Legume Research, 38 (2) 2015 : 157-163
Print ISSN:0250-5371 / Online ISSN:0976-0571

AGRICULTURAL RESEARCH COMMUNICATION CENTRE
www.arccjournals.com/www.legumeresearch.in

Genetic variability, heritability, genetic advance and path analysis in mungbean [*Vigna radiata* (L.) Wilczek]

Aparna Raturi, S.K. Singh*, Vinay Sharma[1] and Rakesh Pathak

Central Arid Zone Research Institute,
Jodhpur-342 003, India.

Received: 20-02-2014 Accepted: 10-08-2014 DOI:10.5958/0976-0571.2015.00024.7

ABSTRACT

To utilize mungbean gene pool effectively, studies on genetic variability, heritability and genetic advance were conducted under rain-fed conditions during *kharif* 2009, 2010 and 2011. The data of ten quantitative characters was recorded. The number of pods per plant and seed yield were recorded with significantly higher heritability (>60%), corresponding PCV (>25%) and GCV (>20%) coupled with more than 30% genetic advance. The correlation studies exhibited highly significant and positive association of all the quantitative characters with seed yield except with that of days to 50% flowering. The number of pods per plant had the maximum direct effect followed by plant height and 1000-seed weight indicating their direct contribution towards seed yield. The present study suggests that seed yield and number of pods per plant are greatly influenced by the additive gene effect and greater proposition of variations are heritable for these traits.

Key words: Correlation, Genetic variability, Mungbean, Path analysis, *Vigna radiata*.

INTRODUCTION

Green gram [*Vigna radiata* (L.) Wilczek]- an Asiatic species of pantropical genus *Vigna*, is an important legume crop, widely cultivated in tropics and sub-tropics for human consumption, animal feed, cover-crop and as supplementary crop in cereal based cropping systems. It is thought to be originated in the Indian sub-continent (De Candolle, 1886). The annual world production area of mungbean is about 5.5 million ha of which about 90% is in Asia (Lambrides and Godwin, 2007). India is one of the major producers of mungbean and accounts for 12% of total pulse area of the country (Singh and Ahlawat, 2005). Mungbean enables land to restore fertility by nitrogen fixation to produce reasonable yields of succeeding crops and provides proteinaceous grain and nutritive fodder (El-Hafiez *et al*., 2003; Dash and Pattanayak, 2007).

The major constraints for achieving higher yields are inherently low yielding potential of the varieties that lack genetic variability, inefficient plant type and low yielding potential, absence of suitable ideotypes for different cropping systems, poor harvest index, low level of crop management, more competition with weeds and susceptibility to biotic and abiotic stresses (Sarobol, 1997; Souframanien and Gopalakrishna, 2004; Srinives, 2006). This is probably due to the utilization of only a few selected genotypes of mungbean in cultivar development programme and underutilization of the gene pool of the Indian subcontinent (Gupta *et al*., 2004; Chattopadhyay *et al*., 2010).

The knowledge of genetic variability existing within the different parameters contributing to yield is an important criterion for yield enhancement but in highly self-pollinated crops like mungbean natural variation is narrow resulting in limited scope for selection opportunity. The efficacy of selection depends upon the existence and magnitude of genetic variability for yield and yield contributing traits in the breeding material (Adewale *et al*., 2010). For any yield improvement programme selection of superior parents possessing better heritability and genetic advance for any quantitative trait is an essential prerequisite (Khan *et al*., 2005). Heritability indicates the relative success of selection (Ortiz and Nq, 2000). Heritability in conjunction with genetic advance is more useful than heritability alone in the prediction of resultant effect of selecting the best individual (Johnson *et al*., 1955; Singh *et al*., 2010).

