



P-ISSN: 2349-8528
E-ISSN: 2321-4902
IJCS 2019; SP6: 77-81

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(Special Issue -6)
3rd National Conference
On

**PROMOTING & REINVIGORATING AGRI-HORTI,
TECHNOLOGICAL INNOVATIONS
[PRAGATI-2019]
(14-15 December, 2019)**

Genetic variability, heritability and genetic advance in mungbean [*Vigna radiata* (L.) Wilczek]

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Abstract

The present investigation was carried out with 36 genotypes of mungbean in summer 2018 at Bihar Agricultural University, Sabour, Bhagalpur, Bihar, India to assess morphological diversity using D² statistics analysis. The analysis of variance revealed highly significant differences among the genotypes for all the traits studied. Thirty six mungbean genotypes (collected from different parts of India) including four checks were analyzed for seed yield and its components by estimating genetic variability. Analysis of variance showed highly significant differences among the genotypes for all the traits under study. In the current study, high heritability coupled with high genetic advance as percent of mean were exhibited by the characters like harvest index followed by seed yield per plant, number of pods per plant, number of clusters per plant, biological yield per plant, number of primary branches, number of secondary branches, number of pods per cluster, plant height and 100 seed weight which depicts that these characters are governed by additive gene action and could go for selection program without progeny testing. High heritability estimates were recorded for the traits viz., 100-seed weight, followed by grain yield per plant, biological yield per plant, number of pods per plant, number of filled pods per plant, number of secondary branches per plant and plant height. In general phenotypic coefficients of variation were observed to be greater than their corresponding genotypic coefficients of variation. Hence these traits could be used by breeders for the improvement of seed yield resulting in the unfolding of high yielding varieties of mungbean.

Keywords: *Vigna radiata*, genetic divergence; D² statistics

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek], generally known as Green gram or Moong, is one of the important pulse crops grown in India. Being a short duration annual, it is grown as a inter-crop and increases cropping intensity. Therefore it became a good profit provider for marginal farmers. Mungbean is utilized as food legumes and good proteinary diet for many vegetarians in India. It is an autogamous diploid plant with $2n = 2x = 22$ chromosomes, having a genome size of 515 Mb (Tangphatsornruang S *et al.* 2009) [35]. In India, the total area covered under mungbean is 30.41 lakh hectares with a total production of 14.24 lakh tonnes and productivity of 468 kg/ha (Tiwarly and Shivhare 2016) [36]. The area covered under mungbean in Bihar is 1.57 lakh hectares with a production of 1.04 lakh tonnes and productivity of 664 kg/ha (Tiwarly and Shivhare 2016) [36]. To increase the production and productivity, there is a need of developing high yielding varieties in mungbean. For developing high yielding varieties, there is a need of variation in the test germplasm.

Genetic diversity is an important element for crop improvement programme. The hybridization programme between two genetically diverse parents is efficient in developing good heterosis in F_1 and able to produce considerable variability in subsequent selfed generations. Grain yield is a quantitative or polygenic trait, which is complex and highly influenced by genetic and environmental factors. The genetic diversity is better estimated by D^2 analysis. Mahalanobis (1936) [20] defined the distance between two populations as D^2 which was obtained by Tocher's method, described by Rao (1952) [30]. D^2 statistics analysis is used for selection of genetically divergent parents for hybridization programme.

Materials and Methods

The present investigation was carried out in summer season, 2018 at Bihar Agricultural University, Sabour, Bhagalpur, Bihar. The experimental material comprised of 36 genotypes were procured from different areas of Bihar, IIPR (Kanpur), G.B.P.U.A.&T (Pantnagar), NBPGR (New Delhi), Kashipur (Uttarakhand), BHU (Varanasi), CSKHPKV, Palampur. The

experiment was conducted in randomized block design (RBD) in three replications with a plot size of 4.8 m². The observations were recorded from five randomly selected plants of each genotype for plant height (cm), number of primary branches, number of secondary branches, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (gm), biological yield per plant (gm), harvest index (%) and seed yield per plant (gm). The data on days to 50% flowering and days to maturity were recorded on plot basis.

The estimation of morphological diversity was done by D^2 analysis (Mahalanobis 1936) [20]. The genotypes were clustered into different clusters with the help of Tocher's method (Rao 1952) [30].

Results and Discussion

The analysis of variance revealed highly significant differences among the genotypes for all the traits studied indicating that there were considerable amount of significant variations present in the breeding materials.

