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Association and inter-relationship among yield and yield contributing characters and screening against *Cercospora* leaf spot in mung bean (*Vigna radiata* L.)

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Thirty-five genotypes of Mung bean (*Vigna radiata* L.) along with check Shalimar Mungbean-1 were evaluated to elicit information on association and interrelationship for yield and its component traits. Seed yield plant⁻¹ showed positive significant association with number of clusters plant⁻¹, number of primary branches plant⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹, pod length, and 100-Seed weight, and negative and significant association with days to 80 % maturity. Path analysis revealed that maximum positive direct contribution to seed yield plant⁻¹ came from number of seeds pod⁻¹ (0.424) followed by 100-Seed weight (0.419), number of pods plant⁻¹ (0.339) and number of primary branches plant⁻¹ (0.177). Significant positive indirect contribution came from all the traits via pod length and number of seeds pod⁻¹. None of the genotypes showed complete resistance to cercospora leaf spot (CLS) however 17 genotypes were rated as moderate tolerant and 15 as moderately susceptible.

Key words: Mung bean, correlation, path-coefficient, *Cercospora* leaf spot.

INTRODUCTION

Mung bean (*Vigna radiata* L. Wilczek) also known as green bean, choroko, mung, mash bean, munggo, green gram and golden gram is one of the most important legume crops of India. It is one of the important crops well suited to dry areas and mainly to irrigated conditions and is cultivated traditionally by small landholders throughout tropical, subtropical and temperate zones of Asia including India, Pakistan, Bangladesh, Sri Lanka, Nepal, Thailand, China, Korea and Japan. Since, it has a short maturity span (60 to 75 days) it is grown under various cropping systems. Hence, contributing to the increase of the small land holder's income and improve the soil conditions as well (Fernandez and Shanmungasundarm, 1988). However, low productivity is

the major constraint for large scale production of this crop. In mung bean, architectural, phenological and yield components are collectively influencing seed yield. The relationships between yield and yield contributing traits on one hand and among themselves on the other hand could be measured by correlation coefficient. The knowledge of this relationship helps to identify traits on which selection can be based for the improvement of yield. Grain yield, being a polygenic complex trait and sensitive to environmental variations, is multiplicative end product of many factors. There are also several component characters of yield. Therefore, for an effective selection for higher yields, a thorough understanding of yield contributing characters and a correlation study

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involving these characters and yield is necessary. It is also necessary to examine whether the effects of different components of yield and other traits on yield are direct or indirect and to what extent. Under such circumstances the path coefficient analysis provides an effective mean of finding direct and indirect causes of an association. Therefore the present investigation was undertaken to study the inter-relationship among yield and its contributions in mung bean.

MATERIAL AND METHODS

An experiment was carried out at experiential farm of Division of Plant Breeding and Genetics, SUAST-K Shalimar Srinagar. 35 genotypes of mung bean including Shalimar mung-1 as check were evaluated in a randomized complete block design (RBD) with 3 replications during *kharif* 2011. Each experimental plot comprised two rows each of 3 m length, with 30 and 10 cm inter- and intra row spacing. Recommended agronomic package of practices were followed to raise a healthy crop. Observations were recorded on eleven morpho-agronomic, yield and quality traits *viz.*, days to 50% flowering, Number of clusters plant^{-1} , Number of primary branches plant^{-1} , Number of pods plant^{-1} , Pod length (cm), days to 80% maturity, plant height (cm), number of seeds pod^{-1} , 100-seed weight (g), Seed yield plant^{-1} (g) and protein content (%). Ten competitive representative plants were selected at random from each experimental plot in each replication and tagged for recording the observations. The genotypic and phenotypic correlation coefficients were estimated by the methodology advocated by Al-Jibouri et al. (1958) and direct and indirect effects were obtained according to the procedure proposed by Dewey and Lu (1959).

Reaction to cercospora leaf spot

Thirty five genotypes of mung bean procured from dry land (Karewa) Agriculture Research Station, Budgam, were laid in RBD with 03 replication having inter-row and inter-plant spacing of 30 x 10 cm, respectively. One local susceptible cultivar included in the screening programme was also sown around the experimental blocks to ensure presence of abundant and uniform inoculum in the field. Five leaves were collected at pod physiological maturity stage from each of the ten randomly selected mung bean plants from each replication for assessing disease reaction. In all 150 leaves of each genotype were assessed for percent disease incidence and intensity.

