CORRELATION AND PATH COEFFICIANT ANALYSIS FOR QUANTITATIVE TRAITS IN GREENGRAM [*Vigna radiate* (L.) Wilczek]

ABSTRACT

Genetic variability, correlation coefficient and path coefficients analysis were carried outin a set of 20 genotypes of Greengram grown in an randomized block design with three replications during *kharif*- 2021. Analysis of variance indicated significant difference among genotypes for the characters plant height (cm), biological yield(g), seedindex(g), number of clusters per plant, days to 50 percent flowering. This indicated existence of variability among the genotype.The high estimates of heritability and genetic advance were found for the characters plant height, number of primary branches per plant. The highest percentage of PCV was observed for number of primary branches per plant and number of pods per plant. The GCV was highest for number of primary branches per plant. The association analysis revealed that the seed yield per plant exhibited positive and significant correlation with number of clusters per plant, seed index, biological yield, number of primary branches, pod length, harvest index and number of pods per plant. Path coefficient analysis revealed that number of clusters per plant followed by seed index (g), biological yield, primary branches, pod length, harvest index, number of seeds per pod, number of pods per plant were effective for the selection of high yielding genotype as they exhibited high positive direct effect along with significant positive correlation with seed yield. Based on the mean performance of the SML-668, PANT MOONG-05, BPMR-145, CO-7, BM 2002-1 were found superior in seed yield. These may be used as parents in crop improvement programs to develop high yielding varieties.

Keywords: Genetic advance, Genotypic coefficient of varience, Phenotyic coefficient of varience, Heritability,Variability ,Correlation,Quantitative traits,path,Greengram

INTRODUCTION

Pulses have been considered as an important constituent of Indian diet, because of their high protein content (25%). Greengram [*Vigna radiata* (L.) Wilczek] also known asmungbean, is an important pulse crop cultivated round the year in almost all parts of India. It is a self-pollinated, diploid (2n=22), legume grown for its dry seeds, which are important sources of easily digestible proteins that supplement the staple rice diet. The foliage and bhusa form nutritious feed to the livestock. In addition, it enriches soil fertility through biological nitrogen fixation and also checks soil erosion. It is also usedas green manure crop.

Mungbean is a short day, warm season crop, grown mainly in semiarid to sub humid tropics and subtropics with 600 to 1000 mm annual rainfall, 22 to 35°C mean temperature during crop production and elevations not exceeding 1800 to 2000 m above mean sea level. For high yield, a warm climate and deep well drained loam or sandy loam soils are desired. Mungbean is rapidly growing, erect or sub-erect annual usually 40 to 120 cm in height. It is frequently much branched with slight tendency of twining in its upper branches. The leaves are trifoliate with large, ovate, entire or rarely lobed membranous leaflets with scattered hairs on both sides. The pods are sub cylindrical, long wide, straight or slightly curved, 10 to 20 cm, small, globular and oblong often green but may be yellow brown and speckled with black coloured seeds.

Narasimham (1929) reported that "pollination in mungbean is completed in all cases by 1.30 pm with an interval of about 4 hours, between the dehiscence of anthers and opening of flower causing self- fertilization".

Mungbean has originated from Indian subcontinent. Maximum diversity amongthe related species is limited to upper Western ghats and Deccan hills. Named mungbean as *Phaseolus mungo*, while wild and yellow variety (Sonamung) as *Phaseolus aureus* Rox

The diploid mungbean (2n = 22, 24) belongs to family Leguminosae, sub family papillionaceae, genus Vigna and species radiata. India is producing 14.76 million tonnes of pulses from an area of 23.63 million hectare, which is one of the largest pulses producing countries in the world. However, about 2-3 million tonnes of pulses areimported annually to meet the requirement of domestic consumption. Thus, there is need to increase production and productivity of pulses in the country by more intensive interventions. States to be covered Rajasthan (30.81%), Maharashtra (19.51%), Karnataka (15.35%), Andhra Pradesh (12.79%), Orissa (7.41%), Tamil Nadu (4.97 %) and Uttar Pradesh (2.09%).

