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Full Length Research Paper

Contribution of morpho-physiological attributes in determining the yield of mungbean

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Field experiments were conducted in 2006 and 2007 under subtropical conditions to investigate the variations in growth and reproductive characters, and yield attributes for selection of important source and sinks characters using correlation and path coefficient analyses in 45 mungbean genotypes. Large genetic variability existed in source characters viz., leaf area index (LAI) (1.22 to 3.80) and sink characters viz., number of racemes plant^{-1} (6.30 to 22.9), flowers plant^{-1} (18.1 to 51.9) and pods plant^{-1} (9.6 to 22.1). Genotypic correlation study revealed that among the traits investigated, LAI was the most important source that determined total dry mass (TDM) yield, and reproductive characters like number of racemes, flowers and pods plant^{-1} were the most important sinks that determined seed yield. Contrarily, reproductive efficiency (RE, % pod set to opened flowers) did not show significant relationship with pod number and seed yield, indicating that selection of high yield based on RE may be misleading. Path coefficient analysis further revealed that number of flowers, pods and 100-seed weight constituted central important sinks which exerted direct positive influence on seed yield. The results indicated that pod yield could be increased by increased raceme and flower production, while seed yield could be increased by increasing pod production. High yielding genotypes, in general, possessed higher earlier mentioned source (LAI) and sink (flower and pod number) characters which resulted in higher seed yield in mungbean. This information could be exploited in the future plant breeding programmes.

Key words: Source-sink, correlation, path analysis, mungbean.

INTRODUCTION

The pod number, seeds pod^{-1} and seed size are the key yield attributes. These attributes in turn depend on raceme and flower numbers, leaf area and total dry mass (TDM) production of a legume plant (Mondal, 2007). Moreover, TDM production depends on the photosynthetic area. Increasing canopy photosynthesis through increase in leaf area during reproductive stage increased TDM and number of fruits (Hamid et al., 1989). It is evident that pod number and seeds pod^{-1} were highly and positively correlated with leaf area and TDM (Ahmed et al., 1993; Hossain et al., 2002; Mondal et al., 2004). Contrarily, reproductive efficiency (% pod set to opened

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Abbreviations: LA, Leaf area; **LAI**, leaf area index; **TDM**, total dry mass; **RE**, reproductive efficiency; **HI**, harvest index.

flowers) and seed size did not show strong relations with pod number and seed yield in legume (Saitoh et al., 2004; Hakim, 2008; Mondal et al., 2009). Efficient plants tend to attain optimum leaf area index (LAI) to maximize light interception. It is suggested that high partitioning efficiency (harvest index) would be advantageous for high yield. Hamid et al. (1989) suggested that the relationship between flower production and podset in mungbean is related to source (LA) and that increased seed yield could be achieved by increasing the source capacity.

On the other hand, component characters for yield are interdependent on each other, while one character may express at the expense of other (Hossain et al., 2002). The importance of correlation study both at genotypic and phenotypic levels in any breeding programme is well documented for various crop species as it provides a basis for effective selection of characters contribution to yield. Path-coefficient analysis further permits the partitioning of correlation coefficient into components of direct and indirect contribution of different contributing characters towards yield (Singh et al., 2008). Therefore, correlations in combination with path co-efficient analysis could be an important index to assess actual association and quantify the direct and indirect influences of different characters (Sarwar et al., 2004, Singh et al., 2008). Some workers have reported on mungbean performance which mainly includes the contribution of various yield components towards yield (Reddy et al., 1991; Sarwar et al., 2004; Hakim, 2008; Singh et al., 2008). Information on identification of important source-sink characters and their correlation with yield is scanty in mungbean (Mondal, 2007). Findings on correlation of seed yield with pod number, pod and seed size are available (Mondal et al., 2004; Siddique et al., 2006; Hakim, 2008), but information on the relationships of pod yield with number of racemes and flower production is scanty in mungbean (Mondal, 2007). Furthermore, racemes and flowers are the important sinks and the key determinant of seed yield in mungbean (Mondal, 2007). The path analysis indicated that number of pods plant^{-1} and 100-seed mass had direct positive influence on seed yield in mungbean (Mondal et al., 2004; Siddique et al., 2006; Singh et al., 2008), but sinks like number of racemes and flowers needs to be investigated to know whether they exert any direct influence on pod and seed yield. Therefore, this study was initiated to investigate variations in some growth and reproductive characters, and yield attributes for selection of important sources and sinks based on correlation and path analysis of 45 mungbean genotypes in the growing seasons and locations [at Mymensingh (24°75´ N latitude and 90°50´ E longitude) and Pabna (24°15´ N latitude and 89°20´ E longitude), Bangladesh].

