JOURNAL OF AGRICULTURE AND BASIC SCIENCE
ISSN Online: 2518-4210
http://www.jabsjournal.com/

Full Length Research Article

Association and path coefficient analysis of different morphological parameters and yield components in mungbean genotypes

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Abstract

Globally mungbean is a very important legume crop having multiple unexploited benefits over other crops. There is a need for improvement in germplasm of this crop for full exploitation of its potential. Keeping in view the importance of this crop current research experiment was launched. Data for different morphological and yield related components were collected during field evaluation of the genotypes. Genotypic correlation coefficients (G_r) and phenotypic correlation coefficients (P_r), phenotypic coefficients of variations (PCV) and genotypic coefficients of variations (GCV) and path coefficient analysis were conducted for analysis of data. Plant height (PH), number of primary branches (NPB), number of secondary branches (NSB), clusters per plant (CPP), number of pods per cluster (NPPC), number of chambers per pod (NCPP), seeds per pod (SPP), 100 seed weight (100SW) and seed yield per plant(SYPP) showed moderate GCV and PCV values. PH, CPP, NPPC, NCPP, SPP, 100SW and SYPP showed high heritability percentage while NPB and NSB showed moderate heritability percentage. PH, NPB, NSB, CPP, NPPC, NCPP and 100SW have positive genotypic and phenotypic correlation with SYPP. PH, NPB, NPPC and 100SW had negative direct effect on SYPP. Positive direct effects of NPB and NCPP on SYPP were observed.

Keywords: Legumes, genotypic correlation coefficients (G_r) and phenotypic correlation coefficients (P_r), path analysis, morphological standards and yield components

Introduction

Mungbean (*Vigna radiate* L.) is a useful legume crop of Pakistan (Sadiq *et al.*, 2005) and is also widely cultivated in India, Bangladesh, Thailand and Sri Lanka. In Pakistan, it is grown as a supplementary and cash crop on 208.5 thousand hectares with an average yield of 546 kg per ha. In Southern Punjab mungbean is grown in both kharif and spring seasons while in Sindh as kharif crop. Kharif crop grows in short period of time than spring crop. High mungbean producing districts are Layyah, Mianwali, Rawalpindi and Bakhar. In Punjab it is mostly cultivated on marginal lands whereas, in Khyber Pakhtunkhwa it is grown as a major pulse crop and its 75% cultivation is in wheat crop rotation. Comparative to 2009, in 2010-11, there was reduction up to 25.25% and 35% in area and production respectively (Anonymous, 2010-11).

Extending or exploring the genetic variability for various traits of interest and developing new genetically improved mungbean cultivars are the dire demand of the day. To improve the yield per unit area, newly developed cultivars must have outstanding performance and uniform maturity. Mungbean being leguminous crop improves soil fertility by fixing the atmospheric nitrogen into nitrates and has remarkably high protein contents *i.e.* 22-24% (Asim *et al.*, 2006).

Any breeding program with aim to increase yield should consider correlation between yield and its attributes through estimation of genotypic and phenotypic correlation. This information helps in formulating selection indices to aid in selection programs.

Estimation of heritability of characters directly affecting yield provides clues on possible improvement and breeding success (Makeen *et al* 2007). Simultaneous estimation of the information on both heritability and correlations among characters will be crucial for obtaining appropriate breeding strategies to achieve breeding goals (Painawadee *et al.*, 2006). Quantification of genetic variability is most suitable biometrical tool to figure out the extent of heritability, genetic coefficient of variation and response to selection using suitable selection intensity for desired traits. Objectives of this study were to assess the extent of genetic variability for quantitative traits, to study the magnitude and nature of correlation between mungbean seed yield and its various components and to determine the contributions of yield components towards seed yield.

Materials and Methods

The seeds of mungbean genotypes (M-2004, AUM-24, AUM-9, M-2002, M-2001, AUM-18, AUM-38, NM-28, AUM-27, M-2006, NM-98, NM-54, 6601, NM21-25, NM20-21, NM-96, NM-2006, NM-51, AUM-28, AUM-31, AUM-21, AUM-6375, AUM-19, and NM-92) collected from different research institutes were sown in research area reserved for the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. Triplicated randomized complete block design was followed with plant to plantand row to row distances 30 cm and 60 cm respectively. The responses of genotypes were assessed on the basis of different morphological standards like plant height (PH), number of primary branches (PB), number of secondary branches (SB), number of clusters per plant (C/P), number of pods per cluster (P/C), number of chambers per pod (Ch/P), number of seeds per pod (S/P), 100 seed weight (100SW), and seed yield per plant (SY/P).

