

Full Length Research Paper

Genotypic association among yield and related attributes in mungbean genotypes

Sabra Begum¹, Muhammad Noor^{*1}, Gulam Hassan¹, Hidayat ur Rahman¹, Durrishawar²,
Hidayat Ullah³ and Masood Jan¹

¹Department of Plant Breeding and Genetics, KPK Agricultural University, Peshawar, Pakistan

²Faculty of Agriculture, Abdul Wali Khan University, Mardan, Pakistan

³Department of Agronomy, KPK Agricultural University, Peshawar, Pakistan

Accepted 03 March, 2012

The research was conducted at the Farm of Plant Breeding and Genetics Department of Khyber Pakhtunkhwa, Agricultural University, Peshawar during the year of 2009. The objectives of this research were to estimate heritabilities and genotypic correlations among traits of 10 mungbean genotypes. A randomized complete block (RCB) design with four replications was used. The parameters included were branches plant⁻¹, plant height, pods plant⁻¹, pod length, number of grains pod⁻¹, number of grains plant⁻¹, grain yield plant⁻¹ and 100-grain weight. Significant variation were observed among the yield and related traits. Pak-22 produced maximum number of branches plant⁻¹ (4.25). NM-51 had maximum pod length (7.82cm) followed by NM-93 (7.42cm). Maximum grain yield was recorded for genotype Ramzan (45.35) while maximum 100-grain weight was recorded for NM-93 (5.85). High heritability was recorded for days 100-grain weight (77.17%), and number of branches plant⁻¹ (68.63%). Low heritability was recorded for grains pod⁻¹ (33.33%), pods plant⁻¹ (29.67%), pod length (35.42), grain plant⁻¹ (30.50%), and grain yield plant⁻¹ (33.50%). Grain yield plant⁻¹ revealed highly significant phenotypic correlation with pods plant⁻¹ (0.65), grains plant⁻¹ (0.61), and with 100-grain weight. Grain yield plant⁻¹ showed significant genotypic correlation with pods plant⁻¹ (0.71). and with days to pods formation (0.70). Based on present studies Ramzan and AEM-96 can be used for further breeding study regarding yield improvement.

Keywords: Mungbean, genetic association, heritability and correlation.

INTRODUCTION

Mungbean (*Vigna radiata* L.) belongs to family leguminosae. Mungbean is tropical or sub tropical warm season legume crop adapted to a variety of soil. Mungbean is successfully grown on sandy and loamy soils. Mungbean varieties based on their seed size can be classified into two groups. One is the bold- seeded varieties (50-70 g/1000 seed), usually called Philippino types, and is predominantly grown in Southeast Asian countries. They possess relatively higher yield potential (1-2 t/ha), large foliage and usually need 2-3 hand pickings to harvest the ripe pods due to pod shattering and lack of uniformity in maturity. These varieties usually fail in south

Asian countries mainly due to their susceptibility to Mungbean Yellow Mosaic Virus (MYMV). The other is the small-seeded varieties (20-35 g/1,000 seed) mainly cultivated in south Asian countries. They have relatively low yield potential (0.5-1.0 t/ha) but are fairly adapted to the local environmental conditions. In Pakistan, it was planted on an area of 2.5 million hectares with a total annual production of 1.8 million tonnes with an average yield of 723 kg ha⁻¹ (MINFAL, 2008-09). Out of the total area of Pakistan, Khyber Pakhtunkhwa covered an area of 10.1 thousand hectares with the production of 6.4 thousand tonnes producing an average yield of 634 kg ha⁻¹.

Mungbean has the potential to make up the gap of protein shortage, but its yield per acre in the country is still marginal. For any yield improvement programme selection of superior parents is an essential prerequisite

*Corresponding Author's E-mail: noor_pbg49@yahoo.com;
Mob: +92-3025258528

i.e. possessing better heritability and genetic advance for various traits (Khan *et al.*, 2005). Correlation analysis provides the information of interrelationship of important plant characters and hence, leads to a directional model for direct and/or indirect improvement in grain yield (Khan *et al.*, 2004). Acharya *et al.* (1993) reported that phenotypic and genotypic coefficients of variation were high for pods per plant and yield per plant. Khan *et al.* (2004) indicated highly significant genetic differences among genotypes for days to 50% flowering, yield and yield related traits. Similarly, Celal (2004) pointed out positive and statistically significant relationships between seed yield per plant and days to flowering, pods per plant, seeds per plant, harvest index and 1000-seed weight. Imrie and Butler (2005) stated that the estimated variance due to environment exceeded than that due to genotypes for all characters.

