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Comparative Study of Quantitative Traits and Association of Yield and its Components in Black Gram (*Vigna mungo*) Genotypes

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Abstract: Studies were conducted on eighteen genotypes of black gram (*Vigna mungo*) to evaluate their comparative performance under rainfed conditions. Highly significant differences were observed for all the traits except leaf area which showed non-significant differences. Leaf area, pods plant⁻¹, plant height and biological yield plant⁻¹ showed high genotypic and phenotypic variances exhibiting greater variability in these traits. The magnitude of heritability was high for 100-seed weight (94%), pods plant⁻¹ (91%), pod length (91%), biological yield (87%), grain yield (85%), days to maturity (80%), harvest index (76%), branches plant⁻¹ (75%) and plant height (71%) indicating additive type of gene action. Pods plant⁻¹, branches plant⁻¹ and biological yield plant⁻¹ showed highly significant and positive correlation with grain yield showing that these traits have good positive effect on grain yield. Selection of genotypes on the basis of these traits can be useful. The present study enabled to identify early to medium duration lines without losing grain weight and yield potential.

Key words: Black gram, mash, *Vigna mungo*, genetic variability, heritability, correlation

INTRODUCTION

Black gram (*Vigna mungo*) or Mash is a member of bean family grown in Southern Asia and is one of the important pulse crops in Pakistan. It is an erect, sub-erect or trailing, densely hairy annual herb. The tap root produces a branched root system with smooth, rounded nodules. The pods are narrow, cylindrical and up to 6 cm long. It is a rich protein food which contains about 26% crude protein, almost three times that of cereals. Black gram supplies a major share of protein requirement of vegetarian population of the country. It is largely used to make dal from the whole or split, dehusked seeds. It is very nutritious and is recommended for diabetics, as are other pulses (Smart, 1990).

Black gram, in Pakistan, has been in cultivation from ancient times and is one of the most highly prized pulses of Pakistan. However, an average yield is very low as compared to other countries. During 2004-05, it was cultivated under an area of 37500 ha with average yield of 491 kg ha⁻¹, while during 2005-06, the area under cultivation was 34600 ha yielding 477 kg ha⁻¹ (Anonymous, 2005-06).

Since the crop is grown in various agro-ecological conditions and cropping systems with diverse cultural practices, no single plant type is appropriate for all production systems (Singh and Satyanarayana, 1994). This calls for an extensive survey of existing germplasm

collections for potential utilization in development of appropriate plant type for the various cropping systems in tropical Asia (Dikshit *et al.*, 2007). In order to develop high yielding cultivars, exploitation of gene pool is very important. The profitable yield can be obtained through genetic improvement for high yield potential and the examination of genetic variability for plant breeder is very important (Malik *et al.*, 2006a). Extent of genetic variability and relationship of traits have been reported by various scientists like Ghafoor *et al.* (2001) and Malik *et al.* (2006b). Khan *et al.* (2004) indicated highly significant differences among genotypes for days to 50% flowering, yield and yield related traits. Malik *et al.* (2006b) examined genetic variability among different genotypes of soybean and found significant differences for all the traits and observed positive and significant correlation of grain yield with leaf area and pods plant⁻¹. High variance was recorded for plant height, days to flowering, days to maturity, number of branches plant⁻¹, number of pods plant⁻¹, pod length, seeds pod⁻¹, biomass yield plant⁻¹, grain yield plant⁻¹ and harvest index (Ghafoor *et al.*, 2002). Malik *et al.* (2006c) stated that the estimated variances due to genotypes exceeded that due to environment for all characters. Similarly, positive and statistically significant relationship between seed yield plant⁻¹ and days to flowering, pods plant⁻¹, seeds plant⁻¹, harvest index and 100-seed weight was pointed out by Celal (2004). Siddique *et al.* (2006)

reported that grain yield was positively correlated with days to maturity, 100-seed weight and grains pod⁻¹. Arshad *et al.* (2002) found high heritability for plant height and showed that grain yield was positively and significantly correlated with pods plant⁻¹, branches plant⁻¹ and biological yield. Present study was conducted to evaluate some promising genotypes of mash for earliness and high grain yield under rainfed conditions.