Statistical Analysis

Analysis of variance (ANOVA) was computed by following (Steel *et al.*, 1997). The values of correlations among various characters were determined by using formulas used by (Kown and Torrie, 1964). Genotypic and phenotypic coefficient of variation was measured according to (Singh and Chaudhary, 1985). Path analysis was performed in accordance with (Wright, 1921); (Dewey and Lu,1959). Heritability was calculated by following (Burton and Devan, 1953).

Results and Discussions

1. Plant height (PH; cm)

ANOVA revealed highly significant difference in mungbean genotypes (Table-1). The maximum mean value of PH was observed in case ofM-2004 (66.66 cm) followed by NM-98 (65.00 cm) whereas, the minimum mean value was shown byNM-2125 (41.00 cm). Plant Height showed moderate genotypic and phenotypic coefficient of variability i.e. 13.48% and 17.78% respectively and high heritability percentage i.e. 60.54 (Table-2). The results were in agreement with (Ram *et al.*, 1997), (Islam *et al.*,1999), (Gill *et al.*,1995), (Gul *et al.*, 2008) and (Sarwar *et al.*,2010). They reported high level of genetic variability among mungbean germplasm regarding plant height. The results were in contradiction with the findings of (Loganathan *et al.*, 2001) who reported low heritability for plant height. Presence of significant genetic variability in plant height at allelic level reflects the presence of chances for improvement.

PH has positive phenotypic and genotypic correlation with CPP, NPPC, NCPP, 100SW and SYPP while has negative genotypic and phenotypic correlation with NSB and SPP. PH has negative genotypic and positive phenotypic correlation with NPB (Table-3). The findings were in accordance to those of (Hassan *et al.*, 2003).

PH had negative direct effect on SYPP. It showed negative indirect effects via NCPP, NPPC, NCPP and 100SW. However, NPB and NSB and SPP had positive indirect effects on SYPP (Table-4). The results are in line with the findings of (Ajmal and Hassan, 2002), (Rasheed *et al.*, 2008) and (Tabasum *et al.*, 2010) while differed from (Pun *et al.*, 1989), (9Kalpande *et al.*, 1997), (Atta et al., 2008) and (Younis *et al.*, 2008) who reported positive direct effect of this trait on seed yields.

2. Number of Primary branches (NPB)

Analysis of variance for NPB revealed non-significant differences in studied genotypes (Table-1). It showed moderate GCV (14.58%) and PCV (31.32%) values with 21.66% heritability and 2.90% CV (Table-2). The results were in line with those of (Malik *et al.*, 1987) and (Younis *et al.*, 2008). These results are in contrast to those of Ghafoor *et al.*, *(*2000), Khan *et al.*, (2001) and Begum *et al.*, *(*2012).

Primary branches were having positive genotypic and phenotypic correlation with NSB, NCPP, SPP, 100SW and SYPP whereas, it had negative phenotypic and genotypic correlation with CPP, and NPPC. It had negative genotypic correlation and positive phenotypic correlation with PH (Table-3). These findings were in accordance with findings of (Pandey *et al.*, 2007) and (Atta *et al.*, 2008) but (Arshad *et al.*, 2004) reported the negative correlation between SYPP and NPB.

Direct and indirect effect matrix showed positive direct effect of NPB on SYPP. However, this trait exhibited negative indirect effect through PH, CPP and NPPC on SYPP. Positive indirect effect was found in case of NSB, NCPP, SPP and 100SW(Table-4). The results were in accordance with the findings of (Tabasum *et al.*, 2010) while differed from (Pun *et al.*, 1989), (Kalpande *et al.*, 1997), (Atta et al., 2008) and (Younis *et al.*,2008) who reported positive direct effect of this trait on SYPP.

3. Numbers of Secondary branches (NSB)

Highly significant differences among all the genotypes regarding numbers of secondary branches were observed (Table-1). The maximum mean value for this trait was shown by AUM-24 (7.33). The minimum number of secondary branches was observed in case of M-2001 (2.66). Moderate heritability percentage (45.72) was recorded with coefficient of variability of 4.01 %. It showed moderate GCV (24.98%) and moderate PCV (36.94%) values (Table-2). Khan *et al., (*2001), Atta *et al., (*2008), Younis *et al., (*2008), Tabasum *et al., (*2010) and Begum *et al., (*2012) reported same results while the results differed from (Ghaviami and Rezai., 2000) who reported sufficient variability. The results were in contrast to (Khan *et al.,* 1985), who reported high heritability percentage.

