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ASSESSMENT OF GENETIC VARIABILITY AND CHARACTER ASSOCIATION FOR YIELD CONTRIBUTING TRAITS IN MUNGBEAN (*Vigna radiata* L.)

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Abstract

The study was conducted to evaluate the genetic variability and correlation between several yield contributing features in mungbean (*Vigna radiata* L.). Fourteen mungbean varieties from different Institutes, were evaluated with nine quantitative traits during the Kharif I season from March to June, 2020 at the Sher-e-Bangla Agricultural University's research farm. The analysis of variance showed significant variation among all the varieties in all the traits studied. The phenotypic variances were greater than the genotypic variances. The Phenotypic coefficient of variance and genotypic coefficient of variance were higher for the no. of branches /plant (19.671; 18.309) followed by weight. of 1000 seed (g) (25.339; 25.254) and yield/plant (g) (31.296; 31.049) respectively. High heritability coupled with high genetic advance as a percent of mean was observed for plant height (cm) (96.073; 21.421), followed by no. of leaves/plant (95.977 ; 31.950), no. of branches /plant (86.636 ; 35.107), no. of pods/plant (99.335; 55.623), pods length/plant (cm) (98.389 ; 29.455), no. of seeds/pod (92.371 ;33.375), weight of 1000 seed (g) (99.331; 51.848) and yield/plant (g) (98.427 ; 63.456), respectively which indicated the effect of additive genes effect. In the correlation co-efficient analysis yield/plant had significant positive relation at both the genotypic and phenotypic level with the number of leaves/plants followed by number of branches/plants, number of pods/plants, number of pods cluster/plant, pods length/plant (cm), number of seeds/pod and weight. of 1000 seed (g) which indicates this character can be considered for future improvement program of mungbean. Path analysis revealed that number of seeds/pod (0.689), number of leaves/plant (0.338), number of branches/plant (0.196), number of pods/plant (0.435) and weight of 1000 seed (g) (0.016) showed positive direct effect on yield/plant. These results suggest that the direct selection of these characters will facilitate the chance of simultaneous improvement of other traits in mungbean. Evaluating the performance among the studied varieties, BINA mung5 and BINA mung8 considered the elite variety.

Keywords: Correlation, Genetic advance, Heritability, Mungbean, Path coefficient.

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Introduction

In Bangladesh mungbean is one of the most important pulse crops because of its easy digestibility and high protein percentage (Azam *et al*. 2018). It is mainly grown for its high protein and consumed as 'Mungdal' along with cereals in South Asian countries also consider it as a vital ingredient for the human diet. Its seeds are also consumed as sprouts in many countries (Singh *et al*. 2014). Dry seeds contain 27% protein (Day, 2013). Mungbean is a very good source of protein, amino acids, carbohydrates, antioxidants and fibers (Bangar *et al*. 2018). One cup of (202 g) boiled mungbean contain 212 calories, 14.2 g of protein, 38.7 g of carbohydrate, 15.4 g of fiber, 0.8 g of fat. It also contains manganese, magnesium, vitamin B1, phosphorus, zinc, vitamin B2, B3, B5, B6 and selenium (Hrubsa *et al*., 2022)

In Bangladesh, the total production is 42000 million tons on 114000 acres of land (BBS, 2022). Singh *et al*. (2014) stated that mungbean production (90%) is mainly located in Asia. Over the last three decades, the global mungbean consumption has increased by 60% with a corresponding growth in production area up to 6 million hectares, concentrated mainly in South, East, and Southeast Asia (Kim *et al.*, 2015).Although mungbean is a nutritious crop, overall production is low due to abiotic and biotic stresses, a low level of crop management by farmers and the shortage of suitable varieties for varying geographical conditions (Singh *et al*. 2015). The present yield is not high enough to meet the demand of consumers and farmers because of its low yield potential, small seed size and susceptibility to disease (Srivastava & Singh, 2013).

