maturity, number pods per plant, and number of seeds per pod. Genetic advance expressed as percent of mean was observed high for seed yield per plant, number of branches per plant. There was high to moderate heritability coupled with high to moderate genetic advance for seed yield per plant, number of pods per plant and number of seeds per pod indicated the involvement of additive gene action and scope of improvement in these traits through selection.

Key words: *Mungbean, GCV, PCV, Heritability, Genetic advance, Genetic advance as per cent of mean.*

INTRODUCTION

Development of high yielding cultivars and improving yield potential, there is a need of systemic breeding approach. Estimation of genetic variability in the germplasm of any crop is pre requisite for making any effective breeding programme. Most of the important yield contributing characters including yield are highly influenced by environment, since they are polygenetically controlled, which make the selection process difficult. Heritability is an index for calculating the influence of environment on the expression of genotypes. Estimates of genetic advance together with heritability would be helpful in assessing the nature of gene action. Therefore, the present investigation was carried out for estimating genetic variability, heritability and predicted genetic gain for various quantitative characters in 26 F_2 populations of mungbean.

Cite this article: Yusufzai, S.A., Pithia, M.S., Raval, L.J. and Vora, Z.N., Genetic Variability, Heritability and Genetic Advance for Seed Yield and Its Components in F_2 Generations of Mungbean (*Vigna radiata* (L.) R. Wilczek), *Int. J. Pure App. Biosci.* **5(2):** 532-535 (2017). doi: http://dx.doi.org/10.18782/2320-

MATERIAL AND METHODS

The material for the present study comprised of 26 F_2 populations of mungbean were evaluated in Randomized Block Design with three replications during *kharif* 2015-16 at Pulses Research Station, Junagadh Agricultural University, Junagadh under irrigated condition. Each of F_2 population was accommodated in two rows of 4.0 m length with line-line and plant–plant spacing of 45x10 cm. Recommended practices were followed to raise a good crop. The data were collected on 20 randomly selected plants in each plot for the traits *viz*., days to flowering, days to maturity, plant height (cm), number of pods per plant, pod length (cm), number of seeds per pod, number of leaves per plant, 100-seed weight (g) and seed yield per plant (g). Average values were subjected to standard statistical procedures, namely analysis of variance, genotypic and phenotypic coefficient of variation, heritability and genetic advance. Analysis of variance[5], GCV and PCV[2] and broad sense heritability and genetic advance[1] were estimated.

RESULTS AND DISCUSSIONS

The analysis of variance revealed significant difference among F_2 populations for all the characters indicating sufficient variability in the genetic material (Table 1). The estimates of genotypic and phenotypic coefficient of variability indicated that the values of phenotypic coefficient of variation was higher than of genotypic coefficient of variation, indicating more influence of environmental factors. Narrow difference was observed between PCV and GCV for days to flowering, days to maturity, pod length and number of seeds per pod. The result are in agreement with Sarkar *et al*.[6] and Hemavathy *et al*.[3]. A high degree of GCV was noticed for seed yield per plant. Similar findings were also reported by Sarkar *et al*.[6] and Hemavathy *et al*.[3]. High magnitude of GCV indicated the presence of wide range of variation for the characters under study to allow further improvement by selection of the individuals. The variation due to phenotypic and genotypic causes is presented in Table 2. Partitioning of total phenotypic variance into heritable and non-heritable components is very useful because only heritable portion of variation is exploitable through selection. It is a property not only a character but also of the population and of the environment to which individuals are subjected. In the experiment, high heritability estimates were obtained for days to flowering, days to maturity, number of pods per plant, number of seeds per pod and seed yield per plant. This high heritability may be due to additive gene effects hence these traits are likely to respond to direct selection. Such type of result was also reported by Singh *et al*.[7] and Narsimhulu *et al*.[4]. Since broad sense heritability represents the upper limit that can be achieved through selection, such estimates should be used judiciously for evaluation studies.

Heritability in conjunction with genetic gain is more useful than heritability alone in predicting the resistant effect for selecting the rest genotype for given trait. In the present experiment, high heritability estimates coupled with high to moderate genetic advance (Table 2) were observed for seed yield per plant, number of pods per plant and number of seeds per pod. This suggest that genotypic variation in the present material for these traits was due to high additive gene effect and direct selection for these traits may be rewarding. Remaining characters had either moderate or low genetic advance besides presence of high heritability, this may be due to non-additive gene effect and presence of high genotypic x environment interaction. Therefore, simple selection would not be rewarding. The expected genetic advance as per cent of mean (Table 2) was observed high for seed yield per plant, number of pods per plant and number of branches per plant. As it provides an idea about the amount of progress than can be achieved by selecting for the concerned trait. Thus, it can be inferred that there exists good variation for most of the traits studied and simple selection can bring significant improvement in seed yield of mungbean and its component traits.

Table 1: Analysis of variance showing mean squares for 10 characters in 26 F_2 populations of mungbean

Source	***df***	**Days to flowering**	**Days to maturity**	**Plant height (cm)**	**Number of branches per plant**	**Number of pods per plant**	**Pod length (cm)**	**Number of seeds per pod**	**Number of leaves per plant**	**100-seed weight (g)**	**Seed yield per plant (g)**
Replication	2	0.190	6.200	6.065	3.021	32.024	0.006	0.849*	264.039*	0.218	2.593*
Genotypes (F_2s)	25	10.035**	15.617**	67.617**	6.647**	109.242**	0.269**	1.410**	168.225**	0.252**	6.087**
Error	50	0.867	2.574	14.592	2.114	18.375	0.083	0.242	61.137	0.073	0.646

*, ** Significant at 5 and 1 % levels, respectively

Table 2: Range, Mean, Phenotypic and Genotypic coefficient of variation, Heritability and Genetic advance for twelve characters in mung bean during summer season

Characters	**Range of variation**	**Mean**	**Phenotypic coefficient of variation (%)**	**Genotypic coefficient of variation (%)**	**Heritability in broad sense (%)**	**Genetic advance**	**Genetic advance expressed as percent of mean**
Days to 50% flowering	34.67 – 39.00	36.84	3.16	2.59	67.22	1.61	4.34
Plant height (cm)	19.48 – 26.70	21.91	4.18	3.98	90.46	1.70	7.79
Number of primary branches per plant	2.47 – 4.62	3.35	18.47	18.14	96.38	1.23	36.68
Number of clusters per plant	2.33 – 6.46	3.58	24.61	23.65	92.36	1.67	46.82
Number of pods per plant	22.27 – 61.38	40.16	24.85	24.64	98.29	20.21	50.32
Length of pod (cm)	5.90– 12.77	8.55	23.28	23.08	97.70	4.01	46.87
Number of seeds per pod	5.80 – 14.47	8.99	22.74	20.66	82.51	3.47	38.65
100- seed weight (g)	4.54 – 7.04	5.82	12.03	12.01	98.66	1.43	24.70
Days to Maturity	66.67 – 77.66	72.66	4.09	3.66	79.98	4.90	6.74
Biological yield per plant (g)	22.33 – 42.47	32.27	20.79	19.84	91.03	12.58	38.98
Harvest Index (%)	16.75 – 30.87	24.28	15.89	14.67	85.19	6.77	27.89
Seed yield per plant (g)	6.53 – 10.06	8.40	8.50	8.10	90.93	1.25	15.92

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