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Estimation of the various genetic variability parameters for seed yield and its component traits in Mothbean germplasm [*Vigna aconitifolia* (Jacq.) Marechal]

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Abstract

Moth bean is mostly grown in the arid zones as an important *kharif* pulse crop. The analysis of variance revealed significant differences for all the twelve quantitative characters of fifty genotypes indicating presence of adequate variability. The higher PCV and GCV was observed for harvest index (38.02%, 36.06%) followed by seed yield per plant (34.18%, 33.82%) and number of pods per plant (23.97%, 17.86%). Most of the characters possessed high heritability. The genetic advance as per cent mean was highest for harvest index (70.47%) followed by seed yield per plant (68.96%), number of seeds per pod (35.64%). Association of high heritability with larger magnitude of expected genetic advance was estimated for traits which might be governed by additive genes. For genetic improvement, their amelioration can be brought by simple selection over a short span of time.

Keywords: Moth bean, quantitative traits, Variability, heritability, genetic advance.

Introduction

Moth bean (*Vigna aconitifolia*) is a native crop of hot and dry habitats of northern and western parts of India. According to De Candolle (1884) [6], Vavilov (1926) [20], Zukovskii (1962) [23] and Jain and Mehta (1980) [11], moth bean was originated in India. Moth bean is a hot weather, drought resistant legume and this fact is supported by its well developed deep root system. It can tolerate high temperature without any adverse effect on flowering and fruit development. Optimum temperature requirement for growth and development is 25-37°c. Bulk of the cultivation of moth bean is confined to dry-lands of arid zone with 250-500 mm rainfall requirement with arrangement of proper drainage. This crop can be grown successfully in sandy loam of low to moderate fertility. It does not require extra care and water. In India moth bean is mainly grown in Rajasthan which contributes about 75 per cent of total area and production in the country. Other important states for cultivation of moth bean are Maharashtra, Gujarat, Jammu & Kashmir and Punjab. Rajasthan ranks first in area and production and occupies 13.87 lakh ha area with annual production of 4.34 lakh tonnes and productivity 310 kg ha^{-1} (Anonymous, 2016-17) [2].

Moth bean is the potential reservoir of protein (22-24 per cent), vitamins, carbohydrates and minerals. In addition to protein rich seeds, it is an important source of hay at par in quality with alfa-alfa (Kennedy and Midson, 1925) [13]. It is cultivated for food as well as dry plants make good fodder. Its green fodder is also superior to guar and cowpea in dry matter digestibility (Das and Arora, 1977) [5].

Moth bean crop till date does not claim to be a national pulse because of its contribution in terms of area and production only 5.9 and 1.6 per cent, respectively. This has been a neglected crop from the evolution view point hence; it is the marginal and secondary choice of the farmers. Furthermore, research efforts, wealth of literature are also scarce, scanty and unsystematically available in respect of this legume.

A plant breeding programme can be divided into three stages *viz.*, creation of a gene pool having variable germplasm, selection of individuals from the gene pool, utilization of selected individuals to evolve as a superior variety. The quantitative measurement of individual character provides the basis for interpreting analysis of variance. The efficacy of selection depends upon the magnitude of genetic variability for yield and yield contributing traits in the breeding material. Collection, maintenance and evaluation of germplasm for studying genetic variability of economically important traits is one of the basic steps for initiating breeding programme. The genetic facts are inferred from phenotypic observations. The observed variability may be grouped with parameters like genotypic and phenotypic coefficient of variation, heritability, genetic gain to form the basis of selection that guides the breeders to select superior parents to initiate an effective and fruitful crossing programme.

Materials and Methods

The present investigation having experimental materials consisting forty eight germplasm along with two check varieties of moth bean procured from AICRP on Moth bean, ARS, SKRAU, Bikaner. The experiment was carried out with three replications in RBD design during *Kharif* 2017. A spacing of 30 cm between rows and 10 cm between plants was adopted respectively. All the recommended package of practices were followed to raise good and healthy crop stand. Data were collected on twelve seed yield and yield contributing quantitative characters *viz.*, days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, pod length, number of pods per plant, number of seeds per pod, 100-seed weight, biological yield per plant, harvest index, seed yield per plant and incidence of yellow mosaic virus. At maturity five plants were selected randomly from each plot and tagged and data were recorded. For observation regarding incidence of yellow mosaic virus scores were given as following (scale 3-7) being 3- resistant, 5- moderately resistant and 7-susceptible.