MATERIALS AND METHODS

Field experiments were conducted on 45 local and exotic genotypes (39 advance lines and 6 varieties) of mungbean at Bangladesh Agricultural University (BAU), Mymensingh (24°75´ N latitude and 90°50´ E longitude) and Bangladesh Institute of Nuclear Agriculture (BINA), Pabna (24°15´ N latitude and 89°20´ E longitude), Bangladesh during 2006 and 2007. The soil of the experimental area of BAU was silty loam, having total nitrogen of 0.06%, organic matter of 1.15%, available phosphorus of 18.5 ppm, exchangeable potassium of 0.28 meq/100 g, sulphur of 18 ppm and pH 6.8. The soil of BINA farm, Pabna was sandy loam, calcareous in nature with pH 7.8, having nitrogen of 0.10%, organic matter of 1.22%, available phosphorus of 12.1ppm, available sulphur of 16 ppm and exchangeable potassium of 0.33 meq/100 g. A randomized complete block design with three replications was followed in both locations. The unit plot size was 2 m x 1.8 m. Seeds were sown, maintaining a spacing of 30 x 10 cm on the 14th and 12th of March 2006 and 2007, respectively at Pabna and 17th and 16th of March 2006 and 2007, respectively at Mymensingh. Management practices were same in both the seasons and locations. Uniform plant stands (30 plants m^{-2}) were maintained in both seasons. Urea, triple superphosphate, muriate of potash and gypsum were used as sources of nitrogen, phosphorus, potassium and sulphur at the rate of 40, 120, 80 and 30 kg ha^{-1}, respectively at the time of final land preparation. First weeding was done followed by thinning at about 21 days after sowing (DAS). A single irrigation was given at 25 DAS at both locations. Insecticide (Ripcord 50 EC, 0.025%) was sprayed at flowering and fruiting stage (55 DAS) to control shoot and fruit borer. Data on growth and yield contributing characters such as TDM, number of raceme and pods, seeds pod^{-1}, single pod, 100-seed weight and seed yield were recorded on 45 randomly selected plants; 15 from each plot. Number of opened flowers plant^{-1} was recorded from 15 randomly selected pants; 5 from each plot. The opened flowers were counted daily. Leaf area index was measured by canopy analyzer (Model: LICOR 2000, USA) at 60 DAS (at pod growth stages). Plant sample was oven dried at 80°C ± 2 for 48 h. The total dry matter plant^{-1} was estimated by summing dry matter of leaves, stem, root and pods dry weight per plant. Harvest index was determined as: (grain yield plot^{-1} ÷ biological yield plot^{-1}) x 100. Percent podset to opened flowers was calculated as follows: % pod set = (number of pods plant^{-1} ÷ number of opened flowers plant^{-1}) x 100. Seed yield was computed on plot yield basis and converted into kilogram hectare^{-1}. The collected data were analyzed statistically following the analysis of variance technique and the mean differences were adjudged by Duncan's multiple range test using MSTAT-C. Phenotypic and genotypic correlations were estimated according to Johnson et al. (1955). Finally, path co-efficient analysis was performed following the method of Dewey and Lu (1959).

RESULTS

The effect of season, location and genotype and their interactions showed highly significant differences for growth, reproduction, yield and yield attributes with few exceptions (Table 1) which means significant differences existed between the genotype, location and season, while some genotypes performed better or worse over a particular location or season.

Growth characters

Mean performance of different growth characters as affected by genotype over locations and seasons is shown in Table 2. LAI varied between 1.22 and 3.89, and that of TDM plant^{-1} varied between 7.39 and 16.8 g. The

Table 1. Mean square of combined analysis of variance for growth, reproductive and yield attributes and yield of 45 mungbean genotypes in locations and years.