Table 1: Analysis of variance for 14 quantitative characters for the design of experiment in 36 Mungbean genotypes

S. No.	Characters	Mean Sum of Squares		
		Replication (df=2)	Treatment (df=35)	Error (df=70)
1.	Days to 50% flowering	106.58	21.00**	5.27
2.	Days to maturity	5.58	87.63**	2.37
3.	Plant height (cm)	89.44	284.82**	22.52
4.	Number of primary branches	0.14	0.87**	0.05
5.	Number of secondary branches	0.07	0.85**	0.07
6.	Number of clusters per plant	0.008	13.04**	0.29
7.	Number of pods per cluster	0.21	1.28**	0.13
8.	Number of pods per plant	207.17	76.38**	2.73
9.	Pod length (cm)	2.50	0.48**	0.06
10.	Number of seeds per pod	3.05	2.52**	0.18
11.	100 seed weight (gm)	0.08	0.67**	0.04
12.	Biological yield per plant (gm)	1.13	110.30**	3.90
13.	Harvest index (%)	8.03	263.69**	7.79
14.	Seed yield per plant (gm)	1.02	10.32**	0.08

d.f.= degree of freedom; * and ** denotes Significance at 5% and 1% probability level, respectively.

The estimates of phenotypic variance (σ^2p) and genotypic variance (σ^2g) calculated for different traits were given in Table 2. The highest (σ^2p) was showed by plant height (109.96) which was followed by harvest index (93.09), biological yield per plant (39.37), days to maturity (30.79) and number of pods per plant (27.28). The pod length showed the lowest phenotypic variance of 0.20. The highest genotypic variance (σ^2g) was found for plant height (87.43) which was followed by characters- harvest index (85.30), biological yield per plant (35.47), days to maturity (28.42) and number of pods per plant (24.55). The lowest genotypic variance (σ^2g) was observed for pod length (0.14) in the experiment.

On detailed observation of Table 2 showed that for days to maturity, number of primary branches, number of secondary branches, number of clusters per plant, number of pods per cluster, pod length, number of seeds per pod, 100 seed weight and seed yield per plant, there were minor differences between phenotypic and genotypic variances indicating the less environmental influence on these characters in the experiment. From the table 4.3, it was observed that in majority of the characters, the genotypic variance was much more greater than environmental variance indicating that these characters were possessing high variance which can be heritable.

Coefficient of variation

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimates of all the traits were given in Table 4.3. The higher values of PCV compared to the GCV denotes the presence of environmental influence. The phenotypic coefficient of variation (PCV) was ranged from 6.18 (days to 50% flowering) to 30.86 (harvest index). The genotypic coefficient of variation (GCV) was ranged from 4.36 (days to 50% flowering) to 29.54 (harvest index).

The high PCV values were observed for harvest index (30.86), number of pods per plant (28.19), biological yield per plant (26.89), seed yield per plant (26.69), number of clusters per plant (26.34), number of secondary branches (22.9) and number of primary branches (22.72). The traits having high phenotypic coefficient of variation showed more influence of environmental factors. Hence care should be taken at the time of selection program as the environmental variations can mislead the expected results or outcomes.

The high GCV values were observed for harvest index (29.54), number of pods per plant (26.74), seed yield per plant (26.38), biological yield per plant (25.52), number of clusters per plant (25.49), number of primary branches (21.01), number of secondary branches (20.43). This showed that these characters are having lesser environmental influences

and priority for these traits can be given in selection programmes.

On detailed observation of table 2, it was showed that seed yield per plant and days to maturity had the least differences between their respective GCV and PCV values indicating that environmental influences on these traits are less and these traits can be given importance in breeding programme.

Heritability (h^2_{bs}) and Genetic Advance

As per data (Table 2), it was proved that the heritability (broad sense) calculated for the fourteen quantitative traits was ranged from 49.90% (days to 50% flowering) to 97.70% (seed yield per plant). High heritability was showed by the characters like seed yield per plant (97.70%) which was followed by number of clusters per plant (93.60%), days to maturity (92.30%), harvest index (91.60%), biological yield per plant (90.10%), number of pods per plant (90.00%), 100 seed weight (85.70%), number of primary branches (85.60%), number of seeds per pod (81.10%), number of secondary branches (79.60%), plant height (79.50%), number of pods per cluster (74.80%) and pod length (70.60%). The days to 50% flowering of 49.90% exhibited moderate heritability (broad sense) in the experiment. Panse and Sukhatme (1967) described that traits having high heritability were controlled by the additive gene action and might be developed by individual plant selection.

Genetic advance in Table 2 for the traits of the experiment was varied from 0.65 (pod length) to 18.21 (harvest index). Moderate genetic advance was showed by the characters like harvest index (18.21) which was followed by plant height (17.18), biological yield per plant (11.64), days to maturity (10.55). The low genetic advance was showed by the characters like number of pods per plant (9.68), number of

clusters per plant (4.11), seed yield per plant (3.76), days to 50% flowering (3.33), number of seeds per pod (1.64), number of pods per cluster (1.10), number of primary branches (1.00), number of secondary branches (0.94), 100 seed weight (0.88), pod length (0.65) in the experiment.