Path coefficient analysis is a standardized partial regression coefficient, which splits the correlation into the measures of direct and indirect effects. It reveals whether the association of these characters with yield is due to their direct effect on yield or it is a consequence of their indirect effect via some other character. If the correlation between yield and

---

*Corresponding author' e-mail: sksingh1111@hotmail.com, [1]Banasthali Vidyapeeth, Banasthali, Rajasthan, India.

other character is due to direct effect of that character, it reflects the true relationship between them (Joshi *et al*., 2005; Yadav *et al*., 2005; Solanki, 2006). The importance of correlation and path coefficient analysis is particularly appreciable when highly heritable characters associated with complex trait like yield are identified and successfully used as criteria for effective selection to achieve high yield (Rani *et al*., 2008). Therefore, identification and utilization of diverse genotypes is essential for breeding new cultivars in a desired direction. To utilize mungbean gene pool effectively, study on genetic variability, heritability and genetic advance analysis in mungbean was carried out in elite set of AVT mungbean genotypes.

MATERIALS AND METHODS

Plant material: Forty-four promising genotypes of mungbean *viz.*, MH-521, RMG-977, AKM-9911, ML-1333, NDM 7-34, COGG -934, PM 04-27, GS 69-99, BGS-9, ML-1405, KM-2262, GM 02-13, PUSA-0771, MH-530, PUSA-0772, SKAM-300, OBGG 11-1, IPM 02-14, PM 04-7, TMB-26, IPM 02-19, NDM 7-31, NDM 5-6, GM-9924, PUSA-0672, KM-2260, RMG-976, ML-1349, HUM-23, PUSA-0671, MH-418, MH-429, COGG-936, PUSA-0571, GM-9925, RGM-34, NVL-1, KM-2241, RMG-267, S-8, K-851, RMG-62 including two check varieties *viz.*, ML-818 (Ch) and Ganga-8 (Ch) of Advanced Varietal Trial (AVT) were procured from All India Coordinated Research Project, Central Arid Zone Research Institute (CAZRI), Jodhpur.

Field experiments: Field experiments were laid out in randomized block design with three replications at Central Research Farm, CAZRI, Jodhpur (27°18' N latitude and 73°01' E longitude) during rainy (*kharif*) season in three consecutive years 2009, 2010 and 2011. Each plot was accommodating three rows of 4 m length with 30 cm and 10 cm distance from rows and plants, respectively. Recommended agronomical practices *viz*., thinning, weeding, uprooting of off-type plants were carried out time to time throughout crop duration. The experiments were carried out strictly under rain-fed conditions and no additional irrigation was provided. A basal dose of 20 kg N and 40 kg of P_2O_5 per hectare was applied during each cropping season.

Morphological parameters: The data of seven morphological characters *viz.*, plant height (cm), number of primary branches, number of secondary branches, number of pods per plant, number of seeds per pod, pod length (cm) and clusters per plant were recorded at maturity, whereas, observations on flowering was recorded for different genotypes as and when they attained 50% flowering stage. The 1000-seed-weight and seed yield per plot were recorded after threshing of the harvested crop.

Estimation of PCV and GCV: The estimation of PCV and GCV was calculated using the formula

$$\mathrm{PCV} = \frac{\sqrt{\sigma_p{}^2}}{\overline{\mathrm{X}}} \text{ x } 100$$

$$\mathrm{GCV} = \frac{\sqrt{\sigma_g{}^2}}{\overline{\mathrm{X}}} \text{ x } 100$$

Where: $ó_p{}^2$= phenotypic variance; $ó_g{}^2$ = genotypic variance; $\overline{\mathrm{X}}$ is the general mean of the character.

Heritability: The heritability in broad sense (h^2_{bs}) was estimated as per the following formula:

$$\text{Heritability broad sense} = \frac{\sigma_g{}^2}{\sigma_p{}^2} \text{ x } 100$$

Where: $ó_p{}^2$= phenotypic variance; $ó_g{}^2$ = genotypic variance.

Expected genetic advance (GA): The expected genetic advance for each character was calculated by the formula:

$$\mathrm{GA} = \mathrm{K}.\ h^2_{bs.}\ ó_p$$

and GA expressed in per cent mean was calculated as-

$$\mathrm{GA}\ (\%) = \frac{\mathrm{GA}}{\overline{\mathrm{X}}} \text{ x } 100$$

Where: h^2_{bs} = Heritability in broad sense; $ó_p$ = Phenotypic standard deviation; K = Selection differential. It is a constant for a given selection intensity (2.06 at 5%);
X= General mean of the character.