Table 1 : Area wise production in Uttar Pradesh and India

PARTICULARS	AREA (lakh ha)	PRODUCTION (lakh tonnes)	PRODUCTIVITY (kg/ha)
INDIA	3347.98	1537.67	459
UTTAR PRADESH	47.00	16.28	346

Like other crops, the mungbean has a complex nature that is influenced by a number of factors, including seed yield. Crop improvement depends on having an understanding of the genetic diversity that exists among several parameters. Understanding the mechanism of inheritance of quantitative features is made easier by the heritability of genetic advancement. A practical method for elaborating the degree and scope of relationships among significant plant traits is correlation coefficient analysis. It also offers fundamental selection criteria and develops directional models based on yield and its constituent parts in field trials. However, the details it provides regarding the type of association are frequently lacking. On the other hand, path coefficient analysis is a powerful statistical method created specifically to quantify the relationships between various components and their direct and indirect effects on seed production.

Keeping all these aspects in view, the present investigation was undertaken withthe following objectives.

1. To study genetic variation among 20 Greengram genotypes.

2.To find out correlation between yield and yield contributing traits.

3. To estimate direct and indirect effect of yield contributing traits in Greengram.

MATERIALS AND METHODS

The experimental materials for present investigation consist of 20 greengram genotypes including one check variety obtained from Department of Genetics and Plant Breeding, Naini Agriculture Institute, SHUATS, Prayagraj, Uttar Pradesh, was evaluated at Field Experimentation Centre, SHUATS, Prayagraj, during *Kharif*-2021 in Randomized Block Design with three replications. Data were recorded for five randomly tagged plants for characters *viz.*, Days to 50% flowering, Days to 50% pod setting, Days to maturity, Number of clusters per plant, Number of primary branches, Plant height(cm), Number of pods per plant, pod length (cm), Biological yield per plant (g), Number of seeds per pod, Harvest index (%), Seed yield per plant(g), Seed index. The genotypic and phenotypic components of variance were calculated according to formulae given for the observed characters.

Genotypic variance (σ^2g) The genotypic variance is due to the differences among genotypes included in the study. Itwas calculated as under:

$$\text{Genotypic variance } (\sigma^2_g) = M_g - M_e / r \tag{1}$$

Phenotypic variance (σ^2_p) It is the sum of variance contributed by genetic causes and environmental factors. It was calculated as under:

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e \tag{2}$$

Coefficient of variation (C.V. %) The coefficient of phenotypic and genotypic variation was calculated by using the formulasuggested by Burton (1952).

Phenotypic coefficient of variation (PCV)

$$\text{P.C.V. (\%)} = \frac{\sqrt{\sigma^2 p} \times 100}{\bar{X}} \tag{3}$$

Genotypic coefficient of variation (GCV)

$$\text{G.C.V. (\%)} = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100 \tag{4}$$

GCV and PCV were categorized as low, moderate and high by following Shivasubramanian and Menon (1973).

Heritability refers to the portion of variability which is heritable in nature out of the total variability. It is due to the genetic causes. Heritability in broad sense (H(b)) was calculated according to the following formula suggested by Burton and De Vane (1953).

$$\mathbf{H_{(b)}\% = (\sigma^2 / \sigma^2\ ) \times 100}$$

Heritability percentage was categorized as demonstrated by Robinson *et al.* (1949).

genetic advance (G.A.)

expressed in percentage of mean was calculated byusing the method suggested by Johnson *et al.* (1955).

$$\textbf{Genetic advance as percent of mean} = \frac{\text{G.A.}}{X} \times 100$$

Correlation coefficients

The phenotypic and genotypic correlation coefficients were computed from the phenotypicand genotypic variance and co-variances according to Searle (1961).

1. Genotypic correlation coefficient:

$$r_{xy}(g) = \frac{Cov.xy\ \ (g)}{\sqrt{Vx(g).Vy(g)}}$$

2 Phenotypic correlation coefficient:

$$r_{xy}(p) = \frac{Cov.xy(p)}{\sqrt{Vx(p).Vy(p)}}$$

RESULT

On the basis of the mean, top five genotype having high seed yield per plant were selected. Among these genotypes SML-668, PANT MOONG-05, BPMR-145, CO-7, BM 2002- 1 were found superior for seed yield. Hence, it is suggested that these genotypes be tested in multi locations trials to confirm their superiority and may also be used as parents in hybridization programme to develop high yielding varieties.

GENETIC ADVANCE

Genetic advance as %of mean varied from 3.36 to 50.56. High genetic advance as % mean (>20%) was recorded for primary branches per plant (50.56), plant height (40.10), number of pods per plant (36.59), seed yield per plant (35.56), pod length (32.55), biological yield (30.13), harvest index (20.60), Moderate genetic advance as % mean (10-20%) was recorded for days to 50% flowering (17.61), seed index (16.03), number of clusters per plant (14.66). Low genetic advance as % mean (<10%) was recorded for number of seeds per pod (9.99) anddays to maturity (3.36).