MATERIALS AND METHODS

An experiment was performed in the research area of Barani Agricultural Research Station, Fatehjang on eighteen genotypes of mash during Kharif 2006 in a randomized complete block design. The plot size was kept 9.0 m² with a row length of 5 m and row to row distance of 30 cm. The seeds were sown with the help of hand drill. Ten plants were selected in each plot to record the data. Data were recorded for traits like leaf area, days to 50% flowering (days from sowing to appearance of 50% flowers), days to maturity (days from sowing to appearance of 90% maturity), pods plant⁻¹, branches plant⁻¹, plant height, pod length, seeds pod⁻¹, 100-seed weight, grain yield plant⁻¹, biological yield plant⁻¹ and harvest index. Data on days to 50% flowering and days to 90% maturity were recorded as a single value for each row. Pods plant⁻¹ (numbers), seeds pod⁻¹ (numbers), seeds plant⁻¹ (numbers), pods branch⁻¹ (numbers), branches plant⁻¹ (numbers), yield plant⁻¹ (g) were recorded from 10 plants that had been randomly chosen in central row and the means of the quantitative data sets were used for analysis. In addition, 100 seed weight was recorded.

Leaf area was recorded using leaf area meter (L1-3000, LICOR, Lambda Instrument Co., USA). Harvest index was calculated by dividing grain yield with biological yield and expressed in % following Wilcox (1974). Means computed from MS-Excel were subjected to analysis of variance (ANOVA) and correlation using computer program MSTATC (Anonymous, 1988) and SPSS-12 respectively. Heritability was calculated by the formula given by Allard (1960).

RESULTS AND DISCUSSION

Highly significant differences were observed for all the traits except leaf area which showed non-significant differences (Table 1). Partitioning of variance into its components revealed that the phenotypic variances were higher than the genotypic and environmental variances. However, the genotypic variances were higher than environmental variances. Siddique *et al.* (2006) also reported similar results. High genotypic and phenotypic variances were recorded for leaf area, pods plant⁻¹, plant height and biological yield plant⁻¹. These results are comparable to the findings of Ghafoor *et al.* (2002) and Malik *et al.* (2006b). Low genetic variance for rest of the traits seems to limit the scope of selection for these traits. The magnitude of heritability (Table 2) was high for 100-seed weight (0.94), pods plant⁻¹ (0.91), pod length (0.91), biological yield (0.87), grain yield (0.85), days to maturity (0.80), harvest index (0.76), branches plant⁻¹ (0.75) and plant height (0.71). These results are supported by the findings of Arshad *et al.* (2002) and Malik *et al.* (2006c).

Results shown in Table 3 showed that maximum leaf area (255.5 cm²) was recorded for genotype 3CM710 while minimum (152.57 cm²) was observed in genotype 3CM716. Two genotypes viz. 3CM705 and 3CM712 gave the highest days to 50% flowering (54.67 days) while lowest (44.33) were given by genotype 3CM702. Early to medium maturity in Mash is desirable without losing yield potential. The check variety Mash-97 matured in the longest duration (92 days) followed by genotype 3CM712 (90 days) and the shortest duration for maturity was given by genotype 3CM707 (66.67 days). These results confirm the findings of Ghafoor *et al.* (2002). Plants that produce more pods per plant along with more seeds per pod would be desirable. In the present collection, 10 accessions had more pods than both checks containing more seeds. Maximum pods plant⁻¹ were observed in genotype 3CM711 (77.8) while minimum were recorded in genotype 3CM713 (9.67). A range between 3.8 (3CM716) and 9.0 (3CM711) was shown by branches plant⁻¹. Highest plant height (170.11 cm) was given by genotype 3CM705 while lowest (76.78 cm) was noted in genotype 3CM716. Dikshit *et al.* (2007) also found similar results.

Table 1: Mean squares of 12 quantitative traits in 18 genotypes of mash (*Vigna mungo*)

SOV	LA	DHE	DMA	PP	BP	PH	PL	SP	100-SW	GY	BY	HI
MS (V)	1508.10 ^{ns}	29.88**	146.40**	812.18**	6.08**	2056.66**	0.27**	0.55**	2.27**	59.41**	623.98**	0.020**
MS (R)	1984.86	26.74	71.72	482.82	14.17	353.97	0.03	0.37	0.16	7.89	48.96	0.008
MS (E)	923.34	9.62	11.04	25.05	0.59	242.50	0.01	0.16	0.05	3.23	29.08	0.002

MS (V) = Variety mean square, MS(R) = Replication mean square, MS(E) = Environmental mean square, LA = Leaf area, DHE = Days to 50% flowering, DMA = Days to maturity, PP = Pods plant⁻¹, BP = Branches plant⁻¹, PH = Plant height, PL = Pod length, SP = Seeds pod⁻¹, 100-SW = 100-seed weight, GY = Grain yield plant⁻¹, BY/plant = Biological yield plant⁻¹, HI = Harvest index **: Significant at p<0.01