The Asian Vegetable Research and Development Center (AVRDC) have made tremendous contribution in improving the world mungbean production through its research and development efforts and a network of active research collaborators in the national programs. The genetic variability, correlation and heritability estimates for quantitative characters are important in selecting suitable genotypes and reliable yield components for efficient yield improvement. Thus, this study was conducted to evaluate mungbean genotypes under Peshawar conditions and estimate heritability for different important parameters and estimate genotypic correlations among various parameters of the mungbean.

MATERIALS AND METHODS

This research was conducted at the experimental Farm of Plant Breeding and Genetics Department of KPK Agricultural University, Peshawar, during the year of 2009. The objectives of this research were to estimate heritabilities and genotypic correlations among traits of 10 mungbean genotypes, viz., Chakwal, NM19-19, NM-28, NM-51, NM-98, 6601, Ramzan, Pak-22, AEM-96 and NM-93. These genotypes were procured from Nuclear Institute for Food and Agriculture (NIFA). The randomized complete block design (RCBD) was used with four replications. Each entry consisted of four row plot with a row length of 5m and a plant to plant distance of 0.3m. The recommended cultural practices were carried out throughout the experiment. Data were recorded on days to 50% flowering, number of branches, days to 50% pods formation, plant height (cm), days to maturity, numbers of pods plant⁻¹, pod length (cm), numbers of grains pod⁻¹, number of grains plant⁻¹, 100-grain weight (g), grain yield plant⁻¹ (g)

Grain yield plant⁻¹ was recorded by threshing all pods from the selected plants and weighing them on single plant basis by electronic balance. Heritability in broad sense was estimated for the parameters according to Singh and Chaudhry (1979).

$$h^2 = \frac{S^2_v}{S^2_e + S^2_v}$$

Where h^2 = Broad sense heritability

$$S^2_v = \frac{\text{Varietal variance} - \text{error variance}}{\text{Number of replications}}$$

$$\text{Broad sense heritability} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}}$$

Phenotypic and Genotypic correlation coefficients were computed by the following formula suggested by Burton and Vane (1953).

1. Phenotypic correlation

$$\frac{(\delta g_{xy} + \delta e_{xy})}{[(\delta^2 g_x + \delta^2 e_x)(\delta^2 g_y + \delta^2 e_y)]^{1/2}}$$

2. Genotypic correlation

$$\frac{(\delta g_{xy})}{[(\delta^2 g_x)(\delta^2 g_y)]^{1/2}}$$

Where $\sigma^2 g_x$ = Variety component of variance for trait x.

$\sigma^2 g_y$ = Variety component of variance for trait y.

$\sigma^2 e_x$ = Error component of variance associated with trait x.

$\sigma^2 e_y$ = Error component of variance associated with trait y.

σ_{xy} = Variety component of variance for trait x and y.

σ_{exy} = Error component of covariance associated with trait x and y.

RESULTS AND DISCUSSION

This research was conducted on ten mungbean genotypes to find out genotypic correlations and heritability estimates for various characters. Mean squares and heritability values are presented in Table 1 whereas, genotypic and phenotypic correlations are presented in Table 2. Mean values of genotypes for different traits are presented in Figure 1 and 2.

Number of branches plant⁻¹

Analysis of variance revealed that highly significant differences among genotypes for branches plant⁻¹ (Table 1). These results are confirmed by the study of Yaqoob *et al.* (1997) who reported significant differences among genotypes for branches plant⁻¹. According to Figure 2, number of branches plant⁻¹ ranged from 2.25 to 4.25. Maximum branches plant⁻¹ were recorded for genotype Pak-22 (4.25) followed by Chakwal (4.0), while minimum branches plant⁻¹ were observed for genotype NM-93 (2.25). Genotypic variance for of branches plant⁻¹ was found higher from phenotypic variance. Arshad *et al.* (2009) and Siddique (2006) also found that genotypic variance is higher than phenotypic variance for branches plant⁻¹. Moderate heritability (68.63%) was found for