The overall mean values of all the genotypes for the characters under study were used for statistical analyses. To test the difference among genotypes, the data obtained for each character were analyzed by the standard procedure given by Panse and Sukhatme (1961) [17]. The coefficient of phenotypic and genotypic variation will be calculated by using the formula suggested by Burton (1952) [3]. Heritability was estimated by the formula as suggested by Johnson *et al.* (1955) [12] and Hanson *et al.* (1956) [8]. Expected genetic advance represents the shift in a population mean towards superior side under selection pressure after single generation of selection. This was estimated as per the formula suggested by Johnson *et al.* (1955) [12].

Results and Discussion

Analysis of Variance

The superiority of performance of germplasm lines of moth bean was judged by analysis of variance of mean for each character. Mean sum of squares of genotypes revealed highly significant difference among all the genotypes for all the twelve characters studied indicating ample amount of genetic variability existing in the germplasm. This is represented in Table no. 1.

Co-Efficient of Variation

The GCV and PCV were categorized as low (10% >), moderate (10-20%) and high (20% <) as suggested by Burton and Devana (1953) [4]. In the present investigation PCV was higher than corresponding GCV. This suggested role of environment in the expression of these characters to some degree or other.

Phenotypic and Genotypic Coefficient of Variation

The higher phenotypic and genotypic coefficient of variance was observed for harvest index (38.02%, 36.06%) and seed yield per plant (34.18%, 33.82%). High PCV with moderate GCV was found for number of seeds per pod (23.97%, 18.15%). This indicates the scope of exploiting variability for further improvement of these traits. Selection based on these characters would facilitate successful isolation of desirable genotypes because response to selection is directly proportional to the variability present in the material. Similar results were reported in the findings of Yogeesh *et al.* (2012) [22]; Kumar *et al.* (2015) [15]; Garg *et al.* (2017) [7]; Kohakade *et al.* (2017) [14] for pods per plant and seed yield per plant.

The occurrence of moderate estimates of GCV and PCV for plant height (16.71%, 17.53%), number of primary branches per plant (14.28%, 17.49%), number of seeds per pod (18.15%, 19.03%), 100-seed weight (14.80%, 15.10%) and biological yield per plant (13.13%, 15.65%) suggested that improvement in these characters might be gained up to reasonable extent.

The lowest GCV and PCV were recorded for days to 50% flowering (6.58 and 7.40%) and days to maturity (9.10 and 9.59%) suggesting narrow range of variation for these characters. Similar results were obtained by Garg *et al.* (2017) [7]; Anand *et al.* (2016) [1] for days to 50% flowering.

The difference between GCV and PCV were minimum for all the characters except number of pods per plant suggesting less influence of environment in the expression of these characters and one may rely upon the phenotypic values for direct selection. This result was in accordance with the findings of Kohakade *et al.* (2017) [14].

Heritability

GCV as such does not give the idea of total variation that is heritable. The relative amount of heritable portion of variation can be assessed through heritable estimates (Comstock et al. 1958). Heritability values were categorized as (low, moderate and high) followed by Robinson et al. (1951); Low: (below 50 per cent), Moderate: (50-70 per cent), High: (above 70 per cent).

The characters namely seed yield per plant (97.93%), 100-seed weight (96.04), number of seeds per pod (90.92%), plant height (90.77%), days to maturity (90.05%), harvest index (89.98%), days to 50% flowering (79.12%) and biological yield per plant (70.34%) possessed high heritability that shows close correspondence between the genotype and the phenotype due to a relatively smaller contribution of the environment to phenotype. This result is in conformity with the results of Vir and Singh (2015) [21], Kohakade *et al.* (2017) [14] and Garg *et al.* (2017) [7], Anand *et al.* (2016) [1] for seed yield per plant, plant height. Thus the above characters will aid in selection programme owing to their high heritability value.

Moderate heritability was observed for number of primary branches per plant (66.59%), incidence of YMV (62.61%), number of pods per plant (55.53%) and pod length (51.05%). Vir and Singh (2015) [21] reported high heritability for incidence of YMV which is contradictory to the above result.

