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Estimation of Genetic Association of Yield and Quality Traits in Mungbean (*Vigna radiata* L. Wilczek)

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Abstract: Morphological and biochemical characterization were carried out in 20 mungbean genotypes. The tested genotypes exhibited significant to highly significant differences with respect to all the morphological and biochemical characters studied. Five genotypes were recorded with significant percent for fat, 16 for fibre, four for ash, six with high protein and eight with carbohydrate contents. Fat and fibre contents were recorded with significantly higher heritability (>90%) with corresponding PCV and GCV (>15%) coupled with genetic advance, which validates that these characters are greatly influenced not only by the additive gene effect but also by greater proportion of heritable variation. No consistency in fat and fibre contents with seed yield indicated that they can be increased or decreased without detrimental effect on seed yield. However, ash and protein contents had negative correlation with nine out of 10 morphological traits, indicating that the genotypes with high protein or ash contents are not essentially high seed yielding as well. Whereas, carbohydrate contents had highly significant and positive correlations with eight out of 10 morphological traits, suggesting its usefulness as an excellent selection marker for improving seed yield.

Keywords: Mungbean, Mean, PCV, GCV, Correlation.

INTRODUCTION

Mungbean is one of the important pulses in India and is suitable for cultivation under different farming situations. Generally, mungbean seeds contain 22-28% protein, 60-65% carbohydrates, 1-1.5 % fat and

3.5-4.5% fibres. However, productivity in the country is still low and there is a need for improvement. Yield is a complex character and is associated with various contributing characters which in turn are interrelated among them. Knowledge of the magnitude and type

of association between yield and its components themselves greatly help in evaluating the contribution of different components towards yield. Yield being a polygenic character is highly influenced by the fluctuations in environment. Hence, selection of plants based directly on yield would not be very reliable. Improvement in yield depends on the nature and extent of genetic variability, heritability and genetic advance in the base population. Hence, the present investigation was undertaken to study the magnitude of genetic variability for various yield parameters and the extent to which the desirable characters are heritable and interrelated among themselves.

MATERIALS AND METHODS

The present study was carried out at The Experimental Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar in a randomized block design (RBD) replicated twice with spacing of 30 cm between rows and 15cm between plants. The recommended agronomic and plant protection practices were followed to maintain healthy stand of the plants. Data were recorded on five randomly selected plants in each genotype for the characters viz., plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, pod length (cm), 100 seed weight and single plant yield (g). Genetic parameters like variance, genotypic and phenotypic coefficient of variation, heritability and genetic advance as per cent mean and character association were calculated as per the standard procedure.

The biochemical analyses of mungbean seeds for crude fibre, fat and ash were performed by A.O.A.C. [1] method. The percentage of 'Carbohydrate' as nitrogen free extract was calculated by subtracting per cent moisture, fat, crude fibre and per cent ash from 100. Seed protein content was done

by Micro kjeldahl's method as described by Yoshida [2]. 0.5 g seeds from the samples of seed protein content were taken from grinded bulk seeds of five plants per replication. The protein from the defatted meal were precipitated with 10% trichloroacetic acid and recovered by centrifugation at 5000 rpm for 30 min at 4°C. The protein content was then determined calorimetrically according to the method of Yoshida *et al.* (1972) using bovine serum albumin (BSA) as standard.

The mean value of the genotypes in each replication was subjected to the analysis of variance [3].

$$\text{Genotypic variance } (\sigma^2g) = \frac{M_g - M_e}{r}$$

$$\text{Phenotypic variance } (\sigma^2p) = \sigma^2g + \sigma^2e$$

Where,

$$\text{Environmental variance} = \sigma^2e$$

M_g = Mean sum of squares due to genotypes

M_e = Mean sum of squares due to error

The mean sum of squares at 'error' was taken as environmental variances (σ^2e).