A critical survey of genetic variability is necessary before initiating an improvement program aiming to develop high yielding varieties of mungbean. The correlation co-efficient between yield components usually show a complex chain of interacting relationships. Path coefficient analysis split the components of the correlation coefficient into direct and indirect effects and visualizes the relationship in a more meaningful way. Considering these above problems and prospects the following objectives were considered; To estimate the nature and magnitude of genetic variations among the mungbean varieties in respect of different yield and yield contributing characters;To estimate the extent of correlation between pairs of characters at genotypic and phenotypic level; and assess the direct and indirect effect of different characters on yield of mungbean.

Materials and Methods

The present study was performed with 14 varieties of mungbean. The varieties were collected from The Pulse Research Centre of Bangladesh Agricultural Research Institute (BARI), Gazipur, BSMRAU, BINA, Lalmonirhat and Barisal. The name and source of studied varieties are presented in Table 1.

Table 1. Sources of 14 (fourteen) varieties of mungbean

Serial number	Variety name	Source
1	BARI mung1	Pulse Research Centre, BARI
2	BARI mung2	Pulse Research Centre, BARI
3	BARI mung3	Pulse Research Centre, BARI
4	BARI mung4	Pulse Research Centre, BARI
5	BARI mung5	Pulse Research Centre, BARI
6	BARI mung6	Pulse Research Centre, BARI
7	BARI mung7	Pulse Research Centre, BARI
8	BARI mung8	Pulse Research Centre, BARI
9	BU mung1	Department of Agronomy, BSMRAU
10	BINA mung5	Plant Breeding Division, BINA
11	BINA mung8	Plant Breeding Division, BINA
12	BINA mung9	Plant Breeding Division, BINA
13	Chaitamung	Lalmonirhat
14	Sonamung	Barishal

Experimental design

The experiment was laid out in randomized complete block design (RCBD) with three replications. Then it was sub-divided into three blocks where 14 varieties were randomly assigned. The plot size was 2.5m with single line. Row to row distance was 30 cm and plant to plant distance was 10 cm. All the recommended agronomic package of practices was followed (thinning, fertilizer application, irrigation, weeding etc.), as recommended for commercial mungbean production according to BARI.

Data recording and analysis

Ten random plants were selected and recorded based on nine yield contributing characters, viz. plant height, number of leaves/plants, number of branches/plants, number of pods/plants, number of pod clusters/plant, pod length, number of seeds/pods, weight of 1000 seed (g). The analysis of variance for different characters was done by using mean data in order to determine the genetic variability among the varieties as given by Cochran and Cox (1957). The level of significance was tested at 5% and 1% using the F test. Estimation of genotypic and phenotypic variance, heritability, and genetic advance in percent of mean were done according to Comstock and Robinson (1952). Genotypic and phenotypic correlation co-efficient was estimated by the formula given by Singh and Chaudhary (1985). Path coefficient was done by the procedure suggested by Dewey and Lu (1959) using phenotypic correlation coefficient values. For statistical analysis statistix 10 software was used.

Results and Discussion

Mean performance

Analysis of variance showed highly significant differences among varieties for all the traits considered. The LSD test also showed that almost all the varieties were significantly different from each other for all the traits studied (Table 2) The mean performance of fourteen varieties is presented in Table-2. The variety BINA mung5 showed the heights mean performance in number of leaves/plant (13.660), number of pod clusters/plant (7.033), number of seeds/pod (13.667) and yield/plant (g) (6.06). BARI mung7 showed maximum performance for the number of branches/plant (3.773) and yield/plant (5.25) whereas Chaitamung performed the lowest (2.440; 2.22). BARI mung6 performed the highest value in case of pod length (10.567) and weight of 1000 seed (51.667) (Table 2) respectively. So, for selection of the elite variety these characters should give more emphasize.