Coefficient of variability: The CV for each character was calculated by the formula:

$$\mathrm{CV} = \frac{\text{Error mean Square}}{\text{Population mean}} \mathrm{X}100$$

Correlation coefficient: Phenotypic correlation coefficients among different quantitative and chemical characters were calculated using INDOSTAT software.

Path coefficient analysis: Seed yield per plot was taken as dependent character, its coefficient of correlation with other independent characters was partitioned in to direct and indirect effects by path coefficient analysis. For path analysis, phenotypic correlation were used. Coefficient of determination (R^2) and residual effect were also calculated using formula given by Dewey and Lu (1959).

RESULTS AND DISCUSSION

The estimates of genotypic and phenotypic coefficients of variation, heritability, genetic advance, coefficient of variation and grand mean (three consecutive years 2009, 2010 and 2011) for 10 morphological traits are presented vide Table 1.

Coefficient of variation: The perusal of data revealed that the maximum coefficient of variation (CV) was observed for

TABLE 1: Genetic variability, heritability, genetic advance for 10 yield attributing traits of 44 mungbean genotypes

Character	Grand mean	MSS	GCV	PCV	h^2	GA	CV
Plant height (cm)	48.06	63.76	0.44	16.57	0.00	0.02	16.56
Primary branches (No.)	7.23	1.71	3.95	14.26	0.08	2.25	13.70
Secondary branches(No.)	8.84	13.78	10.53	29.64	0.13	7.70	27.71
Pods/plant (No.)	15.73	99.30***	20.40	26.15	0.61	32.78	16.36
Seeds/pod (No.)	10.58	19.88***	13.23	19.33	0.47	18.66	14.09
Pod length (cm)	7.90	9.03***	11.78	18.39	0.41	15.53	14.13
Clusters/plant (No.)	4.93	4.31***	11.82	25.64	0.21	11.23	22.75
50% flowering (Days)	36.45	20.79***	11.82	14.52	0.66	19.80	8.44
1000- Seed weight (g)	42.56	223.41***	11.33	14.83	0.62	18.39	8.85
Seed yield (kg/ha)	463.15	117263.59***	23.87	30.16	0.63	38.91	18.43

*** Significant at 0.1% level of significance; MSS= mean sum of square, GCV=Genetic coefficient of variation, PCV=Phenotypic coefficient of variation, h^2= Heritability in broad sense, GA= Genetic advance at 5 per cent of mean, CV= coefficient of variation.

number of secondary branches (27.71%) followed by number of clusters per plant (22.75%), seed yield (18.43%), plant height (16.56%) and number of pods per plant (16.36%). Whereas, the CV for all other morphological characters was less than 15 per cent. The least CV was recorded for days to 50% flowering (8.44%).

Genetic improvement of mungbean is limited to evaluation and selection from segregating progenies involving a few repeatedly used parental lines. This has resulted in relatively low genetic variability in mungbean (Yimram *et al*., 2009). The mean values of different morphological traits reported herein are in accordance with earlier mean values reported in mungbean (Abbas *et al*., 2010; Tabasum *et al*., 2010). The CV represents the ratio of the standard deviation to the mean and it is a useful statistical measure for comparing the degree of variation from one data series to another, even if the means are drastically different from each other. Under present study, the CV indicated that there were significant differences not only among the genotypes but also across the environments for observed morphological characters. The perusal of pooled mean CV revealed that the maximum CV of >20% was observed for number of secondary branches followed by number of clusters per plant. Whereas, moderate CV of >15% were recorded for seed yield, plant height and number of pods per plant. While, for all other morphological characters CV was less than 15%. This indicates that morphological characters measured with low and moderate CV are in general were least influenced with the change in environment. In field experimentations, higher CV values are often accepted due to heterogeneous properties of soil and agro-climatic variations.