The genotypic and phenotypic variance and coefficient of variance were computed based on the expected mean sum of squares from Analysis of Variance (ANOVA).

The co-efficient of variation was worked out by the formula of Burton [4].

$$\text{PCV } (\%) = \frac{(\text{Phenotypic variance})^{1/2}}{\text{General mean } (\bar{x})} \times 100$$

$$\text{GCV } (\%) = \frac{(\text{Genotypic variance})^{1/2}}{\text{General mean } (\bar{x})} \times 100$$

The phenotypic and genotypic coefficient of variation were classified into

High → above 20 per cent
 Moderate → 10 - 20 per cent and
 Low → below 10 per cent

Heritability in broad sense was computed for each character using the formula of Lush [5].

Heritability,

$$h^2 \text{ (BS)} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Where BS = Broad sense

Robinson [6] classified broad sense heritability as

High → above 60 per cent
 Moderate → 30-60 per cent
 Low → below 30 per cent

The extent of genetic advance to be expected by selecting certain proportion of the superior progeny was calculated using the following formula [7].

$$\text{Genetic Advance (GA)} = h^2 \times \sigma_{ph} \times K$$

Where,

h^2 = heritability in broad sense

σ_{ph} = phenotypic standard deviation

K- Selection differential at 5% selection intensity (K = 2.06)

The estimates of inter component correlation was calculated as per the methods suggested by Goulden [8].

$$r_{1,2} = \frac{\text{Sum of Products of 1 and 2}}{(\text{Sum of squares of 1} \times \text{Sum of squares of 2})^{1/2}}$$

Where,

r = Correlation co-efficient

1 and 2 = Characters 1 and 2 respectively.

genotypes, high significant differences for all characters were found in analysis of variance indicating the presence of sufficient variability among different genotype Maximum coefficient of variation was observed for plant height (2.54) followed by number of pods per plant (0.86) and single plant yield (0.55). Under present study, the CV indicated that there were significant differences not only among the genotypes but also across the environments for observed morphological characters. Rao [9], Bharti [10], Mehndi [11] and Sunayana [12] also observed a wide spectrum of variation for yield and yield components in mungbean. Contrarily, Dhananjay [13], reported less genetic variability for pods per cluster, seeds per pod, days to 50% flowering, pods per plant. Similarly, Aziz [14] observed that primary and secondary branches, pods per cluster and pod length showed lesser variability while 100-seed weight exhibited intermediate range of variability and sufficient genetic variability was observed for plant height, pods per plant, total plant weight and seed yield.

Table 1
Grand mean mean sum of square and coefficient of variation for 10 quantitative traits of 20 mungbean genotypes

Character	Grand Mean	MSS	CV (%)
Plant height (cm)	47.55	9.03*	2.54
Number of branches per plant	3.46	1.51**	0.40
Number of clusters per plant	5.19	3.45**	0.29
Number of pods per cluster	4.60	2.32**	0.52
Number of pods per plant	10.67	15.22**	0.86
Number of seeds per pod	8.37	5.87**	0.42
Pod length (cm)	8.36	5.29**	0.18
100 seed weight	3.77	3.14**	0.14
Single plant yield (g)	8.22	9.28**	0.55

RESULTS AND DISCUSSION

The mean sums of squares of nine quantitative traits are presented in table 1. Among the 20 mungbean

The analysis for variation for quantitative characters showed highly significant differences

among them (Table 1). The fat content ranged from 0.93 (WGG 48) to 3.63 (VRMGG 1). Among the genotypes, eight genotypes higher fat content compared to the general mean fat. The fibre, PLM 696 had the least fibre of 1.79 and the genotype GPLM 163 had the maximum fibre of 3.33. Eight genotypes had higher fibre than the fibre mean of 2.55. The ash varied from 3.82 (VBN1) to 5.80 (VGG 7). The mean ash value was 4.39 and only three genotypes excelled it. The protein ranged from 24.89 (VBN 1) to 28.31 (PLM 696). Eleven genotypes showed higher protein when compared to mean protein of 27.06. For carbohydrate content, it ranged from 61.05 (WGG 48) to 64.83 (VRMGG 1) and

eight genotypes exceeded the general mean of 62.66. (Table 2).