NSB had positive phenotypic and genotypic correlation with SPP, 100SW, SYPP, NPPC, and NPB. NSB has negative genotypic correlation and positive phenotypic correlation with CPP. NSB were having negative genotypic and phenotypic correlation with NCPP and PH (Table-3). Thesefindings certified the results of (Atta *et al.*, 2008) who reported that number of secondary branches were strongly and positively correlated with pods per plant and primary branches at genotypic level.

NSB had negative direct effect on SYPP, however this trait showed positive indirect effects through CPP, NCPP and PH. Negative indirect effects were observed through NPPC, NPB, SPP and 100SW(Table-4). The results were in accordance with the results of (Pun *et al.,*1989), (Kalpande *et al.,* 1997), (Atta *et al.*,2008), (Younis *et al.,* (2008) and (Tabasum *et al.*, 2010).

4. Clusters per plant (CPP)

Findingsdepicted the highly significant difference among all studied genotypes for CPP (Table-1). Genotype M-2006 produced maximum number of cluster per plant (17.00) whereas, minimum mean value of clusters per plant was observed in case of genotype NM-92 (6.33).It showed moderate GCV (22.67%) and PCV (23.41%) values and high heritability percentage (93.74). These findings were in accordance with (Sarwar *et al.*, 2010) and (Khajudparn & Tantasawat, 2011) and differed with those reported by (Ram *et al.,* 1997) and (Longanthan *et al.,* 2001) who observed lower heritability for this character.

Clusters per plant were having positive genotypic and phenotypic correlation with NPPC, PH, 100SW and SYPP while were having negative genotypic and phenotypic correlation with primary branches, chambers per pod and seeds per pod (Table-3). (Saeed *et al.*, 2007) reported same results. (Haritha and Sekhar, 2002) reported positive and highly significant correlation of CPP and SYPP.

CPP exhibited positive indirect effect through NPBand NSB, NCPP and SPP. It revealed a positive indirect effect through NPPC, PH and 100SW (Table-4). The results differed with (Malik *et al.*, 1987), (Yaqoob *et al.*,1997), (Ram *et al.*,1997) and (Saeed *et al.,* 2007) while these findings validated the results of Khan *et al.*, (1985), Pun *et al.*, (1989), Haritha and Sekhar, (2002).

5. Number of pods per cluster (NPPC)

Analysis of variance for NPPCelaborated highly significant differences among all the studiedmungbean genotypes (Table-1). AUM-6375 produced maximum NPPC (15.00). The minimum mean value of NPPC was observed for NM-2021 (8.00). It showed moderate GCV (16.83%) and PCV (19.21%) values with high heritability percentage (93.74%). The results were in agreement with (Khan *et al.*, 1985), (Reddy *et al.,* 1991), (Ghafoor *et al.*, 2000), (Khan *et al.*, 2001) and Sarwar *et al.*, 2010).

Number of pods per cluster were observed to have positive genotypic and phenotypic correlation with NSB, PH, 100SW and SYPP whereas, it had negative genotypic and phenotypic correlation with NPB, NCPP and SPP (Table-3). The results were in accordance with (Haritha and Sekhar, 2002) and (Saeed *et al.*, 2007) but in contrast to results of (Tabasum *et al.*, 2010) who observed that NPPCwere correlated significantly and negatively with SYPP. NPPC showed negative direct effect on SYPP. NPPC had positive indirect effects through NPB, CPP and SPP while negative indirect effects through NCPP, NSB, PH and 100SW (Table-4).

6. Number of chambers per pod (NCPP)

Analysis of variance for number of chambers per pod revealed highly significant difference among 24 genotypes. The maximum mean value of number of chambers per pod was observed for M-2001 (15.66) while the minimum mean value of number of chambers per pod was observed for NM-92 (6.33). It showed moderate GCV (23.59 %), PCV (26.75%) and high heritability percentage (77.79 %). The results were in agreements with (Laxmi and Bhattacharya, 2006).

Chambers per pod had negative genotypic and genotypic correlation with clusters per pod, pods per cluster, secondary branches whereas, it had positive genotypic and phenotypic correlation with all other traits (Table-3). (Ghosh and Panda, 2006) reported that NCPP was positively associated with number of pods per plant and SYPP.