A number of researchers have reported low to moderate CV in yield attributing traits among different sets of mungbean genotypes i.e., 2.63-12.07% (Abbas *et al*., 2010), 3.42–16.58% (Rahim *et al*., 2010), 4-11.5% (Siddique *et al*., 2006), 1.95–13.98% (Tabasum *et al*., 2010), 3.25–9.98% (Mondal *et al*., 2011). By contrast Hakim (2008) reported significantly higher ranges of CV (15.26-45.61%) among 350 mungbean germplasm accessions for yield related morphological traits.

Analysis of Variance: The combined pooled ANOVA for morphological characters is given in Table 1. The test genotypes exhibited highly significant differences with regard to number of pods per plant, number of seeds per pod, pod length, number of clusters per plant, days to 50% flowering and seed yield. Whereas, the genotypes had significant differences with regard to 1000-seed weight at 1% level of significance (p=0.01). The morphological characters like plant height, number of primary branches per plant, number of secondary branches per plant did not exhibit significant differences in the pooled analysis of all the three consecutive years.

Most of the yield attributing quantitative traits measured under present study have also been reported to have highly significant variations with regard to different sets of mungbean genotypes (Siddique *et al*., 2006; Abbas *et al*., 2008; Abbas *et al*., 2010; Rahim *et al*., 2010; Tantasawat *et al*., 2010; Mondal *et al*., 2011). The morphological characters *viz*., plant height, number of primary branches and number of secondary branches have been recorded with insignificant variation with regard to genotypes. Similarly, insignificant effects of primary branches per plant vis-à-vis genotypes and that of secondary branches per plant are in accordance with earlier reports (Tabasum *et al*. 2010; Arshad *et al*. 2009).

PCV, GCV, h^2 and GA: The estimates of PCV in all the traits were higher than the estimates on corresponding GCV. The higher estimates (>20%) of GCV were recorded for seed yield (23.87%) followed by number of pods per plant (20.4%). Whereas, higher PCV values (>25%) were recorded for seed yield (30.16%), number of secondary branches (29.64%), number of pods per plant (26.15%) and number of clusters per plant (25.64%). The higher values of heritability in broad sense (>60%) were recorded for days to 50% flowering (66%), seed yield (63%), 1000-seed weight (62%) and number of pods per plant (61%). Higher estimates of genetic advance (>30%) were recorded for seed yield and number of pods per plant.

Higher estimates of PCV measured for all the morphological characters than that of corresponding GCV validates the positive influence of environmental factors in expression of different morphological traits under different environments. Higher values (>20%) of GCV for seed yield and number of pods per plant and in case of PCV (>25%) for seed yield, number of secondary branches, number of pods per plant and number of clusters per plant indicate better chances for selection for these traits to be successful. The GCV variation measures the range of genetic variability shown by the plant traits and helps to compare the genetic variability present in various traits. But higher PCV suggests that the environmental factors were influential in expressing these traits. However, with the GCV alone it is not possible to determine the amount of variation that is heritable (Wani and Khan, 2006; Tabasum *et al*., 2010; Pathak *et al*., 2011).

The heritable portion of variation was determined with the aid of heritable estimates. The values of corresponding heritability and GCV differed from trait to trait. Under present study, two morphological traits viz., number of pods per plant and seed yield were recorded with significantly higher heritability (>60%) with corresponding PCV (>25%) and GCV (>20%) coupled with more than 30% genetic advance which validates that these characters are greatly influenced not only by the additive gene effect but also greater proportion of variation is heritable for these quantitative traits.

The heritability which is ratio of both genetic and phenotypic variance is mainly due to additive gene effects in narrow sense (Tyagi and Khan, 2011). Under present investigation heritability was calculated in broad sense that includes both additive as well as non-additive gene effects of heritable nature of these two characters. Whereas, despite of higher GCV and PCV, number of secondary branches and clusters per plant were recorded with relatively lesser heritability portion of variation indicating that heritability is a property not only of a character but also of the population and the environment to which genotypes were subjected to. Therefore, its ultimate value depends on the magnitude of all the component variance in totality and not to be viewed independent of each other to determine heritable portion of variation. Significantly higher estimates of genetic components (GCV, PCV, h^2 and GA) for seeds per pod, pods per plant and seed yield have also been reported by Tabasum *et al.* (2010), Wani and Khan, (2006), Tyagi and Khan, (2011), Adewale *et al*. (2010) and Yimram *et al*. (2009) in different sets of mungbean germplasm.