Genotypic coefficient of variation (GCV) for qualitative characters ranged from 2.28 % (Carbohydrates) to 29.86 % (Fat). The PVC ranged from 2.46 % (Carbohydrates) to 32.03 % (Fat). Higher magnitude of GCV and PCV was recorded only for Fat; Moderate levels for fibre and low levels for ash, protein and carbohydrate. All characters show maximum heritability in 40 genotypes (table 3). The estimates of heritability (%) in broad sense ranged from 93% to 96%. Maximum heritability was recorded for characters i.e., fibre and protein (96%) followed by ash (94%). Whereas, the minimum

Table 2
Mean values of qualitative traits in 20 genotypes

<i>Sl. No.</i>	<i>Genotype</i>	<i>Fat</i>	<i>Fibre</i>	<i>Ash</i>	<i>Protein</i>	<i>Carbohydrate</i>
1.	VGG 4	1.52	3.11	4.02	26.83	64.52**
2.	GPLM 163	1.55	3.33	4.33	26.58	64.21**
3.	EC 16708	3.02**	2.15	3.85	25.40	61.56
4.	VRMGG Local	3.31**	2.27	4.29	28.30**	64.58**
5.	PDM 89-226	2.12	2.87	4.46	28.06**	62.49
6.	WGG 42	3.51**	3.11	4.02	26.83	61.47
7.	VBN 1	3.02**	2.15	3.82	25.46	64.23**
8.	PLM 696	1.55	1.79	4.04	28.31**	63.15**
9.	CO 4	1.85	3.02**	4.33	27.57**	63.23**
10.	CDM Local	1.34	2.16	4.24	27.62**	62.26
11.	LGG 450	2.12	2.87*	4.46	28.06**	62.08
12.	WGG 17	1.61	2.07	4.02	27.77**	62.46
13.	VRMGG 1	3.63**	2.33	4.06	25.15	64.83**
14.	EC 314292	3.31**	2.27	4.29	28.30**	61.38
15.	WGG 48	0.93	2.65	4.34	27.07	61.05
16.	GPLM 139	2.71**	3.07**	5.72**	27.42**	61.08
17.	EC 30072	1.61	2.07	4.06	27.77**	62.14
18.	ADT 3	2.28	3.08**	4.26	24.89	62.15
19.	VGG 7	2.50	2.07	5.80**	27.69**	61.08
20.	KM 2	2.71**	2.59	5.34**	26.08	63.28**
	Mean	2.38	2.55	4.39	27.06	62.66
	CD (P = 0.05)	0.16	0.25	0.18	0.21	0.28

heritability (%) was recorded for fat and carbohydrate (93 %). The genetic advance (as percent per mean) varied from 4.65 % (Carbohydrate) to 61.17 % for fat. In the present study, the fat and fibre had high heritability (> 90 %) coupled with high PCV and GCV (>15 %) validates that these characters are greatly influenced not only by the additive gene effect but also greater proportion of variation is heritable for these qualitative traits (Table 3). Similar findings were also reported by Marappa [15], Narasimhulu [16] and Sunayana [12] in mungbean for many of these traits. Low values of PCV and GCV were observed for Days to first flowering, Days to first pod, Flower retention, Number of seeds per pod

and photochemical efficiency. Khedar [17] also observed low values of PCV and GCV for days to maturity, days to 50 per cent flowering, seeds per pod. Genotypic coefficient of variation measures the amount of variation present in a particular character. However, it does not determine the proportion of heritable variation present in the total variation. Therefore, heritable variation existing in the character can be find out with greater degree of accuracy with heritability in combination with genetic advance. Parameswarappa [18] indicating that mungbean seed yield expressed high genetic advance coupled with high heritability and genotypic coefficient of variation.