Table 1. Replication mean squares (RMS), Genotypic mean squares (GMS), coefficient of variation and heritability estimates for branches plant⁻¹, grains pod⁻¹, pods plant⁻¹, pod length, grains plant⁻¹, grain yield plant⁻¹ and 100-grain weight of mungbean genotypes

Trait	RMS	GMS	CV	% h ²
Branches plant ⁻¹	0.75	1.55**	12.24	68.63
Pod plant ⁻¹	13.66	1069.45*	21.65	29.67
Pod length	0.16	1.18**	8.86	35.71
Grain pod ⁻¹	0.82	0.78*	6.04	33.33
Grain plant ⁻¹	25192.15	59115.71*	19.67	30.51
Grain yield plant ⁻¹	172.18	188.71*	26.89	33.52
100 grain weight	0.35	3.05**	11.22	77.17

*, ** Significantly different from zero at 5% and 1% levels of probability, respectively.

Table 2. Genotypic correlation coefficients (above diagonal) and phenotypic correlation coefficients (below diagonal) among number of branches plant⁻¹ (BPP), pods plant⁻¹ (PPP), grains pod⁻¹ (GPP), grain yield plant⁻¹ (GYP), 100-grains weight (HGW), grains per plant (GP) and pod length (PL) of 10 mungbean genotypes

	BPP	PPP	GPP	GYP	HGW	GP	PL
BPP		0.14	0.31	-0.22	-0.62*	0.32	-0.79**
PPP	0.12		0.08	0.71*	-0.06	0.83**	-0.00
GPP	0.14	-0.06		-0.25	-0.54	0.32	-0.34
GYP	-0.12	0.65**	-0.03		0.55	0.37	0.37
HGW	-0.56**	-0.01	-0.25	0.45**		-0.43	0.66*
GP	0.16	0.75**	0.16	0.61**	-0.23		0.34
PL	-0.43**	-0.07	-0.19	0.14	0.39*	-0.2	

*, ** Significantly different at 5% and 1% levels of probability, respectively

branches plant⁻¹ (Table 1). Kumar and Chaudhary (2007) have also reported the same type of results and concluded that branches plant⁻¹ has high heritability. Number of branches plant⁻¹ had significant negative genotypic correlation with pod length (-0.79) and 100-grain weight (-0.62) (Table 2). Phenotypic correlation of number of branches plant⁻¹ with plant height (0.31) was significant and positive, while with pod length and 100-grain weight it was highly significant but negative (Table 2). Our results were in agreement with the study of Anwari and Soehendi (1999) who reported strong correlation of branches plant⁻¹ with plant height. Significantly negative association of branches plant⁻¹ with pod length and 100-grain weight was observed. Similarly, Khattak *et al.* (1995) and Arshad *et al.* (2009) have also reported significant negative association of branches plant⁻¹ with pod length and 100-grain weight.

Pods plant⁻¹

Significant differences were observed among the genotypes for pods plant⁻¹, Rahman and Hussain (2003) also reported that pods plant⁻¹ had significant differences among the genotypes. Pods plant⁻¹ ranged between 66.50 and 112.50. Maximum pods plant were recorded for genotype Ramzan (112.5) followed by Chakwal (110.75), while minimum pods plant⁻¹ were recorded for

genotype NM-93 (66.5) (Figure 1). Broad sense heritability was low (29.67%) for pods plant⁻¹ (Table 1). These findings are supported by Anwari and Soehendi (1999) and Rahman and Hussain (2003) who also observed low heritability for pods plant⁻¹. The genotypic correlation coefficient for pods plant⁻¹ revealed highly significant and positive correlation with grains plant⁻¹ (0.83) and days to pods formation (0.99) and with grain yield plant⁻¹ (0.71) its correlation was positive and significant. The rest of the traits were either positive or negative but non-significantly correlated with pods plant⁻¹. Pods plant⁻¹ had highly significant phenotypic correlations with only grains plant⁻¹ (Table 2). Significant correlation of pods plant⁻¹ with grain yield plant⁻¹ was found. Our results are supported by Dikshit *et al.* (2002), Dhuppe *et al.* (2005) and Chaudhury and Rahman (1988) who calculated significant correlation of pods plant⁻¹ and grain yield plant⁻¹.