Genetic advance as Per Cent mean

Genetic advance provides the knowledge about expected gain for a particular character after selection. Genetic advance when expressed as percent of mean is called genetic gain. Genetic advance under selection depends upon the phenotypic variability among different plants or families in the base population, the heritability of the character under selection and the intensity of selection.

The genetic advance as per cent of mean was categorized as suggested by Johnson *et al.* (1955) [12]; 0-10%: Low, 10-20%: Moderate, 20% and above: High.

The genetic advance as per cent mean was highest for harvest index (70.47%) followed by seed yield per plant (68.96%), number of seeds per pod (35.64%) and plant height (32.78%). Similar findings were obtained by Garg *et al.* (2017) [7] for all the above characters except pod length, Hemavathy *et al.* (2015) [9], Kohakade *et al.* (2017) [14] for number of pods per plant and seed yield per plant, Jagdhane *et al.* (2017) [10] for high GAM in number of pods per plant and number of primary branches per plant. The moderate GA was observed for days to 50% flowering (12.07%) followed by pod length (14.49%), incidence of YMV (17.57%), days to maturity (17.80%). This result showed in accordance with Mehandi *et al.* (2013) [16] for days to 50% flowering, pod length.

High GCV, PCV, high to moderate heritability with high genetic advance per cent mean were registered for characters like seed yield per plant, harvest index and number of pods per plant. These characters are said to be governed by additive gene action. These characters are least influenced by environmental effects and offering good promise for future breeding programme using simple breeding methods. Similar findings were observed by Hemavathy *et al.* (2015) [9] for number of pods per plant, plant height, Raturi *et al.* (2015) [18] for seed yield and number of pods per plant.

Moderate heritability with moderate genetic advance per cent of mean was shown by pod length and incidence of YMV. It indicated equal influence of both additive and non-additive gene effects. In such cases recurrent selection and diallel selective mating may be followed.

GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation.

Conclusion

Highly significant differences were obtained through the analysis of variance, reflects ample amount of genetic variability existed in the research material. High estimates of PCV and GCV were observed in harvest index and seed yield per plant. Selection based on these characters would facilitate successful isolation of desirable genotypes. High GCV, PCV, high to moderate heritability with high genetic advance per cent mean was recorded for characters like seed yield per plant, harvest index and number of pods per plant indicated that these were under the control of additive gene effects and selections based on the traits could improve productivity in moth bean directly.

Table 1: Analysis of variance for different characters in Moth bean

S. No.	Characters	Mean sum of squares		
		Replications (df= 2)	Treatments (df=49)	Error (df=98)
1	Days to 50 % flowering	4.81	30.34**	2.45
2	Days to maturity	54.19**	135.90**	4.83
3	Plant height (cm)	0.52	89.07**	2.92
4	Number of primary branches per plant	0.15	1.36**	0.20
5	Pod length (cm)	0.19	0.61**	0.15
6	Number of pods per plant	567.82	1180.58**	248.77
7	Number of seeds per pod	0.08	2.51**	0.08
8	100- Seed Weight (g)	0.00	0.45**	0.01
9	Biological yield per plant (g)	127.44	349.61**	43.08
10	Harvest index (%)	3.45	93.43**	3.34
12	Incidence of yellow mosaic virus(YMV)	10.62**	1.67**	0.28

Table 2: Genotypic and phenotypic coefficient of variation, heritability (broad sense %) and genetic advance for different characters in Moth bean

S. No.	Character	G.C.V.	P.C.V.	Heritability (%)	GA % of Mean
1	Days to 50 % flowering	6.59	7.41	79.12	12.07
2	Days to maturity	9.11	9.60	90.05	17.80
3	Plant height (cm)	16.71	17.54	90.77	32.78
4	Number of primary branches per plant	14.28	17.50	66.59	24.00
5	Pod length (cm)	9.85	13.78	51.05	14.49
6	Number of pods per plant	17.86	23.97	55.53	27.42
7	Number of seeds per pod	18.15	19.03	90.92	35.64
8	100 Seed Weight (g)	14.80	15.10	96.04	29.87
9	Biological yield per plant (g)	13.13	15.65	70.34	22.68
10	Harvest index (%)	36.07	38.02	89.98	70.47
11	Seed yield per plant (g)	33.83	34.18	97.93	68.96
12	Incidence of yellow mosaic virus(YMV)	10.78	13.63	62.61	17.57

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