Table 2. Mean performance of nine characters of 14 (fourteen) varieties of mungbean

varieties	Plant height (cm)	Number of leaves/plants	Number of branches /plants	Number of pods	Number of pods cluster/plant	Pod length(cm)	Number of seeds/pods	Weight of 1000 seed (g)	Yield/plant (g)
BARI mung1	49.300 c	7.553 j	2.777 fg	8.567 g	4.667 d	7.300 f	8.667 hi	27.66f	2.62 h
BARI mung2	48.833 c	8.440 i	2.553 g	8.767 g	5.133 cd	7.367 f	8.333 i	27.333 f	2.52 hi
BARI mung3	53.967 b	10.440 g	3.440 cde	12.913 d	5.600 bcd	8.633 de	9.667 fg	28.333 f	3.84 g
BARI mung4	56.233 a	11.667 ef	3.550 cd	10.303 f	5.533 bcd	8.867 d	10.333 ef	31.000 d	3.94 fg
BARI mung5	45.300 d	12.440 cd	2.660 g	11.417 e	5.333 bcd	10.333 a	11.333 d	40.333 c	4.14 ef
BARI mung6	44.033 de	13.220 ab	3.773 bc	18.327 a	5.667 bcd	10.567 a	12.333 bc	51.667 a	4.85 d
BARI mung7	42.943 ef	12.997 bc	3.773 bc	18.330 a	5.767 bcd	10.333 a	9.333 gh	50.000 b	5.25 c
BARI mung8	41.383 fg	9.773 h	3.440 cde	18.527 a	5.833 bc	8.433 e	10.333 ef	31.667 d	4.95 d
BU mung1	42.403 efg	10.773 g	3.220 de	11.310 e	4.667 d	9.433 bc	11.000 de	29.667 e	4.34 e
BINA mung5	49.187 c	13.660 a	4.110 ab	11.407 e	7.033 a	9.700 b	13.667 a	39.333 c	6.06 a
BINA mung8	41.233 g	12.220 de	4.440 a	15.813 b	5.333 bcd	9.300 c	13.000 ab	30.667 de	6.06 a
BINA mung9	45.257 d	12.333 d	3.107 ef	14.000 c	6.300 ab	8.400 e	11.667 cd	31.000 d	5.55 b
Chaitamung	40.927 g	10.440 g	2.440 g	10.360 f	5.633 bcd	6.467 g	8.333 i	26.000 g	2.22 j
Sonamung	41.703 fg	11.440 f	2.660 g	11.000 e	5.667 bcd	7.567 f	8.333 i	25.667 g	2.32 ij
$lsd_{0.05}$	1.653	0.612	0.396	0.481	1.145	0.271	0.850	1.169	0.29
Mean	45.907	11.243	3.282	12.931	5.583	8.764	10.452	33.595	4.19
Std Error	0.804	0.2976	0.1927	0.2341	0.5572	0.132	0.4134	0.5688	0.14
Stdv	4.852	1.773	0.632	3.429	0.824	1.243	1.797	8.302	1.32
Minimum	40.927	7.553	2.44	8.567	4.6667	6.467	8.333	25.667	2.22
Maximum	56.233	13.66	4.44	18.527	7.0333	10.567	13.667	51.667	6.06

Coefficients of genotypic and phenotypic variations

In this study phenotypic coefficient of variance (PCV) appeared to be higher than the genotypic coefficient of variance (GCV) in case of all the traits viz. plant height, number of leaves/plant, number of branches/plant, number of pod, number of pods cluster/plant, pod length (cm), number of seeds/pod, weight of 1000 seed (g) ,yield/plant

(g) which suggested negligible influence of environment on the expression of genes controlling these traits (Table 3). High magnitude of PCV and GCV were found in number of branches/plant (PCV: GCV= 19.671:18.309;), number of pods/plant (27.182: 27.092), number of seeds/pod (17.540: 16.857), Yield/plant (32.48: 32.22), weight of 1000 seed (25.339: 25.254) (Table 3). The result signifies that selection can be applied for these characters will be more helpful to develop elite variety. Makeen *et al* (2007), Rao *et al*. (2006), Pandey *et al.* (2002) also studied about genotypic and phenotypic coefficient of variations in mungbean.