Grains plant⁻¹

Significant differences (P<0.05) were observed among the genotypes for grains plant⁻¹ (Table 1). Present results are in agreement with the findings of Siddique (2006), Rahman and Hussain (2003) and Mensah and Oludoya (2007) who found significant differences among genotypes for grains plant⁻¹. Grains plant⁻¹ ranged from

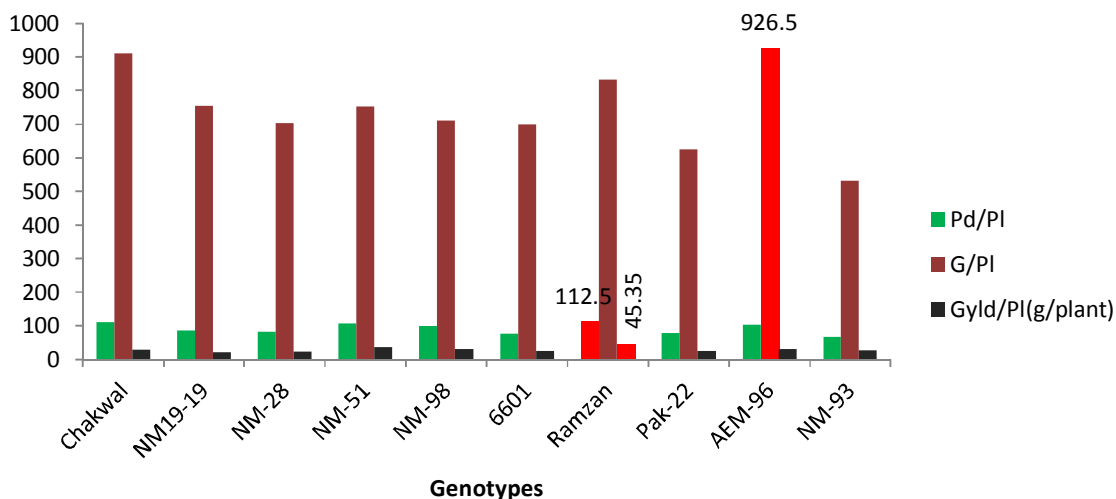


Figure 1. Means for pods per plant, grains per plant and grain yield per plant (g/plant) of ten mungbean genotypes

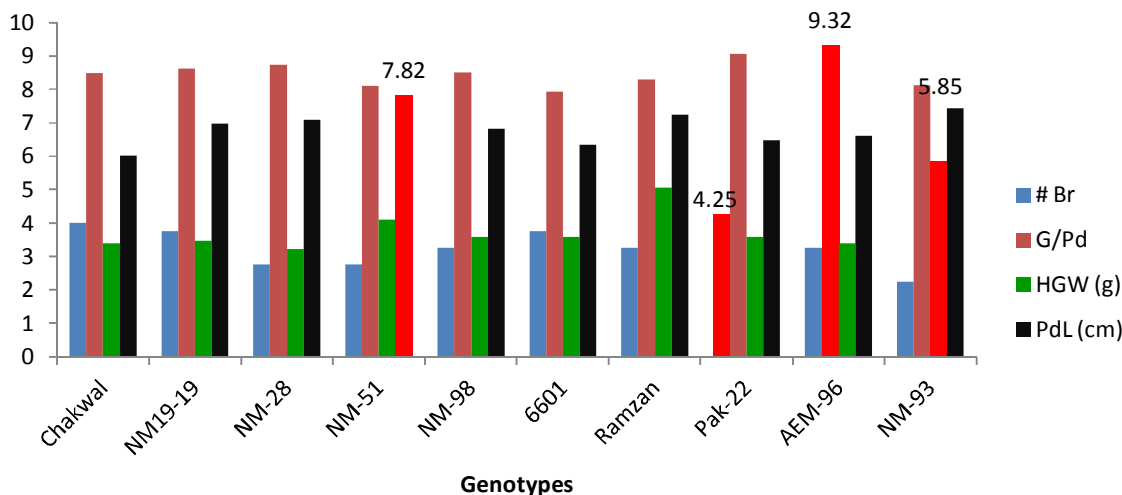


Figure 2. Means for branches per plant, grains per pod, hundred grain weight and pod length of ten mungbean genotypes