Table 2: Variance components of yield and its components

Variance components	LA	DHE	DMA	PP	BP	PH	PL	SP	100-SW	GY	B Y	HI
σ_g^2	194.92	6.75	45.12	262.38	1.83	604.72	0.09	0.13	0.74	18.73	198.30	0.01
σ_p^2	1118.26	16.37	56.16	287.43	2.42	847.22	0.10	0.29	0.79	21.95	227.38	0.01
h^2	0.17	0.41	0.80	0.91	0.75	0.71	0.91	0.46	0.94	0.85	0.87	0.76

σ_g^2 = Genotypic variance, σ_p^2 = Phenotypic variance, h^2 = Heritability

Table 3: Means of 12 quantitative traits studied in 18 genotypes of mash (*Vigna mungo*)

Genotypes	LA (cm)	DHE	DMA	PP	BP	PH (cm)	PL (cm)	SP	100-SW(g)	GY (g)	B Y (g)	HI (%)
3CM702	177.15	44.33	72.33	11.87	4.63	131.11	5.08	5.77	5.87	9.13	16.33	56
3CM703	186.34	46.67	74.67	29.80	5.50	146.11	5.23	6.33	6.57	11.77	31.00	38
3CM704	184.12	49.67	77.00	17.33	5.50	86.11	4.94	6.63	6.23	11.10	28.33	39
3CM705	178.47	54.67	88.33	25.20	4.83	170.11	5.00	5.87	5.73	11.97	29.67	43
3CM706	184.69	52.67	83.67	29.53	5.70	146.67	4.73	6.05	3.63	10.07	32.67	31
Mash97	218.40	57.00	92.00	24.33	4.87	124.11	5.16	6.54	5.53	10.53	31.67	33
CH-Mash	178.14	50.67	81.00	21.33	4.13	143.22	5.06	6.33	5.63	9.53	28.33	34
3CM707	206.66	48.00	66.67	32.73	5.23	112.22	4.97	6.63	7.57	14.00	39.33	36
3CM708	180.14	49.67	72.33	26.20	5.07	90.22	4.77	5.67	6.77	12.30	29.67	41
3CM709	204.33	52.00	73.33	19.87	5.40	117.11	5.43	6.60	6.20	10.83	37.33	30
3CM710	255.50	49.00	78.00	29.60	4.77	90.89	4.41	5.47	6.43	10.60	24.33	45
3CM711	182.00	48.67	75.00	77.80	9.00	97.89	4.42	6.69	7.40	24.33	75.00	32
3CM712	221.59	54.67	90.00	27.00	5.30	83.78	4.26	5.40	5.37	9.90	48.00	21
3CM713	186.15	51.67	81.00	9.67	3.90	106.44	4.71	6.63	6.50	6.03	15.67	40
3CM714	191.39	51.33	81.00	23.53	7.33	91.00	5.07	5.93	6.47	10.70	49.00	22
3CM715	195.07	54.33	87.67	59.13	8.47	116.00	4.84	6.18	5.90	21.20	53.67	39
3CM716	152.57	52.33	82.67	20.67	3.80	76.78	4.90	6.38	6.37	11.83	43.33	27
3CM717	189.48	49.00	74.33	43.40	5.97	125.00	4.78	5.70	5.40	17.73	48.00	37
Mean	192.90	50.91	79.50	29.39	5.52	114.15	4.88	6.15	6.09	12.42	36.74	36

LA = Leaf area, DHE = Days to 50% flowering, DMA = Days to maturity, PP = Pods plant⁻¹, BP = Branches plant⁻¹, PH = Plant height, PL = Pod length, SP = Seeds pod⁻¹, 100-SW = 100-seed weight, GY = Grain yield plant⁻¹, BY/pl = Biological yield plant⁻¹, HI = Harvest index