Interrelationships and path matrices: The interrelationships and path matrices estimated on the basis of values of ten morphological traits consecutively for three years in 44 genotypes of mung bean are presented in Table 2. The data revealed that the seed yield had highly significant and positive correlation with number of pods per plant (0.64), 1000-seed weight (0.50), plant height (0.36), number of primary branches (0.35), number of clusters per plant (0.32), number of seeds per pod (0.21) and pod length (0.19). Whereas, seed yield was recorded with highly significant negative correlation with 50% flowering. Ironically number of secondary branches did not show any significant correlation with seed yield.

The partitioning of phenotypic correlation coefficient of various traits pooled on three year data with seed yield revealed that number of pods per plant had the maximum direct effect (0.55) followed by plant height (0.39)

TABLE 2: Path matrix of seed yield in *Vigna radiata* for 2009, 2010 and 2011

	PH (cm)	PB (No.)	S B (No.)	PPP(No.)	SPP (No.)	PL (cm)	CPP(No.)	DFF	SW(g)
PH (cm)	**0.39**	0.23	0.18	0.03	0.04	0.03	0.07	-0.11	-0.07
PB (No.)	0.05	**0.08**	0.04	0.02	0.01	0.02	0.03	-0.02	0.00
S B (No.)	-0.09	-0.09	**-0.20**	-0.03	-0.04	-0.05	-0.07	0.05	0.02
PPP (No.)	0.04	0.11	0.08	**0.55**	0.30	0.29	0.21	-0.21	0.38
SPP (No.)	-0.02	-0.02	-0.04	-0.10	**-0.18**	-0.09	-0.03	0.06	-0.07
PL (cm)	-0.01	-0.02	-0.03	-0.06	-0.06	**-0.12**	-0.04	0.04	-0.04
CPP (No.)	0.01	0.02	0.01	0.02	0.01	0.01	**0.04**	-0.01	0.01
DFF	0.04	0.04	0.04	0.05	0.04	0.04	0.04	**-0.14**	0.03
SW (g)	-0.04	0.00	-0.02	0.16	0.09	0.08	0.07	-0.05	**0.24**
r^2 with SY(kg/ha)	0.36	0.35	0.05	0.64	0.21	0.19	0.32	-0.40	0.50
Partial R^2	0.14	0.03	-0.01	0.35	-0.04	-0.02	0.01	0.05	0.12

R square = 0.63, Residual effect = 0.61

PH: Plant height; PB: Number of primary branches; SB: Number of secondary branches; PPP: Number of pods/plant; SPP: Number of seeds/pod; PL: Pod length; CPP: Number of clusters/plant; DFF: Days to 50% flowering; SW: 1000-seed weight; SY: Seed yield and 1000-seed weight (0.24). Whereas, 1000-seed weight (0.38), number of seeds per pods (0.30), pod length (0.29), number of clusters per plant (0.21), number of primary branches (0.11), number of secondary branches (0.08) and plant height (0.04) influenced seed yield via number of pods per plant indirectly. Whereas, days to 50% flowering showed negative effect on seed yield via number of pods per plant. The number of primary branches (0.23) and number of secondary branches (0.18) were major traits that influenced seed yield via plant height indirectly. The number of pods per plant (0.16), number of seeds per pod (0.09), pod length (0.08) and number of clusters per plant (0.07) influenced seed yield indirectly via 1000-seed weight.

The correlation of all the morphological characters studied was highly significant and positive with seed yield except with that of days to 50% flowering. Out of all the 10 morphological traits number of pods per plant followed by plant height and 1000-seed weight mainly contributed directly as evident from partial R^2 values of 0.35, 0.14 and 0.12, respectively.