Source of variation	df	Growth character		Reproductive trait		
		TDM plant^{-1} (g)	Leaf area index†	Raceme plant^{-1} (number)	Flower plant^{-1} (number)	% Podset to open flower
Season (S)	1	2436.3**	2.692**	167.45**	23233**	1260.72**
Location (L)	1	42.163^{ns}	----	438.66**	3893.5**	4710.56**
Genotype (G)	44	46.502**	2.394**	198.73**	757.63**	180.89**
S × G	44	44.10**	1.264**	84.79**	284.04**	189.88**
L × G	44	7.770**	----	20.48**	231.39**	192.26**
S × L × G	44	8.760**	----	18.49**	254.88**	121.46**
Error	352	2.220	0.023	3.166	24.959	30.819

*, **, Indicates significant at 5 and 1% probability, respectively; †, Data collected only in one location for two seasons; ns, not significant.

Table 1. Contd.

Source of variation	df	Yield component				Partitioning and yield	
		Pod plant^{-1} (number)	Single pod weight (mg)	Seed pod^{-1} (number)	100-seed weight (g)	Harvest index (%)	Seed yield (kg ha^{-1})
Season (S)	1	4039.9**	24.726*	1.826**	1.077**	4345.1**	1192653**
Location (L)	1	893.5**	1116.3**	9.283^{ns}	0.185^{ns}	901.6**	3854.9^{ns}
Genotype (G)	44	114.1**	823.55**	1.920**	9.662**	91.09**	113137**
S × G	44	47.10 **	49.776**	0.738**	0.116**	88.28**	116467**
L × G	44	20.29**	33.890**	0.686**	0.097**	24.30**	28429.3**
S × L × G	44	21.31**	30.088**	0.463**	0.102**	19.25**	35445.3**
Error	352	4.76	4.475	0.292	0.019	5.699	1714.4

*, **, Indicates significant at 5 and 1% probability, respectively; †, Data collected only in one location for two seasons; ns, not significant.

results revealed that high yielding genotypes, in general, showed greater LAI and TDM plant^{-1} than the low yielding ones. For example, five high yielding genotypes viz., E_4I 913, BMX 956-4, BMX 942-8, BMX 927-3 and VC 6173 showed significantly higher LAI (average 3.73) and TDM (average 15.9 g plant^{-1}) with BMX 942-8 been the highest of all (3.8 and 16.8 g plant^{-1} for LAI and TDM, respectively). In contrast, low yielding genotypes such as MB 300, VC 6372 and VC 3960 produced lower LAI (average 1.42) and TDM (average 9.07 g plant^{-1}) with MB 300 having the lowest (1.22 and 7.39 g plant^{-1} for LAI and TDM, respectively). The remaining genotypes formed different intermediate groups and genotypes also differed within the group. However, the genotypes that produced the highest/higher LAI and TDM, in general, also showed lower/lowest harvest index and vice versa.

Reproductive characters

Mean performance of 45 genotypes with respect to reproductive characters in the two locations and seasons is presented in Table 2. Number of racemes plant^{-1}, flowers plant^{-1} and percent podset to opened flowers (reproductive efficiency, RE) varied between 6.30 and 22.9, 18.1 and 51.9 and 62 and 82%, respectively (Table 2). Results revealed that high yielding genotypes, in general, produced higher number of racemes and flowers plant^{-1} than the low yielding ones. This result indicates that number of racemes and flower are the important sinks that determined seed yield. Like number of racemes and flowers plant^{-1}, RE did not follow any regular pattern. However, the number of flowers showed negative association with RE, that is, genotypes with increased flower production showed lower RE and vice versa (Table 2). In general, RE was higher in the low yielding genotypes than in the high yielding ones.

Yield and yield attributes

Mean performance of different yield attributes and yield as affected by genotypes in locations and seasons is shown in Table 3. The ranges of pods plant^{-1}, seeds pod^{-1}, single pod and 100-seed weight and seed yield were 9.6 to 22.1, 9.61 to 11.5, 374 to 648 mg, 2.91 to 5.94 g and 493 to 957 kg ha^{-1}, respectively (Table 3). Results revealed that high yielding genotypes (E_4I 913, BMX 954-

Table 2. Physiological and reproductive characters as affected by genotypes (averaged over two locations and two seasons).