530.8 to 926.5 (Figure 1). AEM-96 was maximum in grains plant⁻¹ (926.5) followed by Chakwal (910.0) and Ramzan (832.3) (Figure 1). Heritability for grains plant⁻¹ was 30.51% (Table 1). Low heritability for grains plant⁻¹ was found which is confirmed by the study of Empig *et al.* (1970) and Varma and Garg (2001) who recorded low heritability for grains plant⁻¹. Grains plant⁻¹ showed highly significant positive genotypic correlation with pods plant⁻¹ (0.83) and days to pods formation (0.81). Highly significant positive phenotypic correlation of grains plant⁻¹ was observed with pods plant⁻¹ (0.75), grain yield plant⁻¹ (0.16) and days to pods formation (0.72) (Table 2). Grains plant⁻¹ showed significant correlation with pods

plant⁻¹ and days to pods formation. These results are in agreement with the findings of Malik *et al.* (2005) who reported significant correlation with pods plant⁻¹ and days to pods formation.

Pod length

Significant differences were observed for pod length among the genotypes which is supported by the study of Kumhar and Chaudary (2007) who reported significant differences for pod length. Phenotypic variance for pod length is higher than genotypic variance. These findings

are in line with the study of Varma and Garg (2001) who found higher phenotypic variance for pod length than genotypic variance. Pod length of the genotypes ranged between 6.0 cm to 7.82 cm (Figure 2). Genotype NM-51 had maximum pod length (7.82) followed by NM-93 (7.42) and Ramzan (7.25), while minimum pod length (6.0cm) was recorded for Chakwal (Figure 2). Heritability for pod length was 35.71% (Table 1). Arshad *et al.* (2009) have the same type of result and reported low heritability for pod length. At both genotypic and phenotypic levels, the correlation of pod length was positive and significant with 100-grain weight and highly significant but negative with branches plant⁻¹ (Table 2). Significantly negative correlation of pod length with branches plant⁻¹ found. Similar results were also reported by Malik *et al.* (1987) who recorded significant correlation of pod length with branches plant⁻¹. Significant positive association of pod length with 100-grain weight. Bains and Singh (2007) have also reported significant positive correlation of pod length with 100-grain weight.

Grains pod⁻¹

Mean square for grains pod⁻¹ revealed significant differences ($P < 0.05$) among the genotypes (Table 1). Pun and Villareal (1989), Mensah and Oludoya (2007) also reported significant differences among the genotypes for grain pod⁻¹. Grains pod⁻¹ ranged from 7.92 to 9.32 (Figure 2). Maximum grains plant⁻¹ were observed for genotype AEM-96 (9.32) followed by Pak-22 (9.07), NM-28 (8.75) and NM19-19 (8.62), while genotype 6601 showed minimum grains pod⁻¹ (7.92). Broad sense heritability recorded for grains pod⁻¹ was 33.33% (Table 1). Varma and Garg (2001) are in favor of our results who observed low heritability for grains pod⁻¹. Grains pod⁻¹ had negative or positive but non-significant genotypic correlation with all of the traits. Similarly non-significant phenotypic correlations of grains pod⁻¹ with all the traits were observed (Table 2). Negative and non-significant association of grains pod⁻¹ with grain yield plant⁻¹, 100-grain weight and with pod length was observed. These are in agreement with the findings of Malik *et al.* (1987) and Rahman and Hussain (2003) who also found negative and non-significant correlation of grains pod⁻¹ with grain yield plant⁻¹, 100-grain weight and with pod length.