Table 3. Genetic parameters for nine yield and yield contributing characters of mungbean

Serial number	Characters	Phenotypic variance (δ^2_p)	Genotypic variance(δ^2_g)	PCV	GCV	Heritability (h^2b)	GA	GA (%)
1	Plant height (cm)	24.690	23.720	10.824	10.609	96.073	9.834	21.421
2	Number of leaves/plants	3.301	3.168	16.160	15.831	95.977	3.592	31.950
3	Number of branches/plants	0.417	0.361	19.671	18.309	86.636	1.152	35.107
4	Number of pods	12.355	12.273	27.182	27.092	99.335	7.193	55.623
5	Number of pods cluster/plant	0.675	0.209	14.716	8.194	31.007	0.525	9.400
6	Pod length (cm)	1.622	1.596	14.533	14.415	98.389	2.582	29.455
7	Number of seeds/pods	3.361	3.104	17.540	16.857	92.371	3.488	33.375
8	Weight of 1000 seed (g)	72.463	71.978	25.339	25.254	99.331	17.418	51.848
9	Yield/plant (g)	1.85	1.82	32.48	32.22	98.427	2.76	65.85

GCV= Genotypic co-efficient of variation, PCV= Phenotypic coefficient of variation,

GA= Genetic advance, GA (%) = Genetic advance in percent of mean,

δ^2_g= Genotypic variance, δ^2_p= Phenotypic variance

Heritability and genetic advance

The high heritability was found in plant height (96.073), number of leaves/plant (95.977), number of branches/plant (86.636), number of pod (99.335), pod length (98.389), number of seeds/pod (92.371), weight of 1000 seed (99.331) and yield/plant (98.427) in Table 3. The assessment of heritability alone fails to indicate the response to selection (Shompa *et al.*, 2020). Therefore, estimation of heritability will be more efficient when it coexists with estimation of genetic advance and the genetic advance as percent of the mean. High heritability combined with high genetic advance is a good index of genotype selection. Here, selection based on the number of branches/plants, number of pods, number of seeds/pods, weight of 1000 seeds (g) and yield/plant (g) will be effective. High heritability and genetic advance in percent of mean were estimated in 1000-seed weight by Sandhu *et al.* (1979). In case of yield/plant, high heritability estimates coupled with high genetic advance were observed by Rao *et al* (2006), Rohman *et al.* (2003) and Sharma *et al.* (1999). However, genetic advance for the trait number of pod clusters/plant is low that means it revealed non-additive gene action and low heritability. So selection of varieties considering this trait may not be impactful because the trait exhibits low heritability, indicating heavy influenced by the environmental factors as well as non-additive gene action also complicates the selection efforts (Azam *et al*., 2018).

Genotypic and phenotypic correlations

The phenotypic and genotypic correlation indicates the degree of association between different characters, which is helpful for selection. In the majority of cases the genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients which indicating strong inherent association between the characters. However, genetic correlation can result from either pleiotropy or linkage or by Falconer, 1996, while phenotypic correlation is a non-additive combination of both genetic and environmental correlations.

In the present investigation the results showed that the number of leaves/plant showed a highly significant positive correlation with number of branches /plant (0.595 and 0.543), number of pods/plant (0.488 and 0.476), number of pods clusters/plant (0.843 and 0.453), pod length (cm) (0.746 and 0.727), number of seeds/pod (0.704 and 0.663), weight of 1000 seed (0.676 and 0.657) and yield/plant (0.697 and 0.662) (Table 4) at both the genotypic and phenotypic levels. These findings were supported by Govindraj (2001), Parameswarappa (2005) reported the grain yield/plant was showed a highly significant positive correlation with plant height, number of branches/plant, number of pods, number of seeds/pod. The number of branches/plant showed a highly significant positive correlation with the number of pods/plant (0.627 and 0.567), pod length/plant (0.655 and 0.612), number of seeds/pod (0.761 and 0.699), weight of 1000 seed (0.481 and 0.445) and yield/plant (0.872 and 0.799). These findings were supported by Gouda (1977), Govindraj (2001), Parameswarappa (2005) reported the grain yield/plant was showed highly significant positive correlation with number of branches/plant, number of pod, number of seed/pod.The number of pods showed highly significant positive correlation with pod length (0.569 and 0.564), number of seeds/pod (0.394 and 0.372), weight of 1000 seed (0.634 and 0.631) and yield/plant (g) (0.658 and 0.653). Makeen *et al*. (2007) evaluated correlations in respect of various desirable characters in 20 genotypes of mungbean and indicated that pods/plant had significantly positive correlation with seed yield.