Table 3
GCV, PCV, heritability, genetic advance and mean sum of square for qualitative traits

<i>Source of variation</i>	<i>GCV</i>	<i>PCV</i>	<i>h²</i>	<i>GA</i>	<i>MSS</i>
Fat	29.86	32.03	93	61.17	1.33**
Fibre	15.65	16.32	96	31.12	0.62**
Ash	9.27	9.82	94	18.46	0.55**
Protein	4.46	4.64	96	9.01	4.95**
Carbohydrate	2.28	2.46	93	4.65	7.18**

** Significant at 0.1% level of significance, MSS= mean sum of square

Based on the interrelationships of the quality characters on the quantitative characters, it was noted that the fat content was significantly and negatively correlated with plant height, number of branches, number of clusters per plant and number of pod per plant. This suggested that the fat is not related to quantitative characters except for 100 seed weight and single plant yield. The fibre content was negatively associated with number of pods per plant and number of seed per pod whereas, highly positively associated with plant height, number of branches per plant, number of clusters per plant and number of pods per cluster. Similar views have been reported by Srivastava [19], Dhananjay [13], Narasimhulu [15] and Reni [20]. High variation among lentil genotypes for crude fibre in test cultivars

have also been reported by Karadavut and Genç [21], Anjam [22]. The ash content and protein content were in negative association for majority of the quantitative characters.

No correlation between seed yield and protein content was observed in mungbean suggesting that there is possibility of selection for increased protein content without detrimental effect on seed yield [23]. Our results agreed with Fossati [24] who also reported negative correlation of protein with that of yield in wheat. Carbohydrate was significantly positive for all the quantitative characters except for plant height and number of branches per plant (Table 4). Ali [25] also reported positive and highly significant genotypic correlation of carbohydrate with seed yield plant-1. The present study suggests

Table 4
Association between quantitative and qualitative traits in mungbean

	Plant height	Number of branches per plant	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Number of seeds per pod	Pod length	100 seed weight	Single plant yield	Fat	Fibre	Ash	Protein	Carbohydrate
Plant height	1.00													
Number of branches per plant	0.56	1.00												
Number of clusters per plant	0.43	0.39	1.00											
Number of pods per cluster	0.06	0.19	0.13	1.00										
Number of pods per plant	0.09	0.10	0.21	0.42	1.00									
Number of seeds per pod	0.07	0.10	0.25	0.48	0.44	1.00								
Pod length	0.16	0.18	0.32	0.29	0.17	0.33	1.00							
100 seed weight	0.26	0.36	-0.25	0.35	-0.30	-0.30	-0.26	1.00						
Single plant yield	0.33	0.26	-0.14	0.55	0.35	0.17	0.26	0.42	1.00					
Fat	0.27**	-0.19**	-0.24**	-0.59**	-0.17**	0.14	0.25	0.15*	0.27*	1.00				
Fibre	0.23**	0.32**	0.21**	0.17*	-0.05	-0.06	0.30**	0.21*	0.35**	-0.15	1.00			
Ash	-0.26**	-0.38**	-0.30**	-0.14	-0.21*	-0.06	0.20*	0.08	0.06	0.05	-0.15	1.00		
Protein	-0.30**	0.29**	-0.14	-0.32**	-0.23*	-0.26*	-0.19	-0.25*	-0.32**	-0.08	0.02	0.05	1.00	
Carbohydrate	-0.33**	-0.19*	0.26*	0.31**	0.30**	0.26**	0.24*	0.19	0.28*	-0.12	-0.05	-0.02	-1.34	1.00

that the mungbean genotypes with high protein contents are not essentially high seed yielding. Whereas, carbohydrate contents being directly proportional to seed yield can serve as an excellent marker for large scale screening of high yielding mungbean genotypes.

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