Grain yield plant⁻¹

Significant differences ($P < 0.05$) were observed in genotypes for grain yield plant⁻¹ (Table 1). Similarly, Aslam and Ajmal (2002) and Rahman and Hussain (2003) have also reported significant differences for grain yield plant⁻¹. Grain yield plant⁻¹ ranged from 21.87 to 45.35. Genotype Ramzan showed maximum grain yield

plant⁻¹ (45.35) followed by genotype NM-51 (35.40), while genotype NM19-19 had minimum grain yield plant⁻¹ (Figure 1). Low heritability (33.52%) was recorded for grain yield plant⁻¹ (Table 1). Low heritability (33.52) was recorded for grain yield plant⁻¹. These results are in line with the study of Empig *et al.* (1970) and Anwari and Soehendi (1999) who also reported low heritability for grain yield plant⁻¹. Grain yield plant⁻¹ had positive and significant genotypic correlation with pods plant⁻¹ and days to pod formation while non-significant correlations with all other traits. Grain yield plant⁻¹ showed highly significant phenotypic correlation with pods plant⁻¹, grains plant⁻¹ and days to pods formation and significant correlation with 100-grain weight (Table 2). Our results are supported by Dikshit *et al.* (200), Kumar *et al.* (2004) and Malik *et al.* (1987) who also reported positive and significant correlation of grains yield plant⁻¹ with pods plant⁻¹ and days to pods formation. Grain yield had significantly positive correlation with 100-grain weight. Our results are in agreement with Rahman and Hussain (2003) and Khattak *et al.* (1999) who also reported significant positive correlation of grain yield with 100-grain weight.

100-grain weight (g)

Highly significant differences were observed for 100-grain weight among the genotypes. These results are supported by the findings of Mensah and Oludoya (2007), Dhuppe *et al.* (2005) and Khattak *et al.* (1999) who observed highly significant differences for 100-grain weight. The range of 100-grain weight was 3.22 g to 5.85 g. The maximum 100-grain weight (5.85g) was observed for NM-93 followed by Ramzan (5.07), while minimum 100-grain weight was observed for NM-28 (3.22g) (Table 2b). High heritability (77.17%) was recorded for 100-grain weight. Heritability estimates for 100-grain weight is high. Higher heritability was also reported by Empig *et al.* (1970), Varma and Garg (2001) and Yimram *et al.* (2009) for 100-grain weight. 100-grain weight showed significant and positive genotypic correlation with pod length (0.66) and significant and negative correlation with branches plant⁻¹ (-0.62) (Table 2). Phenotypic correlation of 100-grain weight was positive and highly significant with grain yield plant⁻¹ (0.45) and positive and significant with pods length (0.39). While highly significant but negative correlation was observed with days to flowering, plant height, branches plant⁻¹ and days to maturity (Table 2). Significant positive correlation of 100-grain weight with pod length were found. Our findings are supported by the study of Arshad *et al.* (2009) who stated significant positive correlation of 100-grain weight with pod length. Significant positive association of 100-grain weight with grain yield plant⁻¹. Our results are in line with the findings of Khattak and Haq (1999) and Pun and Villareal (1989) who reported significant positive correlation of 100-grain

weight with grain yield plant⁻¹. Highly significant and negative correlation of 100-grain weight with days to flowering and days to maturity were observed. Rahman and Hussain (2003), and Chaudhary and Rahman (1988) also reported significant negative correlation of 100-grain weight with days to flowering and days to maturity.