The information on correlation of the quantitative characters like seed yield with related traits is the pre-requisite to form an effective selection strategy aimed at its improvement. Perusal of interrelationship correlation matrix of three consecutive years (environments) revealed that the seed yield had highly significant and positive correlation with number of pods per plant, 1000-seed weight, plant height, number of primary branches, number of clusters per plant, number of seeds per pod and pod length. This indicates that mungbean genotypes with taller plants, more number of (primary branches, clusters per plant, seeds per pod, pods per plant) with longer pod lengths and more 1000-seed weights have greater possibilities of producing higher yields.

Nevertheless, highly significant negative correlation of days to 50% flowering *i.e.*, early flowering may not always demonstrate higher yield in mungbean genotypes tested. Whereas, number of secondary branches did not show any significant correlation with the seed yield suggests that both the characters assort independent to each other and may contribute indirectly via other quantitative traits. Positive correlation occurs due to the changes of gene supplying precursors. On the other hand negative correlations arise due to competition among traits for common precursors which are having restricted supply (Madhur and Jinks, 1994).

A number of researchers have established correlation of various quantitative traits with seed yield facilitating indirect selection strategies for improvement in mungbean. Siddique *et al*. (2006) reported significantly positive correlation of number of seeds per pod and 1000-seed weight while significant negative correlation with pods per plant and days to 50% flowering with seed yield in eight genotypes of mungbean. Agarwal *et al*. (2001) elaborated the fact that positive correlation with seed yield and clusters per plant was consistent. The positive correlation of seed yield with pods per plant, biological yield, plant height and seed weight was additionally supported by Hamdi *et al*. (2003) and Luthra and Sharma, (1990). High positive correlation of pods per plant with seed yield is attributed to the sink strength (Tyagi and Khan, 2011). While Rahim *et al*. (2010) reported highly significant positive correlation and positive correlation of pod length and number of seeds per pod with seed yield in 26 mungbean genotypes.

Knowledge of correlation alone is often misleading as the correlation observed may not be always true. Two characters may show correlation just because they are correlated via a common third character. In such cases, it becomes necessary to study a method which takes into account the casual relationship between the variables in addition to the degree of such relationship. Therefore, Path coefficient analysis measures the direct influence of one variable upon the other and permits separation of correlation coefficient into components of direct and indirect effects. Partitioning of total correlation into direct and indirect effects provides actual information on contribution of characters and thus forms the basis of selection to improve the yield (Tyagi and Khan, 2011).

Path coefficient measured vide Table 2 of seed yield revealed that the number of pods per plant had the maximum direct effect followed by plant height and 1000-seed weight. It means a slight increase in any of these traits may directly contribute towards seed yield. Positive direct effect of pods per plant on seed yield via indirect positive effect through 1000-seed weight, number of seeds per pod, pod length, number of clusters per plant, number of primary branches, number of secondary branches and plant height. Our findings are in accordance with previous reports (Rao *et al*., 2006; Makeen *et al*., 2007; Hakim, 2008; Tabasum *et al*., 2010 and Mondal *et al*., 2011).

Positive direct effect of plant height on seed yield via indirect positive effects through number of primary and secondary branches observed in this study have also been reported by Solanki (2006); Yadav *et al*. (2005); Joshi *et al*. (2005) and Tyagi and Khan (2011). Positive direct effect of 1000-seed weight via indirect positive effects through pods per plant, number of seeds per pod, pod length and number of clusters per plant influenced seed yield indirectly reported here in have also been observed by Mondal *et al*. (2011) and Biradar

(2007). The residual effect of 0.61 was observed under present study indicating the contribution of component characters was 39% and the rest 61% was the contribution of other factors. The present study suggests that seed yield and number of pods per plant are greatly influenced by the additive gene effect and greater proposition of variations are heritable.

REFERENCES

Abbas, G., Asghar, M.J., Shah, T.M. and Atta, B.M. (2010). Genetic diversity in mungbean (*V. radiata* (L.) Wilczek] germplasm. *Pak. J. Bot.* **42**:3485-3495.

Abbas, G., Manzoor, B., Mahmood, T., Siddique, M. and Ahsanul Haq, M. (2008). Stability analysis for seed yield in mungbean [*Vigna radiata* (L.)Wilczek]. *J. Agri. Res.* **46**:223-228.