Genotype	Growth and partitioning			Reproductive characters		
	Leaf area index	**Total dry matter plant^{-1} (g)**	**Harvest index (%)**	**Raceme plant^{-1} (number)**	**Flower plant^{-1} (number)**	**Pod set to open flowers (%)**
N_2J 207	2.32	13.2	32.12	17.5	37.2	69
N_2J 210	2.44	14.4	31.79	18.1	43.0	69
N_2M 402	2.49	13.9	34.40	16.1	34.2	72
N_5J 521	2.27	14.3	26.51	19.3	38.3	68
E_1J 608	2.05	12.6	29.94	16.1	32.5	73
E_4I 901	2.63	13.5	28.48	19.6	37.1	73
E_4I 913*	3.42	15.7	30.28	20.4	44.1	74
MB 293	2.31	12.3	29.68	9.03	22.5	69
MB 298	2.30	10.0	32.28	12.7	23.7	77
MB 300	1.22	7.39	35.14	6.30	18.1	75
BMX 954-24*	3.21	14.8	36.86	16.6	36.3	82
BMX 966-8	3.12	12.9	22.78	18.0	33.8	72
BMX 941-3	2.58	11.3	34.44	11.9	33.0	70
BMX 956-18	2.48	12.0	31.98	16.2	34.8	72
BMX 956-17	3.19	13.2	25.64	11.1	36.0	74
BMX 952-18	2.33	11.8	32.63	13.2	32.8	78
BMX 967-1	1.82	10.6	26.75	10.6	25.6	66
BMX 941-10*	2.66	13.5	29.54	14.9	31.3	71
BMX 944-2	2.88	13.2	25.48	16.1	30.8	72
BMX 954-12	2.91	12.7	30.08	15.9	51.9	66
BMX 956-4	3.89	15.0	26.41	13.8	39.2	72
BMX 942-8*	3.86	16.8	27.18	22.9	48.7	68
BMX 959-30	2.68	14.0	27.73	16.5	38.0	72
BMX 959-10	3.52	13.4	28.76	15.1	38.0	74
BMX 954-18	2.77	13.7	28.28	16.4	45.1	68
BMX 963-1	3.80	15.7	24.44	13.2	25.3	75
BMX 927-3	3.74	15.4	26.99	16.1	37.9	68
BMX 953-9*	3.31	12.8	29.38	15.7	39.0	67
VC 6372	1.57	10.0	30.22	6.55	23.0	74
VC 6173 (B 6)*	2.98	12.7	31.12	12.7	24.9	68
VC 6144C	3.05	12.2	23.86	9.40	25.0	75
VC 6173 (B13)	3.15	14.8	26.01	14.2	28.2	76
VC 3960	1.50	9.81	27.47	7.18	24.7	68
VC 6379 (B11)	2.74	14.3	28.53	11.8	32.4	77
VC 6173*	3.72	16.6	26.42	19.6	51.2	65
VC 6173A	2.07	11.0	28.18	8.02	19.4	71
VC 6153 (B19)	2.55	12.2	29.97	14.4	39.2	73
VC 6379(23-11)	2.04	12.1	30.62	9.15	29.5	65
VC 3960 (A89)	2.17	11.0	31.88	10.2	23.2	68
BINA moog 2*	3.01	14.6	30.31	22.2	41.4	70
BINA moog 4	2.62	10.7	34.64	16.3	40.8	70
BARI moog 2	2.61	13.2	32.97	12.5	33.5	74
BARI moog 3	1.92	10.4	36.99	14.7	41.2	62
BARI moog 4	3.22	10.7	31.94	12.6	33.4	69
BARI moog 5	2.25	10.0	34.57	7.54	25.6	76
LSD (0.05)	0.24	1.89	2.59	2.22	5.67	6.3
SE (±)	0.09	0.61	0.97	0.73	2.04	2.3
CV (%)	3.65	9.55	8.21	13.2	10.3	15.2

*, High yielding genotypes (HYV).

Table 3. Yield components and seed yield as affected by genotypes (averaged over two locations and two seasons).