COEFFICIENT OF GENOTYPIC AND PHENOTYPIC VARIATIONS

Genotypic coefficient of variation (GCV):-

Genotypic coefficient of variation (GCV) for 12 characters ranged from 2.30% for days to maturity to 28.41% (Number of primary branches). High GCV (>20%) was recorded for Number of primary branches (28.41%), Moderate GCV (10-20%) was recorded for plant height (19.62%), Number of pods per plant (19.57%), seed yield per plant (18.44%), pod length (17.60%), biological yield (15.24%), harvest index (12.36%), number of clusters per plant (10.98%), seed index (10.33%). Low GCV was recorded for Days to 50% flowering (9.31%), seeds per pod (5.95%) and days to maturity (2.30%).

Phenotypic coefficient of variation (PCV):-

Phenotypic coefficient of variation (PCV) for 12 characters ranged from 3.25% for days to maturity to 32.89% (Number of primary branches). High PCV (>20%) was recorded for number of primary branches (32.89%), Number of pods per plant (21.56%), Moderate PCV (10-20%) was recorded for plant height (19.76%), seed yield per plant (19.70%), pod length (19.61%), number of clusters per plant (16.95%), biological yield (15.88%), harvest index (15.28%), seed index (13.71%), Days to 50% flowering (10.15%). Low GCV was recorded for seeds per pod (7.30%) and days to maturity (3.25%).

Heritability

The results of heritability for all the 12 characters are presented inThe estimates of heritability (%) in the broad sense for 12 characters studied, which ranged from 42.10 to 98.50%. High heritability (broad sense) (>60%) was recorded for character plantheight (98.50%), biological yield (92.11%), seed yield per plant (87.60%), days to 50%flowering (84.28), number of pods per plant (82.40%), pod length (80.59%), number ofprimary branches (74.62%), seed per pod (66.41%), harvest index (65.41%).

CORRELATION BETWEEN TRAITS

Genotypic correlations of the components characters with seed yield per plant:-

Analysis of correlation coefficient revealed that seed yield per plant exhibited positive and significant correlation associated with number of clusters per plant (0.844**), seed index (0.833**), biological yield (0.736**), number of primary branches (0.722**), pod length (0.702**), harvest index (0.601**), number of pods per plant (0.522*), While the negative non-significant association with plant height (-0.197), days to 50% flowering (-0.186) and days to maturity (-0.093).

Phenotypic correlation of the components characters with seed yield / plant:-

Analysis of correlation coefficient revealed that seed yield per plant exhibited positive and highly significant correlation with seed index (0.657**), biological yield (0.657**), harvest index (0.617**), number of primary branches per plant (0.597*), pod length (0.570**), number of clusters per plant (0.536**), number of seeds per pod (0.534**), number of pods per plant (0.480**) and Negative non-significant correlation exhibited plant height (-0.184), days to 50% flowering (-0.128) and days to maturity (-0.111).

DISCUSSION

The present investigation was carried out to identify proper accessions from the germplasm for future breeding programme. Prior to breeding crop for higher yield, it is essential to generate information regarding interrelationship between different plant characters with seed yield and among themselves, since its facilities the quicker assessment of high yielding genotypes in selection programme. Yield is a complex character controlled by polygenes. Therefore, selection made on the basis of its phenotypic expression alone is likely to be misleading. It is, hence, essential to measure the contribution of various traits to the yield through correlation and partitioning the correlation coefficient into the components of direct and indirect effects.

Genetic variability

Genotypic differences were highly significant for all the characters in the present study, indicating presence of considerable amount of variability. A wide range of variability for various traits has also been observed earlier by **Garje *et al*. (2013), Kumar *et al.* (2013), Narasimhulu *et al*. (2013, Hemavathy *et al.* (2015), Bhutia *et al.* (2016), Asari et al. (2019).**