Percent disease incidence was calculated as under:

$$\text{Disease incidence (\%)} = \frac{\text{Number of diseased leaves}}{\text{Total number of leaves}} \times 100$$

Per cent disease intensity was calculated by adopting Ahmad and Ahmad (2000) scale with slight modification and leaves grouped into six categories where 0= No infection, 1= one spot to 20% diseased area, 2 = 21 to 40% diseased area, 3= 41 to 60% diseased area, 4 = 60 to 75 % diseased area and 5 = above 75 % diseased area. Percent disease intensity was calculated by using the formula:

$$\text{Disease intensity (\%)} = \frac{\sum (nv)}{NG} \times 100$$

Where:

n = number of leaves in a category

v = category value

N = total number of leaves

G = maximum rating (scale)

The genotypes were categorized into five different reaction groups on the basis of percent disease intensity on leaves as per the scale given by Sindhan et al. (1999) as show in Table 1.

RESULTS AND DISCUSSION

Analysis of variance and association among traits

The analysis of variance revealed highly significant differences for all characters under study among the 35 genotypes, indicating the presence of sufficient variability in the material tested (Table 1). Perusal of Table 2 revealed that days taken to 50% flowering exhibited significant and positive correlation with days to 80% maturity at both genotypic and phenotypic levels suggesting that number of days to flowering can be used as a criterion for selecting genotypes with short life span by selecting for fewer number of days to flowering (Vir and Gupta, 2002). Days to 80% maturity revealed significant and negative correlation with number of seeds pod^{-1} and protein content at both the levels. Number of clusters plant^{-1} revealed positive and significant correlation with number of primary branches plant^{-1} , number of pods plant^{-1} , number of seeds pod^{-1} and seed yield plant^{-1} but was significant and negatively correlated with 100-seed weight. These reports were in agreement with the earlier reports in mung bean (Vikas et al., 1999; Afiah and Muhammad, 2000; Rajan et al., 2000 and Kumar et al., 2004). Number of primary branches plant^{-1} had significant and positive correlation with number of pods plant^{-1} , number of seeds pod^{-1} , and seed yield plant^{-1} at both the levels but it was significant and negatively correlated with 100-seed weight. Number of pods plant^{-1} exhibited positive and significant correlation with number of seeds pod^{-1} and seed yield plant^{-1} at both the levels while it was significant and negatively correlated with 100-seed weight at both genotypic and phenotypic levels. Similar results were observed in mung bean by Upendra et al. (2005), Wani et al. (2007) and Rahim et al. (2010). Pod length had significant and positive correlation with number of seeds pod^{-1} , 100 seed weight and seed yield plant^{-1} at both the levels but significant and negatively correlated with plant height. Number of seeds pod^{-1} revealed positive and significant correlation with number of clusters plant^{-1} , number of primary branches plant^{-1} , pods plant^{-1} , pod length and seed yield plant^{-1} but negative and significant correlation with days to 80% maturity at both levels. 100-seed weight is significant and positively correlated with pod length at both the levels but negatively correlated with number of clusters plant^{-1} found to have positive and significantly association with

Table 1. Analysis of variance for quality, yield and yield component traits in mung bean (*Vigna radiata* L. Wilczek).

Source of variation	d.f	Mean square				
		Days to 50% flowering (1)	Days to 80% maturity (2)	No. of clusters plant ⁻¹ (3)	No. of primary branches plant ⁻¹ (4)	No. of Pods plant ⁻¹ (5)
Replication	2	4.40	1.60	0.03	0.20	0.21
Treatment	34	86.63**	199.09**	3.52**	0.81**	56.84**
Error	68	2.04	3.81	0.10	0.10	1.43

Source of variation	d.f	Pod length (cm)	Plant height (cm)	No. of Seeds pod ⁻¹	100 – seed weight (g)	Seed yield plant ⁻¹	Protein content (%)
		(6)	(7)	(8)	(9)	(10)	(11)
Replication	2	0.01	7.52	0.15	0.11	0.28	0.001
Treatment	34	2.06**	1014.45**	2.60**	1.05**	3.05**	0.74**
Error	68	0.05	8.20	0.04	0.03	0.55	0.11

*, ** Significant at 5 and 1 per cent levels respectively.

all other traits except days to 50% flowering, days to 80% maturity, plant height and 100-seed weight. Positive and significant correlations of seed yield with number of clusters plant⁻¹, number of branches plant⁻¹, number of pods plant⁻¹, pod length and number of seed pod⁻¹ had also been reported by Kumar et al. (2004), Rao et al. (2006), Wani et al. (2007), Hakim (2008) and Rahim et al. (2010). Protein content did not reveal any significant correlation with the important economic character that is, seed yield plant⁻¹. Similar trend was found with other traits except negative and significant association with days to 80% maturity.