Genotype	Pods plant^{-1} (number)	Seeds pod^{-1} (number)	Single pod Weight (mg)	100-seed weight (g)	Seed yield (kg ha^{-1})
N$_2$J 207	18.6	10.2	394	3.35	748
N$_2$J 210	16.7	10.5	411	3.41	757
N$_2$M 402	16.4	10.4	387	3.40	642
N$_5$J 521	18.8	10.1	389	3.46	747
E$_1$J 608	14.8	10.6	404	3.43	716
E$_4$I 901	18.0	10.4	406	3.48	709
E$_4$I 913*	20.0	10.4	419	3.50	902
MB 293	9.60	10.2	618	5.59	579
MB 298	11.6	10.4	594	5.21	714
MB 300	10.4	10.0	550	5.74	555
BMX 954-24*	18.0	11.1	392	2.91	789
BMX 966-8	12.6	11.2	470	3.65	641
BMX 941-3	18.5	10.7	430	3.58	632
BMX 956-18	19.0	10.5	466	3.90	772
BMX 956-17	15.3	11.2	472	3.94	656
BMX 952-18	15.9	10.6	374	3.22	650
BMX 967-1	11.0	10.7	494	4.23	558
BMX 941-10*	13.0	10.2	614	5.66	779
BMX 944-2	13.1	10.4	462	3.81	635
BMX 954-12	19.3	10.8	424	3.36	749
BMX 956-4	15.7	11.5	502	3.82	763
BMX 942-8*	22.1	10.6	458	3.65	957
BMX 959-30	15.7	10.6	429	3.60	767
BMX 959-10	19.8	10.4	406	3.35	692
BMX 954-18	20.5	11.2	382	2.85	746
BMX 963-1	14.1	10.5	514	4.53	643
BMX 927-3*	17.3	9.90	499	4.91	838
BMX 953-9*	15.5	11.0	502	3.74	804
VC 6372	11.3	10.6	592	4.88	625
VC 6173 (B 6)*	11.9	9.99	649	5.94	813
VC 6144C	11.9	10.2	564	5.21	554
VC 6173 (B13)	13.0	10.1	648	5.90	707
VC 3960	11.4	9.80	544	4.96	493
VC 6379 (B11)	13.5	10.2	646	5.94	762
VC 6173*	18.5	10.7	530	4.76	899
VC 6173A	12.5	10.2	569	5.09	576
VC 6153 (B19)	16.8	10.4	407	3.51	655
VC 6379(23-11)	12.5	10.7	603	5.46	620
VC 3960 (A89)	11.1	11.1	514	4.09	598
BINA moog 2*	17.7	10.3	394	3.53	789
BINA moog 4	17.1	9.61	448	4.32	741
BARI moog 2	15.5	10.6	472	3.89	753
BARI moog 3	18.3	10.5	408	3.66	695
BARI moog 4	15.7	11.0	422	3.61	654
BARI moog 5	11.9	10.7	507	4.15	661
LSD (0.05)	1.75	0.61	28.0	0.16	66.5
SE (±)	0.89	0.22	0.86	0.06	23.9
CV (%)	9.98	3.25	4.51	3.65	7.33

*, High yielding genotypes; the last six genotypes are varieties and the rest are advance lines.

24, BMX 942-8, BMX 953-9, VC 6173 and BINA moog 2) produced increased number of pods plant^{-1}, medium to small pod and seed sizes. In contrast, the low yielding genotypes [MB 293, MB 298, MB 300, VC 6144C, VC 6173 (B13), VC 6372, VC 6173A, VC 6379 (23-11) and BARI moog 5] produced fewer pods plant^{-1} with larger pod and bolder seed. The highest seed yield was observed in BMX 942-8 (957 kg ha^{-1}), followed by E_4I 913 (902 kg ha^{-1}) and VC 6173 (899 kg ha^{-1}), and these three genotypes held similar statistical rank, although, was significantly different from the remainders. However, BMX 954-18 appeared to be an exception as it had higher number of pods plant^{-1} (20.2), yet showed intermediate seed yield (746 kg ha^{-1}). This is because it possessed smaller pod and seed size than other high yielders. In contrast, VC 3960 produced the lowest seed yield (493 kg ha^{-1}) which was statistically similar to VC 6144C (554 kg ha^{-1}) and MB 300 (555 kg ha^{-1}). The remaining genotypes once again formed different intermediate groups, and genotypes also differed within the group. However, number of seeds pod^{-1} between high and low yielding genotypes did not follow any regular pattern like single pod weight and 100-seed weight (Table 3).

Correlation coefficient

The results revealed that genotypic correlations were higher than those of the phenotypic ones for all the attributes (Table 4). Seed yield showed significant and positive genotypic correlations with TDM (r = 0.85**), LAI (r = 0.63**), pods number (r = 0.77**), racemes number (r =0.72**) and flowers number (r = 0.59**). In contrast, seed yield had negative association with seed size (100-seed weight) (r = - 0.35**). Again, seed yield and related traits were positively and significantly correlated with TDM, and TDM was found to be positively and significantly correlated with LAI, both at the genotypic and phenotypic levels. It means TDM production depended on LAI. The prime yield attribute, pods number showed significant and positive association with number of flowers (r = 0.83**) and racemes (r = 0.84**), both at the genotypic and phenotypic levels, indicating that pods number depend on raceme and flower numbers. In contrast, pod number showed significantly negative association with seed (r = - 0.83**) and pod sizes (r = - 0.64**). However, RE showed negative relation with number of raceme, flowers and pods.