Adewale, B.D., Okonji, C., Oyekanmi, A.A., Akintobi, D.A.C. and Aremu, C.O. (2010). Genotypic variability and stability of some grain yield components of Cowpea. *African J. Agri. Res.* **5**:874-880.

Agarwal, A.P., Patil, S.A. and Satimath, P.M. (2001). Variability, heritability and genetic advance of some quantitative characters over the season in soybean. *Madras J. Agri.* **88:**1-3.

Arshad, M., Aslam, M. and Irshad, M. (2009). Genetic variability and character association among morphological traits of mungbean, *Vigna radiata* L. Wilczek genotypes. *J. Agri. Res.* **47**:121-126.

Biradar, K. (2007). Genetic studies in green gram and association analysis. *Karnataka J. Agri. Sci.* **20**:843-844.

Chattopadhyay, N., Ghosh, T., Sinha, S., Chattopadhyay, K., Karmakar, P. and Ray, B. (2010). Polysaccharides from *Turbinaria conoides*: Structural features and antioxidant capacity. *Food Chem.* **118**:823-829.

Dash, D. and Pattanayak, S. K. (2007). Effect of seed treatment with cobalt on nodulation, growth and yield of green gram crop through improving biological nitrogen fixation. *J. Soils Crops.* **17**:24-29.

De Candolle, A. (1886). *Origin of Cultivated Plants*. Hafner Publishing, New York.

Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* **51**:515-518.

El Hafiez, A., Zohry, A. and El, Aal AINA. (2003). Soil morphological features and competition of intercropping mung bean with sugarcane in upper Egypt. *Egyptian J. Agri. Res.*. **81**:1-14.

Gupta, S., Kumar, S. and Singh, B.B. (2004). Relative genetic contributions of ancestral lines to Indian mungbean cultivars based on coefficient of parentage analysis. *Indian J. Genet*. **64**:299-302.

Hakim, L. (2008). Variability and correlation of agronomic characters of mungbean germplasm and their utilization for variety improvement programme. *Indonesian J. Agri. Sci.* **9**:24-28.

Hamdi, A., El-Ghareib, A.A., Shafey, S.A. and Ibrahim, M.A.M. (2003). Direct and indirect relationships among lentil characters. *J. Agri. Res.*. **81**:224-229.

Johnson, H.F., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybean. *Agron. J.* **47**:314-318.

Joshi, M., Singh, S. and Singh, I. (2005). Variability and association studies in lentil (*Lens culinaris* Medik). *Indian J. Pulses Res.* **18**:144-146.

Khan, M.Q., Awan, S.I. and Mughal, M.M. (2005). Estimation of genetic parameters in spring wheat genotypes under rainfed conditions. *Indus J. Biol. Sci.* **2**:367–370.

Lambrides, C.J. and Godwin, I. (2007). Mungbean. In: Genome Mapping and Molecular Breeding in Plants, Volume 3: Pulses, sugar and tuber crops (Kole, C. eds), Springer, Berlin and Heidelberg, pp. 69–90.

Luthra, S.K. and Sharma, P.C. (1990). Correlation and path analysis in lentils. *Lens Newsletter*. **17**:5-8.

Madhur, J. and Jinks, C. (1994). Study of different days of sowing on yield parameters of green gram (*V. mungo*). *Agri. News*. **12**:53-56.

Makeen, K., Abrahim, G., Jan, A. and Singh, A.K. (2007). Genetic variability and correlations studies on yield and its components in mungbean (*Vigna radiata* (L.) Wilczek). *J. Agron.* **6**:216-218.

Mondal, M.M.A., Hakim, M.A., Juraimi, A.S., Azad, M.A.K. and Karim, M.R. (2011). Contribution of morpho-physiological attributes in determining the yield of mungbean. *African J. Biotechnol.* **10**:12897-12904.