The correlations at the phenotypic level were similar in direction though lower in magnitude as compared to genotypic correlations. Higher magnitude of genotypic correlation coefficients among different characters in mung bean has also been reported by Rao et al. (2006), Wani et al. (2007) and Hakim (2008). Higher magnitude of genotypic correlation helps in selection of

genetically controlled characters and gives a better response for seed yield improvement that would be expected on the basis of phenotypic associations alone (Robinson, 1966).

Johnson et al. (1955) proposed that besides genotypic and phenotypic variances, estimation of genotypic and phenotypic correlations are also important for the improvement of a trait as these parameters provides an understanding of relationship between different traits. Newell and Eberhart (1961) observed that when two characters are showing negative association at both phenotypic and genotypic levels, simultaneously selection for the improvement of these characters becomes difficult and accordingly a judicious breeding programme need to be drawn up. Adams (1967) reported that negative association between developing traits may arise from the development of one character at the cost of the suppression of the other, because of competition for common resources for development of a plant and its component traits.

Cause and effect relationship (path coefficient analysis)

Seed yield is a polygenic trait hence direct selection for this character may often be misleading. The components that determine the yield are the best indices for selection. Therefore, knowledge of the association between important yield attributes and seed yield may help the breeder to identify suitable donors for any successful breeding programme. Path analysis can provide an effective means of partitioning the correlation coefficient into direct and indirect effects.

Considering the direct effect of each character on seed yield, (Table 3) number of seeds pods⁻¹ had the highest positive direct effect (0.42), followed by 100-seed weight (0.41) and number of pods plant⁻¹ (0.33). Number of clusters plant⁻¹ and pod length recorded low positive direct effect, while number of primary branches plant⁻¹ exhibited a moderate direct effect. The indirect

Table 2. Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficient for quality, yield and yield component traits in mung bean (*Vigna radiata* L. Wilczek).

Traits	Days to 50% flowering	Days to 80% maturity	No. of clusters plant ⁻¹	No. of primary branches plant ⁻¹	No. of pods plant ⁻¹	Pod length (cm)	Plant height (cm)	No. of Seeds pod ⁻¹	100- seed weight (g)	Seed yield plant ⁻¹ (g)	Protein content (%)
Days to 50% flowering	-	0.6125**	0.0858	-0.1136	-0.0121	-0.0192	0.1069	-0.1351	-0.0805	-0.0731	-0.2121
Days to 80% maturity	0.6030**	-	-0.1173	-0.2505	-0.2240	0.0243	-0.1838	-0.3846*	0.0396	-0.2134	-0.4839**
No. of clusters plant ⁻¹	0.0793	-0.1003	-	0.7815**	0.8924**	0.2931	-0.0192	0.6248**	-0.3825**	0.6368**	0.0823
No. of primary branches plant ⁻¹	-0.0984	-0.2008	0.6674**	-	0.9392**	0.1285	0.0920	0.6472**	-0.3403*	0.6899**	-0.0942
No. of pods plant ⁻¹	-0.0134	-0.2084	0.8840**	0.8193**	-	0.2945	0.0265	0.7381**	-0.3406*	0.7599**	0.0159
Pod Length (cm)	-0.0203	0.0158	0.2828	0.1174	0.2836	-	-0.3446*	0.4959**	0.4173**	0.6146**	-0.0055
Plant height (cm)	0.1021	-0.1798	-0.0164	0.0737	0.0269	-0.3309*	-	-0.1037	-0.3572*	-0.2059	-0.0207
No. of seeds Pod ⁻¹	-0.1341	-0.3638*	0.5933**	0.5137**	0.7008**	0.4652**	-0.1014	-	0.0838	0.9089**	0.2009
100-Seed weight (g)	-0.0546	0.0407	-0.3562*	-0.2844	-0.3238*	0.4052*	-0.3371*	0.0750	-	0.2910	0.1590
Seed yield plant ⁻¹ (g)	-0.0688	-0.2044	0.6186**	0.5717**	0.7380**	0.5923**	-0.2018	0.8877**	0.2792	-	0.1631
Protein content (%)	-0.2039	-0.4698**	0.0789	-0.0813	0.0157	-0.0048	-0.0202	0.1893	0.1483	0.1595	-