Positive direct effect of NCPP on SYPP was observed in present study. There were indirect negative effects through clusters per plant, secondary branches and pods per cluster; however, NPB, SPP, PH and 100SW had positive indirect effects (Table-4). The results were in agreement with (Gill *et al.*,1995), (Ram, 1997), (Yaqoob *et al*., 1997) and (Sharma, 1999).

7. Seeds per pod (SPP)

Highly significant differences among all the genotypes of mungbean were revealed (Table-1). The maximum mean value of seeds per pod was observed for AUM-6375 (11.33) followed by NM-92 (11.00) while the minimum mean value of seeds per pod was observed for NM-28 (2.00). It showed moderate GCV (34.31%) and PCV (45.69%) values but high heritability percentage (56.39%).The results were in accordance with (Laxmi and Bhattacharya, 2006), (Islam *et al.*, 1999), (Sharma., 1999), (Loganathan *et al.*, 2001), and (Begum *et al.*,2012).

SPP were noted to have negative phenotypic and genotypic correlation coefficients with clusters per plant, pods per cluster and plant height but had positive phenotypic and genotypic correlation with NPB, NSB, NCPP, 100SW and SYPP (Table-3). These results were in accordance with the study of (Ghosh and Panda, 2006) but contradict to the study of (Gul *et al.*, 2008) who observed that PH at maturity was significantly and positively correlated with SPP.

SPP had positive direct effect on SYPP. NPB, NSB, NCPP and 100SW had positive indirect effects while PH, CPP and NPPC had negative indirect effects (Table-4). The results were in agreement with (Khan *et al.*, 1985) and (Pun *et al.*,1989) but differed from (Malik *et al.*,1987) and (Tabasum *et al.*, 2010).

8. 100 seed weight (100SW)

Analysis of variance for 100 seed weight revealed highly significant difference among genotypes (Table-1). Maximum mean value of 100 seed weight was observed for NM-2006 (8.1g) while the minimum mean value was observed for M-2006 (3.30g). It showed moderate GCV (22.44%) and moderate PCV (22.53%) with heritability percentage i.e. 99.23 (Table-2). The results were verified the study of (Reddy *et al.*, 1991), (Sharma, 1999), (Gul *et al.*, 2008) and (Rasheed *et al.*, 2008).

Hundred (100) seed weight were observed to have positive phenotypic and genotypic correlation with clusters per plant, pods per cluster, primary branches, secondary branches, chambers per pod, SPP, PH and SYPP (Table-3). These findingsadvocated the presentation of (Arshad *et al.*, 2004), (Atta *et al.*, 2008) and opposed findings of (Hassan *et al.*, 2003).

Negative direct effect and indirect effects through all the traits was exerted by 100 seed weight (Table-4). These findings validated the results of (Rasheed *et al.*, 2008) while differed from (Arshad *et al.*, 2004), Younis *et al.*, 2008) and (Tabasum *et al.*, 2010) who found positive direct effect of this trait on SYPP.

9. Seed yield per plant (SYPP)

Analysis of variance for seed yield per plant revealed highly significant variation in all studied genotypes of mungbean (Table-1). The maximum mean value of seed yield per plant was observed for NM-2006 (25.33g) which is at par with M-2004 (22.33g) while the minimum mean value was observed for NM-92 (10.66g). It showed moderate GCV (24.42%) and PCV (25.84%) values with high heritability percentage i.e. 89.28% (Table-2).The results were in line with results of (Gul *et al.*,2008), (Ram *etal.*,1997), (Reddy *et al.*, 1991) and Loganathan *et al.*, 2001).

SYPP was found to have positive genotypic and phenotypic correlation with CPP, NPPC, NPB, NSB, NCPP, SPP, PH and 100SW (Table-3). The results were in line to those presented by (Arshad *et al.*, 2004, (Ghosh and Panda, 2006) (Pandey *et al.*, 2007) and (Atta *et al.*, 2008).