Genotypic and phenotypic coefficients of variation:-

The estimates of genotypic and phenotypic coefficient of variation indicated that the values of phenotypic coefficient of variation were higher than their corresponding genotypic coefficient of variation. Indicating the influence of environmental factors less differences were observed between phenotypic and genotypic coefficient of variation in certain cases such as daysto 50% flowering, plant height, biological yield. Which indicated that these characters were less influenced by the environment. Similar results were also obtained by **Mehandi *et al.* (2013**), **Yadav *et al.* (2017), Govardhan *et al.* (2018), Sushmitharaj *et al.* (2018), Sneha *et al*. (2019).**

Heritibility:-

The high heritability value was registered by the characters under study viz., plant height,biological yield, seed yield per plant, days to 50% flowering, number of pods per plant, pod length, number of primary branches, seed per pod, harvest index. Similar finding were also reported by **Kumar *et al.* (2013), Narasimhulu *et al*. (2013), Pathak *et al*. (2014), Yadav *et al.* (2017), Pulagampalli and Lavanya (2017), Sushmitha and Jayamani (2018), Asari *et al*. (2019)**, **Ramakrishnan *et al*. (2018), Sandhiya and Saravanan (2018.**

Correlation coefficients:-

The study of genotypic correlation gives an idea of the extent of relationship between different characters. This relationship among yield contributing characters as well as their association with yield provides information for exercising selection pressure for bringing genetic improvement in seed yield.

In the present study, seed yield per plant was found to be significantly and positively correlated with seed index, biological yield, harvest index, number of primary branches per plant, pod length, number of clusters per plant, number of seeds per pod and number of pods per plant at phenotypic levels and genotypic level. Such positive interrelationship between seed yield and these attributes has also been reported in Greengram by **Tnippani *et al.* (2013), Lal and Singh(2014), Das and Barua (2015), Raturi *et al.* (2015), Baisakh *et al*. (2016), Dhoot *et al.* (2017) Kate *et al.* (2017), Pulagampalli and Lavanya (2017), Sushmitharaj *et al.* (2018), Jayaprada *et al.* (2019), Muthuswamy *et al.* (2019), Sneha *et al*. (2019).**

Path coefficient analysis:-

The Genotypic path coefficient analysis revealed that the highest direct and positive effect on seed yield was exhibited by number of clusters per plant followed by seed index (g), biological yield, primary branches, pod length, harvest index, number of seeds per pod, number of pods per plant. Such positive and high direct effects of these variables had also been reportedby **Kate *et al.* (2017), Tabasum *et al.* (2010), Garje *et al.* (2014)**, **Baisakh *et al.* (2016)** for pods per plants, **Tnippani *et al.* (2013)** for number of primary branches**, Das and Barua. (2015), Muralidhara *et al.* (2015)** for seeds per pod**, Bhutia *et al*. (2016)** for pod length**,** similar results were also obtained by **Garg *et al.* (2017)** for harvest index. The residual effecton seed yield per plant was low.

Table 2: Analysis of Variance (ANOVA) for 12 characters in Greengram genotypes during *Kharif*-2021

Characters	Mean sum of Squares		
	Replication (df=2)	**Treatment (df=19)**	**Error (df=38)**
Days to 50% flowering	2.22	19	38
Days to maturity	0.1	46.28**	2.71
Plant height	1.76	8.01**	1.99
No. of primary branches	0.55	305.52**	1.54
No. of cluster per plant	0.16	3.19**	0.33
No. of Pods per plant	1.44	0.59**	0.19
Seeds per pod	0.11	7.79**	0.52
Pod length	0.14	1.17**	0.17
Biological yield	0.73	5.77**	0.43
Harvesting index	3.38	83.01**	2.3
Seed index	0.01	71.78**	10.76
Seed yield per plant	0.68	0.63**	0.13

*,** = Significant at 5 and 1 per cent, respectively

Table 3: Genetic parameter of characters of Green gram evaluated during *kharif* 2021-22

Sr. No.	Characters	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation(%)	Heritabilityin broad sense (%)	Genetic advance	Genetic Advance as percentage of mean
1.	Days to 50% flowering	9.31	10.15	84.28	7.21	17.61
2.	Days to maturity	2.30	3.25	50.21	2.07	3.36
3.	Plant height	19.62	19.76	98.50	20.58	40.10
4.	No. of primary branches	28.41	32.89	74.62	1.74	50.56
5.	No. of cluster per plant	10.98	16.95	42.01	0.49	14.66
6.	No. of Pods per plant	19.57	21.56	82.40	2.91	36.59
7.	Seeds per pod	5.95	7.30	66.41	0.97	9.99
8.	Pod length	17.60	19.61	80.59	2.47	32.55
9.	Biological yield	15.24	15.88	92.11	10.25	30.13
10.	Harvest index	12.36	15.28	65.41	7.51	20.60
11.	Seed index	10.33	13.71	56.75	0.64	16.03
12.	Seed yield per plant	18.44	19.70	87.60	4.38	35.56