Table 4: Correlation coefficients among 12 quantitative traits

Quantitative traits	LA	DHE	DMA	PP	BP	PH	PL	SP	100-SW	GY	B Y
DHE	-0.04										
DMA	0.08	0.55**									
PP	0.02	0.05	0.04								
BP	0.01	-0.11	-0.03	0.73**							
PH	-0.14	0.08	0.11	-0.05	-0.15						
PL	-0.19	0.00	-0.17	-0.31	-0.21	0.42					
SP	-0.27	-0.04	-0.09	-0.01	0.10	0.01	0.32				
100-SW	0.06	-0.28	-0.50*	-0.07	-0.12	-0.24	0.20	0.04			
GY	-0.04	-0.08	-0.10	0.77**	0.63**	-0.08	-0.21	0.10	0.08		
B Y	-0.04	0.10	0.10	0.65**	0.66**	0.25	-0.29	0.08	-0.05	0.810**	
HI	0.02	-0.35	-0.33	-0.10	-0.24	0.26	0.14	-0.08	0.19	0.002	-0.55*

LA = Leaf area, DHE = Days to 50% flowering, DMA = Days to maturity, PP = Pods plant⁻¹, BP = Branches plant⁻¹, PH = Plant height, PL = Pod length, SP = Seeds pod⁻¹, 100-SW = 100-seed weight, GY = Grain yield plant⁻¹, BY/pl = Biological yield plant⁻¹, HI = Harvest index
*: Significant at p<0.05, **: Significant at p<0.01

However, these findings are somewhat contradictory to those of Ghafoor *et al.* (2002) who showed relatively low mean plant height (37.5 cm). The difference in results might be due to the excessive rainfall during the growing season which resulted in prolonged vegetative period and increased plant height. Maximum pod length was recorded in genotype 3CM709 (5.43 cm) while minimum was recorded in genotype 3CM712 (4.26 cm). Seeds pods⁻¹ were between 5.4 (3CM712) and 6.69 (3CM711). These are supported by Ghafoor *et al.* (2001). 100-seed weight is the major contributor to the final grain yield. High 100 seed weight was noted in genotype 3CM707 (7.57 g) while lowest 100 seed weight was given by genotype 3CM706 (3.63 g). Grain yield is the ultimate output of any crop.

Genotype 3CM711 out yielded other genotypes for grain yield plant⁻¹ (24.33 g) while genotype 3CM713 least yielding (6.03 g). Verma and Katna (1998) reported a large variability in yield tested in both monocrop and intercrop conditions. Biological yield is a major contributor to total output which depends upon species, growing season and various other factors. For biological yield plant⁻¹, genotype 3CM711 was at top (75.0 g) while genotype 3CM713 was at the bottom (15.67 g). Harvest index in legumes is unpredictable and sensitive to environment. Harvest index ranged from 0.21 (3CM712) and 0.56 (3CM702). Ghafoor *et al.* (2001) also found that biological yield and harvest index had a mean value of 44.44 g and 23.28%, respectively.

Correlation coefficients (Table 4) revealed that highly significant and positive correlation was observed between days to 50% flowering and days to maturity. Days to maturity showed negative and significant correlation with 100 seed weight. Siddique *et al.* (2006) also showed positive correlation between days to 50% flowering and days to maturity and negative correlation between days to maturity and 100-seed weight. The number of pods per plant can be increased by increasing branches plant⁻¹, because a strong positive correlation ($r = 0.73$) existed between them. Similarly, pods plant⁻¹ and branches plant⁻¹ were also highly significantly and positively correlated with grain yield plant⁻¹ and biological yield plant⁻¹. Singh and Satyanarayna (1994) and Sood and Garton (1994) also discussed similar relationships. Grain yield plant⁻¹ showed highly significant and positive correlation with biological yield plant⁻¹ showing that increased biomass results in increased grain yield. Biological yield plant⁻¹ and harvest index were also positively and significantly correlated with each other. These results are well confirmed by the findings of Arshad *et al.* (2002), Khan *et al.* (2004), Malik *et al.* (2006a, c) and Celal (2004).

CONCLUSION

It was concluded that the genotypes showed greater variability for leaf area, pods plant⁻¹, plant height and biological yield plant⁻¹. Traits showing lesser influence of environment and high heritability were 100-seed weight, pods plant⁻¹, pod length, biological yield, grain yield, days to maturity, harvest index, branches plant⁻¹ and plant height. Pods plant⁻¹, branches plant⁻¹ and biological yield plant⁻¹ can be used as selection criteria as they showed highly significant and positive correlation with grain yield. Black gram has been reported as a crop highly influenced by environmental fluctuations, but the selected genotypes performed better and were least affected by the environment. The high yielding genotypes viz., 3CM711 and 3CM715 proved their superiority over checks as had higher pods plant⁻¹, grain yield plant⁻¹ and biological yield plant⁻¹ than checks. These can be used in crossing programme to induce earliness and high yield.

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