Path analysis

The results of path analysis revealed that the number of pods contributed maximally to seed yield with the highest positive direct effect (0.929) (Table 5). The genotypic correlation of pods with flowers was also high and it contributed to seed yield in positive direction, indirectly through flower number. The characters, 100-seed weight and flower numbers also had considerable high positive and direct effects on seed yield (0.603 and 0.543, for 100-seed weight and flowers plant^{-1}, respectively). RE showed very weak relation with the number of flowers.

DISCUSSION

In general, harvest index (HI) was higher in the low yielding genotypes than in the high yielding ones, indicating that even though yield performance was not good, dry matter pertaining to economic yield was better. These results therefore, suggest that selection of higher yielding genotypes on the basis of HI may be misleading (Poehlman, 1991). In contrast, LAI and TDM had positive relation with seed yield as most of the higher LAI producing genotypes also produced higher TDM. This result has also been reported by Pawar and Bhatia (1980) and Mondal (2007) in mungbean. Unlike TDM and LAI, RE was higher in the low yielding genotypes than in the high yielding ones and this suggests that selection of genotypes on the basis of RE may be misleading for high yield. Further, high yielding genotypes also had increased number of racemes and flowers and this could be explained by the fact that high yielding genotypes had increased number of branches (data not shown), leading to increased flower (sink size) production. However, higher flower producing genotypes vis-à-vis, high yielding genotypes had lower RE. This result might be explained in a way that less competition is seen for assimilates amongst the flowers/pods in the low yielding genotypes that had fewer sinks (flowers).

Results of yield attributes versus yield revealed that high yielding genotypes had higher number of pods plant^{-1} with medium to small pod and seed sizes. In contrast, the low yielding genotypes produced fewer pods plant^{-1}, although in most cases, showed larger pods and seeds. It means pod number and seed size were inversely related with each other. Furthermore, the higher number of pods in high yielding genotypes was attributed to the increased number of pod bearing organ, raceme (Table 2). This result agrees with Saitoh et al. (2004) and Mondal (2007) who also observed inverse relations between pod number and seed size in soybean and mungbean, respectively. Dry matter (DM) is the end product of many plant processes where LA/LAI plays central role (Hamid et al., 1989). In the current investigation, TDM was found to be positively and significantly correlated with LAI, both at the genotypic and phenotypic levels, indicating that TDM can be increased by increasing LAI. Pods number, in this study, showed significant and positive association with number of flowers and racemes, both at the genotypic and phenotypic levels, indicating that pods number depend on raceme and flower numbers. This suggests that increasing sink (racemes and flowers) production would increase pod yield and this agrees with

Table 4. Genotypic (G) and phenotypic (P) correlation coefficients between yield components, reproductive and growth characters of 45 mungbean genotypes in two locations for two seasons.

Character	Correlation type	Pods plant^{-1} (number)	Seeds pod^{-1} (number)	100-seed Weight (g)	Single pod weight (g)	Raceme plant^{-1} (number)	Flowers plant^{-1} (number)	% Pods to open flower	TDM/ Plant (g)	Leaf area index
Seed yield (kg/ha)	G	0.77**	0.20 *	- 0.35**	- 0.11	0.72**	0.59**	0.12	0.85**	0.63**
	P	0.72**	0.15 *	- 0.35**	- 0.10	0.67**	0.53**	0.08	0.77**	0.57**
Pods/plant (number)	G		0.18 *	- 0.83**	- 0.64**	0.84**	0.83**	- 0.06	0.81**	0.58**
	P		0.16 *	- 0.67**	- 0.58**	0.72**	0.72**	- 0.05	0.68**	0.54**
Seeds/pod (number)	G			- 0.47**	- 0.40**	0.23**	0.36**	- 0.05	0.35**	0.05
	P			- 0.31**	- 0.24*	0.16 *	0.22**	- 0.04	0.21 *	0.17 *
100-seed weight (g)	G				0.79**	- 0.57**	- 0.68**	- 0.02	- 0.50**	- 0.48**
	P				0.77**	- 0.54**	- 0.63**	- 0.02	- 0.44**	-0.40**
Single pod weight (g)	G					- 0.54**	- 0.67**	0.16 *	- 0.27*	- 0.08
	P					- 0.46**	- 0.60**	0.14 *	- 0.23**	- 0.32**
Racemes/plant (number)	G						0.78 **	- 0.016	0.80 **	0.67**
	P						0.73 **	- 0.014	0.73 **	0.59**
Flowers/plant (number)	G							- 0.21 *	0.84**	0.57**
	P							- 0.15 *	0.74**	0.54**
% Pods to open flowers	G								- 0.006	0.17 *
	P								- 0.014	0.13 *
TDM/plant (g)	G									0.72**
	P									0.65**