Table 4. Genotypic (rg) and phenotypic (rp) correlation co-efficient among different pairs of yield and yield contributing characters for 14 varieties of mungbean

Characters		Plant height (cm)	Numberof leaves/plant	Number of branches /plant	Number of pod	Number of pods cluster/plant	Pod length (cm)	Number of seeds/pod	Weight of 1000 seed (g)
Number of leaves/plant	r_g	-0.163^{NS}							
	r_p	-0.156^{NS}							
Number of branches /plant	r_g	0.045^{NS}	0.595**						
	r_p	0.056^{NS}	0.543**						
No of pod	r_g	-0.438**	0.488**	0.627**					
	r_p	-0.431**	0.476**	0.567**					
Number of pods cluster/plant	r_g	0.047^{NS}	0.843**	0.523**	0.382*				
	r_p	0.038^{NS}	0.453**	0.265^{NS}	0.235^{NS}				
Pod length (cm)	r_g	-0.021^{NS}	0.746**	0.655**	0.569**	0.260^{NS}			
	r_p	-0.018^{NS}	0.727**	0.612**	0.564**	0.167^{NS}			
No of seeds/pod	r_g	-0.049^{NS}	0.704**	0.761**	0.394**	0.586**	0.709**		
	r_p	-0.026^{NS}	0.663**	0.699**	0.372*	0.353*	0.668**		
Weight of 1000 seed (g)	r_g	-0.123^{NS}	0.676**	0.481**	0.634**	0.400**	0.835**	0.457**	
	r_p	-0.121^{NS}	0.657**	0.445**	0.631**	0.228^{NS}	0.827**	0.436**	
Yield/plant (g)	r_g	-0.116^{NS}	0.697**	0.872**	0.658**	0.656**	0.736**	0.878**	0.541**
	r_p	-0.108^{NS}	0.662**	0.799**	0.653**	0.405**	0.722**	0.843**	0.537**

* and ** indicate significant at 5% and 1% level of probability and NSindicates non-significant respectability. r_g= genotypic correlation co- efficient, r_p= phenotypic correlation co-efficient

The number of pods cluster/plant showed highly significant positive correlation with Number of seeds/pod (0.586 and 0.353) and yield/plant (g) (0.656 and 0.405) (Table 4) at both genotypic and phenotypic level. Pod length showed a highly significant positive correlation with number of seeds/pod (0.709 and 0.668), weight of 1000 seed (0.835 and 0.827) and yield/plant (0.736 and 0.722) at both genotypic and phenotypic level. The number of seeds/pods showed a highly significant positive correlation with weight of 1000 seed (0.457 and 0.436) and yield/plant (0.878 and 0.843) at both genotypic and phenotypic level. Thousand seed weight showed significant positive correlation with yield/plant (0.541 and 0.537) at both genotypic and phenotypic level. A higher number of pods per plant with longer pod and seed size and diameter directly contributed towards the seed yield. Moreover, high correlation of 100-seed weight and with seed yield also obtained in mungbean mentioned by Anwari and Sochandi (1999); Makeen *et al.* (2007); Tabassum *et al* .(2010). For selection of the best variety the component characters viz. number of pods clusters/plant, number of seeds/pods, weight of 1000 seed are very important.