Ortiz, R. and Nq, N.Q. (2000). Genotype x Environment interaction and its analysis in germplasm characterization and evaluation. In: Genotype x Environment interaction analysis of IITA mandate crops in sub–Saharan Africa. (Ekanayake, I.J., Ortiz, R. eds). IITA, Ibadan. pp 32-40.

Pathak, R., Singh, M. and Henry, A. (2011). Genetic diversity and interrelationship among clusterbean (*Cyamopsis tetragonoloba*) genotypes for qualitative traits. *Indian J Agri. Sci.* **81**:402-406.

Rahim M.A., Mia, A.A., Mahmud, F., Zeba N. and Afrin, K.S. (2010). Genetic variability, character association and genetic divergence in mungbean (*Vigna radiata* L. Wilczek). *Plant Omics J.* **3**:1-6.

Rani, C.I., Veeraragavathatham, D. and Sanjutha, S. (2008). Studies on correlation and path coefficient analysis on yield attributes in root knot nematode resistant F1 hybrids of tomato. *J. App. Sci. Res.* **4**:287-295.

Rao, G.R., Rao, Y.K. and Rao, C.M. (2006). Genetic divergence in mungbean. *Indian J. Pulses Res.* **19**:61-63.

Sarobol, N. (1997). Mungbean: Past, present and future. In: Proceedings of the National Mungbean Research Conference VII held at Golden Grand Hotel, Thailand, 2-4 December 1997, pp: 1-20.

Siddique, M., Malik, M.F.A. and Awan, S.I. (2006). Genetic divergence, association and performance evaluation of different genotypes of mungbean (*Vigna radiata*). *Internatl J. Agri. Biol.* **8**:793-795.

Singh, D.P. and Ahlawat, I.P.S. (2005). Greengram (*Vigna radiata*) and blackgram (*Vigna mungo*) improvement in India past, present and future prospects. *Indian J. Agri. Sci.* **75**:243–250.

Singh, M., Singh, T.P., Sharma, S.K. and Thakur, H.L. (2010). Influence of cropping system on combining ability and gene action for grain yield and its components in black gram (*Vigna mungo*). *Indian J. Agri. Sci.* **73**:356-357.

Solanki, Y.S. (2006). Comparision of correlations and path coefficients under environments in lentil (*Lens culinaris* Medik). *Crop Improv.* **33**:70-73.

Souframanien, J. and Gopalakrishnan, T. (2004) A comparative analysis of genetic diversity in black gram genotypes using RAPD and ISSR markers. *Theoretical Appl. Genet*. **109**:1687-1693.

Srinives, P. (2006). Research direction and legume crop development. In: Proceedings of the National Legume Crop Research Conference I, held at Rimkok Resort Hotel, Chiang Rai, Thailand, August 2006, pp: 389.

Tabasum, A., Saleem, M. and Aziz, I. (2010). Genetic variability, trait association and path analysis of yield and yield components in mungbean (*Vigna radiata* (L.) Wilczek). *Pak. J. Bot.* **42**:3915-3924.

Tantasawat, P., Trongchuen, J., Prajongjai, T., Thongpae, T., Petkhum, C., Seehalak, W. and Machikowa T. (2010). Variety identification and genetic relationships of mungbean and black gram in Thailand based on morphological characters and ISSR analysis. *African J. Biotechnol.* **9**:4452-4464.

Tyagi, S.D. and Khan, M.H. (2011). Correlation, path-coefficient and genetic diversity in lentil (*Lens culinaris* Medik) under rainfed conditions. *Internatl Res. J. Plant Sci.* **2**:191-200.

Wani, M.R. and Khan, S. (2006). Estimates of genetic variability in mutated populations and the scope of selection for yield attributes in *Vigna radiata* (L.) Wilczek. *Egyptian J. Biol.* **8**:1-6.

Yadav, S.S., Phogat, D.S., Solanki, I.S. and Malik, B.P.S. (2005). Genetic divergence under two environments in lentil. *Indian J. Pulses Res.* **18**:150-152.

Yimram, T., Somta, P. and Srinives, P. (2009). Genetic variation in cultivated mungbean germplasm and its implication in breeding for high yield. *Field Crops Res.* **112**:260-266.