* and **, Indicates significance at 5 and 1% level, respectively.

the result of Mondal (2007) in mungbean who also observed that pod yield increased with increased number of flowers. Negative relations of pod number with pod and seed sizes indicate that there should be a compromise between the number of pods, and pod and seed size. Seed yield was also positively and significantly correlated with LAI, TDM and pod number, and was negatively associated with pod and seed sizes in mungbean as reported by Mondal et al. (2004) which support this finding. Interestingly, percent podset to opened flowers, that is, reproductive efficiency (RE) showed negative relationship with number of raceme, flowers and pods. Contrarily, the RE showed positive relationship with number of pods plant^{-1} in groundnut (Mondal and Hamid, 1998). Here in this study with mungbean, pod yield was improved by increasing raceme and flower production since RE had weaker relationship (non-significant) with yield. This further suggests that sink production and flowers number, were more important than survivability (RE) in mungbean.

It appears from this investigation that the greater number of leaves, racemes, flowers and pods could be good indexes of selection for mungbean improvement. It was thus obvious that flower and pod numbers, and seed sizes are the principal determinants of seed yield in mungbean (Reddy et al., 1991; Sarwar et al., 2004; Siddique et al., 2006; Mondal, 2007). This mean that increased flower and pod production, and large seed size should be used for selection indexes for varietal improvement programme in mungbean. This result agrees with the report of Hossain et al. (2002) and Hakim (2008) who also reported significant direct effect of pod number and seed size on seed yield in mungbean.

From the results, it may be concluded that: (i)

Table 5. Direct (bold) and indirect effects of yield attributes, growth and reproductive characters on seed yield of 45 mungbean genotypes studied in two locations for two seasons (estimated from genotypic correlation).

Character	Pods plant^{-1} (number)	Seed pod^{-1} (number)	100-seed weight	Single pod weight	Flower plant^{-1} (number)	TDM plant^{-1} (g)	% Pod to open flower	Raceme plant^{-1} (number)	Leaf area index	Seed yield plant^{-1}
Pod plant^{-1} (number)	0.929	0.015	- 0.298	- 0.039	0.440	0.264	- 0.015	- 0.179	0.071	0.765
Seed pod^{-1} (number)	0.161	0.136	- 0.381	- 0.054	0.197	0.118	-0.012	- 0.110	0.011	0.205
100-Seed weight	- 0.783	- 0.064	0.603	0.267	- 0.368	- 0.171	- 0.004	0.790	0.009	- 0.355
Single pod weight	- 0.610	- 0.054	0.474	0.061	- 0.364	0.092	0.059	0.293	-0.071	- 0.106
Flower plant^{-1} (number)	0.788	0.046	- 0.410	- 0.341	0.543	0.220	0.051	- 0.416	0.009	0.593
TDM plant^{-1} (g)	0.764	0.047	- 0.643	- 0.317	0.338	0.488	- 0.215	-0.499	0.163	0.850
% Pod to open flower	- 0.059	- 0.007	- 0.04	0.280	- 0.114	0.141	0.242	0.044	- 0.121	0.121
Racemes plant^{-1} (number)	0.755	0.031	- 0.686	- 0.413	0.462	0.278	- 0.700	0.489	0.140	0.614
Leaf area index	0.742	0.044	- 0.338	- 0.500	0.044	0.278	- 0.056	- 0.533	0.221	0.630

leaf area index was the most important sources that determined TDM yield, (ii) raceme number was the main sink that determined the organ of flowers and pods production and (iii) correlation and path-coefficient analysis indicated that number of flowers plant^{-1}, pods plant^{-1} and 100-seed mass contributed maximally to seed yield in mungbean, and the genotypes E$_4$I 913, BMX 942-8, BMX 953-9, VC 6173 and BARI moog 2 maintained superiority in the earlier mentioned characters, except 100-seed mass, which had higher seed yield.

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