*, ** Significant at 5 and 1 per cent level respectively.

effects of number of clusters plant⁻¹ via number of pods plant⁻¹ (0.30) was high and positive followed by number of primary branches plant⁻¹ (0.13), while it was high and negative via 100-seed weight. Number of primary branches plant⁻¹ had the highest positive in direct effect via number of pods plant⁻¹ (0.31) followed by number of seeds pod⁻¹ (0.27). Number of pods plant⁻¹ showed high and positive direct effect on seed yield via. Number of seeds pod⁻¹ (0.31) followed by number of primary branches plant⁻¹ (0.16). Indirect effect of pod length on seed yield was positive and high plant height and pods plant⁻¹. Plant height had significant and positive correlation with 100-seed weight but significant and negative correlation with pod length. Positive and significant association has been reported in mung bean for plant height with 100-seed weight. Seed yield plant⁻¹ was via number of seeds pod⁻¹ (0.21) followed by 100-seed weight (0.17). 100-seed weight showed

negative indirect effects on seed yield via all the traits except pod length (0.03) and number of seeds pod⁻¹ (0.03). Reddy et al. (1994) observed that number of pods plant⁻¹, number of pods cluster⁻¹ and number of seeds pod⁻¹ had strong positive direct effect on seed yield. Byregoda et al. (1997) and Gill et al. (2000) reported high direct effect of number of pods plant⁻¹, number of seeds pod⁻¹ and 100-seed weight on seed yield plant⁻¹. It may therefore be argued that if other characters are held constant, an increase in these characters which are showing positive and direct effect with seed yield individually would be reflected in increased seed yield.

Disease response

Thirty five genotypes assessed for the occurrence of *Cercospora* leaf spot disease under natural

conditions were arbitrarily categorized into different reaction groups on the basis of percent disease intensity. The data collected on differential response (Tables 4 and 5) revealed that none of the genotypes exhibited tolerant reaction to the pathogen. The genotypes were either moderately tolerant or susceptible to pathogen infection to varying extents. There existed a significant difference in disease intensity among different genotypes which ranged between 5.2 to 32.5% (Table 4). The maximum disease intensity of 30.81, 31.4 and 32.5% was recorded on genotypes SKUM-110, SKUM-114, SKUM-133 respectively. The disease intensity was next highest on SKUM-131, SKUM-127 and SKUM-125 exhibiting intensities of 26.6, 26.0, 25.8 and 25.4% respectively. Least disease intensity of 5.2, 5.6 and 5.7 per cent was recorded on genotypes SKUM-101, SKUM-103, SKUM-105 and SKUM-106, respectively.

Table 3. Direct and indirect effects (genotypic level) for major yield contributing traits on grain yield plant⁻¹ (g) in mung bean (*Vigna radiata* L. Wilczek).

Traits	No. of clusters plant ⁻¹	No. of primary branches plant ⁻¹	No. of pods plant ⁻¹	Pod length (cm)	No. of Seeds pod ⁻¹	100- Seed weight (g)	Genotypic correlation coefficient with seed yield plant ⁻¹
No. of clusters plant ⁻¹	0.0657	0.1383	0.3025	0.0255	0.2654	-0.1606	0.6368**
No. of primary branches plant ⁻¹	0.0513	0.1771	0.3183	0.0112	0.2749	-0.1429	0.6899**
No. of Pods plant ⁻¹	0.0586	0.1663	0.3390	0.0256	0.315	-0.1431	0.7599**
No. of pod length (cm)	0.0193	0.0227	0.0998	0.0869	0.2107	0.1752	0.6146**
No. of seeds pod ⁻¹	0.0410	0.1146	0.2502	0.0431	0.4248	0.0352	0.9089**
100-seed weight (g)	-0.0251	-0.0602	-0.1155	0.0363	0.0356	0.4199	0.2910

R square = 0.9832, Residual effect = 0.129.