REFERENCES

- Acharya S, SK Gupta, BS Jamwal (1993). Evolution of local germplasm of urbeans from Jammu. *Indian J. Pulses Res.* 6: 198–199.
- Anwari M, R Soehendi (1999). Improvement of component technology to increase legume and tuber plants productivity. Malang (Indonesia) BALITKABI. 12(1): 46-51.
- Arshad M, M Aslam, M Irshad (2009). Genetic variability and character association among morphological traits of mungbean genotypes. *J. Agric. Res.* 47(2): 367-70.
- Aslam M, SU Ajmal (2002). Genetic Variability and character association of yield components in mungbean (*Vigna radiata* L. (Wilczek). *Pak. J. Arid Agric.* 5(2): 69-72.
- Bains TS, S Singh (2007). Breeding for ideal plant types in Spring/Summer mungbean. *Acta Hort.* 752: 417-422.
- Burton GW, EH De Vane (1953). Estimating heritability in tall fascue from replicated clonal material. *Agron. J.* 45: 478-481.
- Celal Y (2004). Correlation and path coefficient analysis of seed yield components in the narbon bean (*Vicia narbonensis* L.). *Turk J. Agric.* 28: 371–376
- Chaudhury MA, MM Rahman (1988). Variability and correlations among some yield contributing characters in mungbean (*Vigna radiata* L. Wilczek). *Bangladesh J. Plant Breeding and Genetic* 1(1-2): 62-65.
- Dhuppe MV, IA Madrap, GD Chandankar (2005). Correlation and path analysis in mungbean. *J. Soils and Crops* 15: 84-89.
- Dikshit HK, BB Singh, RP Dua (2002). Genetic variation in mungbean. *Indian J. Pulse. Res.* 15(2): 125-127.
- Empig LT, RM Lantican, PB Escuro (1970). Heritability estimates of quantitative characters in mungbean [*Vigna radiata* (L.) Wilczek]. *Crop Sci.* 10:240-241.
- Imrie BC, KL Butler (2005). An analysis of variability and genotype environment interaction in mungbean (*Vigna radiata* L) in southeastern Queensland. *Australian J. Agric. Res.* 33: 523–30.
- Khan MD, IH Khalil, MA Khan, Ikramullah (2004). Genetic divergence and association for yield and related traits in mash bean. *Sarhad J. Agric.* 20: 555–561.
- Khan MQ, SI Awan and MM Mughal 2005. Estimation of genetic parameters in spring wheat genotypes under rainfed conditions. *Ind. J. Bio. Sci.* 2: 367–370.
- Khattak GS, MA Haq (1999). Genetic variability and correlation studies in mungbean (*Vigna radiata* L. Wilczek). *Suranaree. J. Sci. Tech.* 6(2): 65-69.
- Khattak GSS, M Ashraf, M Irfan (1999). Yield and yield components in mungbean. *J. Sci. and Tech. (Thailand)* 21: 387-391.
- Khattak GSS, S Perrasak, DK Kim (1995). Yield partitioning in high yielding mungbean genotypes. *Kasetsart J. Natural Sci. (Thailand)* 29(4): 494-497.
- Kumar R, R Kant, CB Ojha (2004). Character association and cause of effect analysis for spring season genotypes of mungbean. *Legume Res.* 27: 32-36.
- Kumhar SR and BR Chaudhary 2007. Genetic Diversity and Variability in Mungbean [*Vigna radiata* L.] Wilczek]. *Indian J. Plant Genetic Resources*, 20 (2): 971-974.
- Malik BA, M Tahir, M Zubair, AH Chaudhury (1987). Genetic variability, character correlation and path analysis of yield components in mungbean (*Vigna radiata* L. Wilczek). *Pak. J. Bot.* 19(1): 89-97.
- Mensah JK, RT Oludoya (2007). Performance of mungbean grown in mid-West Nigeria. *American Eurasian J. Agric. Environ. Sci.* 2(6): 696-701.
- MINFAL (2008-09). *Agric. Statistics of Pak.* Ministry of Food, Agric. and Livestock, Economic wing, Islamabad pp. 46-47.
- Pun L, RL Villareal (1989). Inter-relationships and path coefficient of some quantitative traits in mungbean under post-rice growing conditions. *Philippine J. Crop Sci.* 14(3): 91-95.
- Rahman MM, Hussain (2003). Genetic variability, correlation and path analysis in mungbean. *Asian J. Plant Sci.* 2(17): 1209-1211.
- Siddique M (2006). Genetic divergence, association and performance evaluation of different genotypes of mungbean. *Inter. J. Agric. Bio.* 8(6): 793-795.
- Singh RK, Chaudhary BD (1979). *Biometrical methods in quantitative genetics analysis.* Kalyani Pub. Ludhiana and New Dehli India: 304.
- Varma P, DK Grag (2001). Estimation of genetic parameters among a set of mungbean (*Vigna radiata* (L.) Wilczek) genotypes. *Annals of Agri. Res.* Department of Plant Breeding and Genetics, College of Agriculture, Rajasthan Agri. Uni. Beechwal, Bikaner, India. 2(4) 334.
- Yaqoob M, AJ Malik, BA Malik, HU Khan, K Nawab (1997). Path coefficient analysis in some mungbean genotypes under rainfed conditions. *Sarhad J. Agric.* 13(2): 129-133.
- Yimram T, P Somta, P Srinives (2009). Genetic Variation in cultivated mungbean germplasm and its implication in breeding for high yield. Faculty of Agriculture at Kamphaeng Saen, Kas