Genetic advance as percent of mean in Table 2 was varied from 6.35 (days to 50% flowering) to 58.25 (harvest index). High genetic advance as percent of mean was exhibited by the characters like harvest index (58.25) which was followed by seed yield per plant (53.7), number of pods per plant (52.26), number of clusters per plant (50.81), biological yield per plant (49.89), number of primary branches (40.05) and number of secondary branches (37.55), number of pods per cluster (29.89), plant height (29.53), 100 seed weight (22.06). The moderate genetic advance as percent of mean was exhibited by the characters like number of seeds per pod (16.43), days to maturity (15.53). The low genetic advance was showed by the characters like pod length (9.5) and days to 50% flowering (6.35) in the experiment.

High estimates of heritability may or may not have the high genetic advance. Johnson *et al.* (1955) described that heritability estimates coupled with the genetic advance as percent of mean would give a much better result apart from heritability alone in finding the resultant effect of selection. In the current study, high heritability coupled with high genetic advance as percent of mean were exhibited by the characters like harvest index followed by seed yield per plant, number of pods per plant, number of clusters per plant, biological yield per plant, number of primary branches, number of secondary branches, number of pods per cluster, plant height and 100 seed weight which depicts that these characters are governed by additive gene action and could go for selection program without progeny testing.

Table 2: Genetic parameters of 14 characters of Mungbean genotypes

S. No.	Characters	Mean	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Environmental variance (σ^2_e)	GCV (%)	PCV (%)	h^2 (Broad sense) (%)	Genetic Advance (GA) at 5%	GA as% of mean at 5%
1.	Days to 50% flowering	52.47	5.24	10.51	5.27	4.36	6.18	49.90	3.33	6.35
2.	Days to maturity	67.92	28.42	30.79	2.37	7.85	8.17	92.30	10.55	15.53
3.	Plant height (cm)	58.16	87.43	109.96	22.52	16.08	18.03	79.50	17.18	29.53
4.	Number of primary branches	2.50	0.28	0.32	0.05	21.01	22.72	85.60	1.00	40.05
5.	Number of secondary branches	2.50	0.26	0.33	0.07	20.43	22.90	79.60	0.94	37.55
6.	Number of clusters per plant	8.09	4.25	4.54	0.29	25.49	26.34	93.60	4.11	50.81
7.	Number of pods per cluster	3.69	0.38	0.51	0.13	16.78	19.41	74.80	1.10	29.89
8.	Number of pods per plant	18.53	24.55	27.28	2.73	26.74	28.19	90.00	9.68	52.26
9.	Pod length (cm)	6.86	0.14	0.20	0.06	5.49	6.53	70.60	0.65	9.50
10.	Number of seeds per pod	9.97	0.78	0.96	0.18	8.86	9.83	81.10	1.64	16.43
11.	100 seed weight (gm)	3.99	0.21	0.25	0.04	11.57	12.50	85.70	0.88	22.06
12.	Biological yield per plant (gm)	23.34	35.47	39.37	3.90	25.52	26.89	90.10	11.64	49.89
13.	Harvest index (%)	31.26	85.30	93.09	7.79	29.54	30.86	91.60	18.21	58.25
14.	Seed yield per plant (gm)	7.00	3.41	3.49	0.08	26.38	26.69	97.70	3.76	53.70

Conclusion

Genetic variability parameters revealed that number of pods per plant, number of filled pods per plant and 100 seed weight could be the deciding factors for the improvement of

mungbean genotypes for grain yield. The PCV and GCV values were high for grain yield per plant, biological yield per plant, number of secondary branches per plant, number of pods per plant, number of filled pods per plant and 100-seed

weight suggesting the probability of refinement of these traits through selection. High heritability coupled with high expected genetic advance as per cent of mean for 100 seed weight, grain yield per plant, biological yield per plant, number of pods per plant, number of filled pods per plant and number of secondary branches per plant, these characters show least environmental affect which could be improved more easily than the other characters for more productivity of lentil. The genotypes BRM-1, Banka local mung -7, Banka local mung -2, SML668, DMG-1105-1-2, and BRM-8-1 were identified as genetically divergent, which can be utilized for future crop improvement programme in mungbean. The above results indicated that these genotypes have maximum genetic diversity and useful for developing a large number of segregants through crossing programme by using maximum diverse parents.

Acknowledgment

Authors are grateful to the Bihar Agricultural University, Sabour, Bhagalpur, India for providing the required facilities for the experimental work.

Competing Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

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