Table 4: Genotypic correlation coefficient between yield and its component characters in Greengram during *Kharif* 2021

Characters	Days to 50% Flowering	Days to maturity	Plant height	No. of primary branches	No. of cluster per plant	No. of Pods per plant	Seeds per pod	Pod length	Biological yield	Harvest index	Seed index	Seed yield per plant
Days to 50% Flowering	1.00	0.640^{**}	0.049	-0.100	0.139	-0.253	-0.260^{*}	-0.432^{**}	-0.330^{*}	0.073	0.018	-0.186
Days to maturity		1.00	-0.156	-0.187	-0.235	-0.306^{*}	0.122	-0.642^{**}	-0.623^{**}	0.618^{**}	0.174	-0.093
Plant height			1.00	-0.377^{**}	-0.304^{*}	0.015	-0.259^{*}	0.037	-0.224	-0.072	-0.274^{*}	-0.197
No. of primary branches				1.00	0.921^{**}	0.784^{**}	0.822^{**}	0.292^{*}	0.523^{**}	0.434^{**}	0.779^{**}	0.722^{**}
No. of cluster per Plant					1.00	0.818^{**}	0.675^{**}	0.628^{**}	0.540^{**}	0.574^{**}	0.637^{**}	0.844^{**}
No. of Pods per plant						1.00	0.639^{**}	0.500^{**}	0.437^{**}	0.216	0.486^{**}	0.522^{**}
Seeds per pod							1.00	0.187	0.261^{*}	0.512^{**}	0.583^{**}	0.565^{**}
Pod length								1.00	0.778^{**}	0.197	0.308^{*}	0.702^{**}
Biological yield									1.00	-0.076	0.428^{**}	0.736^{**}
Harvest index										1.00	0.720^{**}	0.601^{**}
Seed index											1.00	0.833^{**}
Seed yield per plant												1.00

*, ** significant at 5% and 1% significance level, respectively

Table 5: phenotypic correlation coefficient between yield and its component characters in Greengram during *Kharif* 2021

Characters	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of cluster per plant	No. of Pods per plant	Seeds per pod	Pod length	Biological yield	Harvest index	Seed index	Seed yield per plant
Days to 50% Flowering	1	0.440**	0.039	-0.126	0.054	-0.164	-0.154	-0.385**	-0.272*	0.077	0.063	-0.128
Days to maturity		1	-0.133	-0.037	-0.119	-0.189	-0.068	-0.396**	-0.375**	0.214	0.058	-0.111
Plant height			1	-0.326*	-0.181	0.019	-0.203	0.043	-0.205	-0.066	-0.192	-0.184
No. of primary branches				1	0.651**	0.623**	0.661**	0.257*	0.406**	0.338**	0.561**	0.597**
No. of cluster per plant					1	0.488**	0.461**	0.340**	0.350**	0.348**	0.499**	0.536**
No. of Pods per plant						1	0.480**	0.460**	0.380**	0.208	0.328*	0.480**
Seeds per pod							1	0.152	0.186	0.486**	0.537**	0.534**
Pod length								1	0.674**	0.111	0.194	0.570**
Biological yield									1	-0.151	0.358**	0.657**
Harvest index										1	0.523**	0.617**
Seed index											1	0.657**
Seed yield per plant												1

*, ** significant at 5% and 1% significance level, respectively

CONCLUSION

1. Significant variation to all the characters were observed in the present study.
2. Based on present investigation, it can be concluded that maximum yield was recorded in SML-668 (0.0018 kg/ha) genotype
3. Number of primary branches, number of pods per plant had the highest magnitude of phenotypic and genotypic coefficient of variation
4. Seed yield per plant showed significant and positive association with clusters per plant, seed index, biological yield, number of primary branches at both phenotypic and genotypic level hence, these can be utilized in indirect selection of genotypes for high seed yield
5. Path coefficient at phenotypic and genotypic level reveled that have direct positive effect on seed yield per plant for Number of clusters per plant, seed index (g), biological yield, primary branches, Pod length
6. Therefore,these traits may be given during selection for yield improvement in green gram.

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