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Assessment of genetic variability in mung bean [*Vigna radiata* (L.) Wilczek.]

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Abstract

The present investigation was carried out during rabi 2020-2021 at B-block of Regional agriculture research station, Warangal to assess genetic variability in forty four mungbean genotypes. Observations were recorded on 14 quantitative characters *viz.*, days to 50% flowering, days to maturity, plant height, branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, 100 seed weight and seed yield per plant, harvest index, preharvest sprouting, and protein content. The analysis of variance revealed that significant differences were found among genotypes for all fourteen characters which indicates the presence of substantial amount of variability among the germplasm. An examination of genetic parameters confirms that high estimates for GCV and PCV obtained for branches per plant, preharvest sprouting, pods per cluster and seed yield per plant. High heritability along with high genetic advance in per cent of mean was noted for seed yield per plant, number of pods per cluster, weight of 100 seed, plant height, number of branches per plant, number of branches per plant and preharvest sprouting which indicates that these traits were under the control of additive gene action and such characters could be improved through simple selection strategies.

Keywords: PCV, GCV, heritability, genetic advance

Introduction

Green gram (*Vigna radiata* (L.) Wilczek) is a legume crop which is also known as mung bean (2n=22) or maash (Persian;), “pesalu” (In A.P and Telangana). An active normal body requires about 40 grams of pulse per day or 14.6 kg per person per year (Narasinga Rao, 2010) [18]. Green gram is often preferred to other pulses due to its better digestibility and lower content of stachyose, verbacose and raffinose leading to less flatulence (Poehlman 1991) [20]. Mungbean is an excellent source of quality protein and due to its easy digestibility and palatableness it is most liked pulse in India. The grain contains approximately 25% protein, 4.1% fiber, 3.5% minerals and 56% carbohydrates. It is bagged with healthy nutrition which affords a number of health benefits. Genetic improvement of crop mainly depends on magnitude of genetic variability as well as extent to which desirable characters are heritable as it is the basis for effective selection Garje *et al.* (2014) [18]. Hence, it is necessary to study various genetic parameters like phenotypic and genotypic coefficients of variability, genetic advance and heritability, as they help in conducting a breeding program efficiently.

Material and Methods

Field experiment was carried out at Regional Agricultural Research Station, Warangal, during *Rabi*, 2020. Forty-four genotypes were evaluated at Regional Agricultural Research Station (RARS), Warangal. Experiment was performed in Randomized Block Design with three replications during *Rabi* season, 2020. Each entry was sown in two rows of five meters length with 30 cm X 10 cm spacing., keeping plot size 500 m^2. Tillage operations such as ploughing and harrowing were performed to prepare a fine tilth. Fertilizers were applied to the crop as a basal application with a fertilizer dosage of 20:50:0 NPK kg/ha. All cultural practices that are recommended for green gram cultivation were followed. Data was recorded on five randomly tagged plants in each genotype at various stages of crop growth. The phenotypic coefficient of variations (PCV) and genotypic coefficient of variations (GCV) for fourteen characters were calculated with the formulae proposed by Burton (1952) [4]. Heritability in broad sense was estimated as described by Allard (1960) [1]. Genetic advance was estimated from the heritability values using the formula suggested by Burton (1952) [4].

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Results and Discussion

Genetic parameters *viz*., variability, genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV), Heritability (in broad sense), genetic advance, genetic advance in percent of mean (GAM at 5%) were estimated among green gram genotypes for fourteen quantitative characters and the results are presented in Table 1.

Table 1: Genetic parameters for yield and component traits in Mung bean (*Vigna radiata*)

S. No	Character	General Mean	Range		Coefficient of variation		Heritability (in broad sense) (H_{bs})	Genetic Advance	GA as per cent of mean (5%)
			Maximum	Minimum	Genotypic (%)	Phenotypic (%)			
1	Days to 50% flowering	37.09	42.33	30.67	6.46	8.51	57.50	3.74	10.09
2	Days to maturity	70.94	80.00	62.33	4.73	5.24	81.60	6.25	8.80
3	Plant height (cm)	27.56	37.40	18.60	13.58	15.44	77.40	6.79	24.62
4	Number of branches per plant	1.33	2.40	0.53	35.79	38.04	88.50	0.93	69.36
5	Number of Clusters per plant	5.79	7.93	4.07	12.27	17.42	49.60	1.03	17.81
6	Number of pods per cluster	5.39	8.47	3.40	21.33	22.39	90.80	2.26	41.87
7	Number of pods per plant	20.62	29.26	13.73	16.20	19.97	65.90	5.59	27.09
8	Number of seeds per pod	10.72	14.87	7.87	11.50	13.15	76.50	2.22	20.73
9	Pod length (cm)	7.50	10.10	6.07	11.13	12.19	83.40	1.57	20.94
10	Test weight (gm)	3.60	5.44	2.84	15.87	15.97	98.80	1.17	32.48
11	Harvest index (%)	32.73	40.30	24.48	9.78	11.09	77.70	5.81	17.76
12	Preharvest Sprouting (%)	52.94	100.00	11.40	44.87	45.79	96.00	47.95	90.58
13	Protein content (%)	21.59	24.76	18.46	6.90	7.34	88.50	2.89	13.37
14	Grain yield per plant (gm)	5.94	8.80	3.41	18.37	21.12	75.60	1.95	32.90