Path coefficient analysis

In order to find out a clear picture of the interrelationship between yield/plant and other yield attributes, path analysis was done. Direct and indirect effects were worked out using path analysis at the genotypic level which also measured the relative importance of each component. From the present study it was clear that the number of branches/plants showed positive indirect effect on yield/plant via number of seeds/pod (0.524), number of pod (0.273), number of leaves/plant (0.201), weight of 1000 seed (0.008) and plant height (cm) (0.007) (Table 5). Kritika and Yadav (2017) revealed that, path co-efficient analysis indicated number of pods/plants, number of seeds/pods, biological yield/plot and harvest index had the maximum direct contribution to seed yield and these characters should be given importance while formulating selection criteria for seed yield. Plant height (0.160) and number of branches /plant (0.338) were recorded as having a high positive indirect effect on seed yield via number of pods/plants. The number of pods showed a positive direct effect (0.435) on yield/plant via number of leaves/plant (0.165), number of branches /plant (0.123), number of seeds/pod (0.271) and weight of 1000 seed (0.010). Alom *et al.* (2014) showed that pods/plant contributed the maximum positive direct effects on seed yield. Plant height, pod length and 1000 seed weight had also positive direct effect on seed yield. Thus, selection based on pods/plant, days to first flowering, plant height and 1000 seed weight might be effective for improving seed yield in mungbean. Garje *et al.* (2014) reported that number of pod/plants had the maximum direct effect on seed yield followed by number of cluster/plant and Number of secondary branches/plant. The number of seeds/pods showed positive direct effect (0.689) on yield/plant. Path analysis revealed that number of pod/ plant and 100-seed weight exerted a high magnitude of positive direct effect on seed yield. These results were corroborating with the findings of Rohman *et al*. (2003) and Makeen *et al. (*2007). Weight of 1000 seed showed a positive direct effect (0.016) on yield/plant. Path analysis revealed that number of 1000-seed weight exerted a high magnitude of positive direct effect on seed yield. These results were corroborating with the findings of Rohman *et al*. (2003) and Makeen *et al. (*2007). The residual effect (R) of path co-efficient analysis was noted as 0.10 which indicated that there were also some other characters which although not studied in the present investigation but have an impact on the yield per plant.

Table 5. Path analysis showing direct and indirect effects of different characters on fruit yield of 14 mungbean varieties

Trait	Plant height	Number of leaves/plant	Number of branches /plant	Number of pods/plant	Number of pods cluster/plant	Pod length	Number of seeds/pod	Weight of 1000 seed	Genotypic correlation with yield/plant
Plant height (cm)	0.160	-0.055	0.009	-0.190	-0.011	0.007	-0.034	-0.002	-0.116^{NS}
Number of leaves/plant	-0.026	0.338	0.116	0.212	-0.193	-0.247	0.485	0.011	0.697**
Number of branches /plant	0.007	0.201	0.196	0.273	-0.120	-0.217	0.524	0.008	0.872**
Number of pod	-0.070	0.165	0.123	0.435	-0.088	-0.188	0.271	0.010	0.658**
Number of pods cluster/plant	0.008	0.285	0.102	0.166	-0.229	-0.086	0.403	0.006	0.656**
Pod length (cm)	-0.003	0.252	0.128	0.248	-0.060	-0.331	0.488	0.013	0.736**
Number of seeds/pod	-0.008	0.238	0.149	0.171	-0.134	-0.235	0.689	0.007	0.878**
Weight of 1000 seed (g)	-0.020	0.229	0.094	0.276	-0.092	-0.276	0.314	0.016	0.541**

Conclusion

The variation is present among the varieties. The variety BINA mung5 and BINA mung8 could be selected for the number of leaves/plants, number of branches /plants, number of pods cluster/plant, number of seeds/pod and yield/plant as they have strong positive correlation on yield. For future hybridization program, the traits, number of branches /plants, number of pods cluster/plant, number of seeds/pods, weight of 1000 seed (g) will be a good selection index for future breeding program of mungbean.

Author's contribution

Sharmin, S. designed, planned, and executed the experiment and drafted the manuscript; Shompa, B.N. and Parveen, S. edited and reviewed the manuscript; Siddikee, M.A. supervised the experiment, analyzed the data, and edited and reviewed the manuscript.

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