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Table 1. Analysis of variance

SOV	Df	PH	NPB	NSB	CPP	NPPC	NCPP	SPP	100SW	SYPP
Rep/Block	2	34.125	2.097	2.680	0.125	0.264	3.014	0.0139	0.0263	2.63
Genotypes	23	178.406**	1.55ns	5.724**	22.38**	11.90**	19.0121**	20.577**	5.44**	48.64**
Error	46	31.835	1.344	1.622	0.487	1.090	1.652	4.2168	0.0139	1.8714
Total	71									

Plant height (PH), number of primary branches (NPB), number of secondary branches (NSB), clusters per plant (CPP), number of pods per cluster (NPPC), number of chambers per pod (NCPP), seeds per pod (SPP), 100 seed weight (100SW) and seed yield per plant (SYPP)

Table 2. Heritability, Coefficient of variation, genotypic coefficient of variation and phenotypic coefficient of variation of different traits

	PH	NPB	NSB	CPP	NPPC	NCPP	SPP	100SW	SYPP
H^2 (%)	60.54%	21.66	45.72	93.74	93.73	77.79	56.39	99.23	89.28
CV (%)	10.89%	2.90	4.01	2.20	5.26	4.05	6.47	0.37	4.31
GCV (%)	13.48%	14.58	24.98	22.67	16.83	23.59	34.31	22.44	24.42
PCV (%)	17.78%	31.32	36.94	23.41	19.21	26.75	45.69	22.53	25.84

Plant height (PH), number of primary branches (NPB), number of secondary branches (NSB), clusters per plant (CPP), number of pods per cluster (NPPC), number of chambers per pod (NCPP), seeds per pod (SPP), 100 seed weight (100SW) and seed yield per plant (SYPP)

Table 3. genotypic and phenotypic correlation coefficients of different traits

		CPP	NPPC	NPB	NSB	NCPP	SPP	PH	100SW	SYPP
CPP	Rg	1								
	Rp	1								
NPPC	Rg	0.8185**	1							
	Rp	0.7734**	1							
NPB	Rg	-0.3373	-0.2415	1						
	Rp	-0.1018	-0.1193	1						
NSB	Rg	-0.0479	0.1106	0.3926	1					
	Rp	0.0004	0.0862	0.3173	1					
NCPP	Rg	-0.2879	-0.2571	0.2399	-0.2245	1				
	Rp	-0.2252	-0.1069	0.0411	-0.1889	1				
SPP	Rg	-0.3598	-0.0575	0.2417	0.1664	0.1052	1			
	Rp	-0.2676	-0.0132	0.1152	0.0051	0.0266	1			
PH	Rg	0.5445**	0.4645*	-0.1011*	-0.1809*	0.2162*	-0.3276*	1		
	Rp	0.4175*	0.3227*	0.0228*	-0.1049*	0.1533*	-0.2609*	1		
100SW	Rg	0.0586	0.0269	0.4926*	0.1094*	0.2411*	0.0229*	0.1492*	1	
	Rp	0.0580	0.0258	0.2088	0.0757	0.224	0.0218	0.1112	1	
SYPP	Rg	0.3387	0.1864	0.7896**	0.303**	0.07**	0.0751**	0.1432**	0.5591**	1
	Rp	0.2963	0.1235	0.2911	0.1975	0.064	0.0529	0.0991	0.5311**	1

Plant height (PH), number of primary branches (NPB), number of secondary branches (NSB), clusters per plant (CPP), number of pods per cluster (NPPC), number of chambers per pod (NCPP), seeds per pod (SPP), 100 seed weight (100SW) and seed yield per plant (SYPP)

Table 4. Direct and Indirect values of Path coefficient analysis

Traits	CPP	NPPC	NPB	NSB	NCPP	SPP	PH	100SW
CPP	**1.2793**	-0.4055	-0.3487	0.0017	-0.0211	-0.0711	-0.0956	-0.0002
NPPC	1.0471	**-0.4954**	-0.2497	-0.0038	-0.4371	-0.0114	-0.0815	-0.0001
NPB	-0.4371	0.1196	**1.0338**	-0.0136	0.0176	0.0478	0.0177	-0.002
NSB	-0.0613	-0.0548	0.4059	**-0.0346**	-0.0165	0.0329	0.0318	-0.0004
NCPP	-0.3684	0.1274	0.2480	0.0078	**0.0734**	0.0208	-0.4603	-0.001
SPP	-0.4603	0.0285	0.2499	-0.0058	0.0077	**0.1976**	0.0575	-0.0001
PH	0.6965	-0.2301	-0.1045	0.0063	0.0159	-0.0647	**-0.1755**	-6.000
100SW	0.075	-0.0133	0.5092	-0.0038	0.0177	0.0045	-0.0262	**-0.004**

Plant height (PH), number of primary branches (NPB), number of secondary branches (NSB), clusters per plant (CPP), number of pods per cluster (NPPC), number of chambers per pod (NCPP), seeds per pod (SPP), 100 seed weight (100SW) and seed yield per plant (SYPP)