Table 4. Reaction of mung bean genotypes to *Cercospora canescens* causing *Cercospora* leaf spot disease under natural conditions in 2011.

S/N	Genotypes	Percent disease incidence	Percent disease intensity
1.	SKUM-101	12.6	5.2
2	SKUM-102	31.3	15.7
3.	SKUM-103	13.3	5.3
4.	SKUM-105	14.6	5.6
5	SKUM-106	15.3	5.7
6.	SKUM-107	17.3	6.1
7.	SKUM-108	32.0	16.8
8.	SKUM-109	18.0	6.6
9.	SKUM-110	53.3	30.8
10.	SKUM-111	19.3	7.6
11.	SKUM-112	33.3	18.0
12.	SKUM-113	34.6	19.9
13.	SKUM-114	56.0	31.4
14.	SKUM-115	20.0	8.5
15.	SKUM-116	36.0	21.3
16.	SKUM-117	20.6	8.6
17.	SKUM-118	21.3	9.0
18.	SKUM-119	37.0	22.3
19.	SKUM-120	22.0	9.8
20.	SKUM-121	24.6	10.8
21.	SKUM-122	37.3	23.7

Table 4. Contd.

22.	SKUM-123	38.7	24.5
23.	SKUM-124	25.3	11.7
24.	SKUM-125	40.0	25.4
25.	SKUM-126	26.0	11.8
26.	SKUM-127	42.0	25.8
27.	SKUM-130	43.3	26.0
28.	SKUM-131	46.7	26.6
29.	SKUM-132	26.6	12.8
30.	SKUM-133	57.3	32.5
31.	SKUM-134	48.7	26.9
32.	SKUM-135	50.0	28.0
33.	SKUM-136	52.0	28.6
34.	SKUM-137	28.6	12.9
35.	Shalimar Mung-1	30.6	14.2
36.	Local cultivar	54.8	32.50

Table 5. Grouping of mung bean genotypes (*Vigna radiata* LWilczek) in to different reaction categories based on per cent disease intensity.

Reaction	Category	Percent disease intensity	Genotypes
Resistant	R	0.1 to 5.0	-NIL-
Moderate resistant	MR	5.1 to 15.0	SKUM-101, SKUM-103, SKUM-105, SKUM-106, SKUM-107, SKUM-109, SKUM-111, SKUM-115, SKUM-117, SKUM-118, SKUM-120, SKUM-121, SKUM-124, SKUM-126, SKUM-132, SKUM-137 and Shalimar Mungbean-1
Moderate susceptible	MS	15.1 to 30.0	SKUM-102, SKUM-108, SKUM-112, SKUM-113, SKUM-116, SKUM-119, SKUM-122, SKUM-1123, SKUM-125, SKUM-1127, SKUM-1130, SKUM-131, SKUM-134, SKUM-135 and SKUM-136
Susceptible	S	30.1 to 50.0	SKUM-110, SKUM-114, SKUM-133 and Local cultivar
Highly susceptible	HS	>50	-Nil-

Based on disease intensity, the assessed mung bean genotypes were grouped in to different categories (Table 5). None of the genotypes could be rated as tolerant, however seventeen genotypes viz., SKUM-101, SKUM-103, SKUM-105, SKUM-106, SKUM-107, SKUM-109, SKUM-111, SKUM-115, SKUM-117, SKUM-118, SKUM-

120, SKUM-121, SKUM-124, SKUM-126, SKUM-132, SKUM-137, Shalimar mung bean-1, were rated as moderately tolerant and fifteen other genotypes viz., SKUM-102, SKUM-108, SKUM-112, SKUM-113, SKUM-116, SKUM-119, SKUM-122, SKUM-123, SKUM-125, SKUM-127, SKUM-130, SKUM-131, SKUM-134, SKUM-135, SKUM-

136, as moderately susceptible. The other three genotypes viz, SKUM-110, SKUM-114, SKUM-133, were categorized as susceptible. Resistance to major biotic stresses including cercospora leaf spot (CLS) have been identified (Sarker et al., 2008). Hence efforts need to incorporate these sources into high yielding susceptible cultivars to

increase overall production and productivity of mung bean.

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