*Significant at 5 percent level; ** Significant at 1 percent level

Variability

Variability results confirms that the Preharvest sprouting recorded high estimates for coefficient of variation (GCV: 44.87% and PCV: 45.79%) followed by number of branches per plant (GCV: 35.79% and PCV 38.04%), number of pods per cluster (GCV: 21.33% and 22.39%). Seed yield per plant recorded moderate GCV (18.37%) and high PCV (21.12%). These results were in agreement with Kate *et al*. (2017) [17] for branches per plant, Lamichaney *et al*. (2018) [14] for preharvest sprouting, Payasi *et al*. (2015) [19] for pods per cluster, Das and barua (2015) [5] for seed yield per plant. Moderate values for coefficient of variation were noticed in traits such as plant height (GCV: 13.58% and PCV: 15.44%), number of clusters per plant (GCV: 12.27% and PCV: 17.42%), test weight (GCV: 15.87% and PCV: 15.97%), number of pods per plant (GCV: 16.20% and PCV: 19.97%), number of seeds per pod (GCV: 11.50% and PCV: 13.15%) and pod length (GCV: 11.13% and PCV: 12.19%). Similar results were published by Varma *et al*. (2018) [25] for pods per plant, Kumar *et al*. (2013) [13] for test weight, Muthuswamy *et al*. (2019) [17] for plant height, Hemavathy *et al*. (2015) [9] for clusters per plant, Mohammed *et al*. (2020) [16] for seeds per pod, Ramakrishnan *et al*. (2018) [22] for pod length. Lowest estimate for GCV and PCV were recorded in days to maturity (GCV: 4.73% and PCV: 5.24%) followed by days to 50% flowering (GCV: 6.46% and PCV: 8.51%), protein content (GCV: 6.90% and PCV: 7.34%). Harvest index was recorded with low GCV (9.78%) and moderate PCV (11.09%). These experimental results were in agreement with Mohammed *et al*. (2020) [16] for days to maturity, Varma *et al*. (2018) [25] for days to fifty percent flowering, Gadakh *et al*. (2013) [7] for harvest index, Gadakh *et al*. (2013) [7] for protein content.

Heritability

Heritability among the different characters ranged between 49.60% to 98.80%. All characters have shown high heritability except days to fifty percent flowering and clusters per plant. Highest heritability was recorded for test weight (98.80%) followed by preharvest sprouting (96%), number of pods per cluster (90.80%), protein content (88.50%), number of branches per plant (88.50%), pod length (83.40), days to maturity (81.60%), harvest index (77.70%), plant height (77.40%), number of seeds per pod (76.50%), seed yield per plant (75.60%), number of pods per plant (65.90%). Moderate estimates were observed for days to fifty percent flowering (57.50%), number of clusters per plant (49.60%). These findings were in accordance with Sandhiya and Saravanan (2018) [24] for test weight, Muthuswamy *et al.* (2019) [17] for branches per plant, Das and barua (2015) [5], for pod length. Rao *et al.* (2016) [23] for preharvest sprouting, Alom *et al.* (2014) [2] for pods per cluster, Kate *et al.* (2017) [17] for Seed yield per plant, Alom *et al.* (2014) [2] for pods per plant, Payasi *et al.* (2015) [19] for days to maturity, Degefa *et al.* (2014) [6] for harvest index, Mohammed *et al.* (2020) [16] for plant height, Sandhiya and Saravanan (2018) [24] for seeds per pod, Gadakh *et al.* (2013) [7] for protein content.

Genetic advance as percent of mean

Highest genetic advance as percent of mean was recorded in preharvest sprouting (90.58%) followed by number of branches per plant (69.36%), number of pods per cluster (41.87%), seed yield per plant (32.90%), test weight (32.48%), number of pods per plant (27.09%), plant height (24.62%). Genetic advance as percent of mean was found to be moderate in pod length (20.94%), number of seeds per pod (20.73%), number of clusters per plant (17.81%), harvest index (17.76%), protein content (13.37%), days to fifty percent flowering (10.09%) and low estimates were documented in days to maturity (8.80%). These experimental results were parallel with Suresh *et al.* (2010) [10], Sandhiya and Saravanan (2018) [24] for branches per plant, Lamichaney *et al.* (2018) [14] for preharvest sprouting, Hemavathy *et al.* (2015) [9] for pods per clusters and pods per plant. Rahim *et al.* (2010) for seed yield per plant, test weight and plant height. Baisakh *et al.* (2016) [3], Kumar *et al.* (2013) [13] for pod length, Reddy *et al.* (2011) [12] for seeds per pod, Mehandi *et al.* (2013) [15] for clusters per plant, Jagdhane *et al.* (2017) [10] for harvest index, Reddy *et al.* (2011) [12] for protein content, Jagdhane *et al.* (2017) [10] for days to 50% flowering, Hemavathy *et al*. (2015) [9] for low estimates of days to maturity.

Conclusion

High GCV and PCV values were observed in preharvest sprouting, number of branches per plant, number of pods per cluster and seed yield was found with moderate GCV and high PCV. All characters have exhibited high heritability except days to fifty percent flowering and clusters per plant which declares high influence of genetic components. High heritability at broad sense along with high genetic advance in percent of mean was noted in seed yield per plant, pods per cluster, weight of 100 seed, pods per plant, plant height, branches per plant and preharvest sprouting which indicates that these traits were under the control of additive gene action and such characters could be improved through simple selection strategies. High heritability with moderate values of genetic advance under mean was observed in seeds per pod, length of pod, harvest index and protein content whereas, high heritability by the side of low genetic advance under mean was recorded for days to maturity. These characters are governed by non-additive genes and selection might be less rewarding for improvement of these component characters.

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