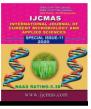


International Journal of Current Microbiology and Applied Sciences ISSN: 2319-7706 Special Issue-11 pp. 1479-1486 Journal homepage: <u>http://www.ijcmas.com</u>



Original Research Article

Mean Performance and Correlation Analysis for Seed Yield and Components Traits in Mungbean [*Vigna radiata* L. Wilczek] Genotypes

Pandit Praveen Kumar^{1,2}*, G. Roopa Lavanya¹, Sanjay Kumar Sanadya², K. Priyatham¹, C.S. Kazipyo¹ and B.G. Suresh¹

¹Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad-211007 (Uttar Pradesh) India
²Department of Genetics and Plant Breeding, Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176062 (Himachal Pradesh) India

*Corresponding author

ABSTRACT

Keywords

Correlation, Mungbean, Path analysis, Seed yield Mungbean [*Vigna radiata*] belongs to the family *leguminoceae* is an excellent source of easily digestible proteins with low flatulence which complements the staple rice diet in Asia. A field experiment with 40 genotypes of mungbean was conducted at Experimental Farm, SHUATS Allahabad during *Kharif*-2017 to study the correlation and mean performance for seed yield and its component traits. Genotypes were evaluated in Randomized Block Design with a single check SAMRAT. Mean performance for earliness revealed that Genotype JLM-1758 and JLM-1757 were earlier over check. In the case of seed yield per plant, genotypes PM 9-11, BPMR 145 and RMG 1030 exhibited significant performance over the check. Therefore, these genotypes can be utilized for mungbean improvement program. The correlation of seed yield per plant, was positive and significant at the phenotypic level with days to 50% flowering, clusters per plant, pod length, seeds per plant. Therefore, selection based on these component traits would results in improvement in seed yield of mungbean. Protein content showed a negative correlation with clusters per plant and non-significant with other traits.

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek], is an ancient pulse crop widely cultivated in India. It can be grown in various crop rotation practices (Singh *et al.*, 2015) because of its short duration nature, wider adaptability, low water requirement and photo insensitiveness can be utilized in low rainfall areas or good rainfall areas. Mungbean is short day, warm season crop, grown mainly in tropical and sub-tropical regions. It is drought tolerant and has ability to grow under harsh climate and medium to low rainfall situation. It is tolerant to moisture stress and heat as well. It has ability to grow under low input conditions. It can be grown on several types of soils such as black cotton, red lateritic, gravelly and sandy soils. Well drained fertile sandy loam soil with a pH between 6.2-7.2 is the best for mungbean cultivation. Water logged and saline soils are not suitable for mungbean cultivation (Sharma 2016). Correlation coefficient analysis is a statistical technique that helps to measures the degree and association between two or more variables. Estimates of the correlation coefficient are useful in identifying the component traits,

which can be used for yield or other agronomically important traits improvement of mungbean. To accumulate optimum contribution of yield contributing characters, it is essential to know the association of various characters (Bhutia *et al.*, 2016). Earlier numerous studies have been reported in legumes recently such as Kumar *et al.*, (2018), Kumar *et al.*, (2020), Sahoo *et al.*, (2018) and Sahoo *et al.*, (2019) in moth bean. Therefore, the present study was conducted to assess correlation to identify component traits for developing high yielding varieties of mungbean.

Materials and Methods

The present investigation was carried out during Kharif-2017 at experimental farm, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad (Figure 1). The experimental material consisted of 40 genotypes was evaluated in Randomized Block Design with three replications accommodating 3 meter long two rows per replication at 30 cm spacing (Table 1). Observations were recorded for thirteen characters viz., Days to 50% flowering (DF), Days to maturity (DM), Plant height (PH), Number of primary branches per plant (PBP), Number of clusters per plant (CPP), Number of pods per plant (PPP), Pod length (PL), Seeds per pod (SPP), Biological yield per plant (BYP), Protein Content (PC), Seed Index (SI), Harvest Index (HI) and Seed yield per plant (SYP). Phenotypic and genotypic correlation coefficient estimated by Johnson et al., (1955). Softwares used for analysis were OPSTAT and Microsoft Excel 2007.

Results and Discussions

Mean performance

Mean performance of 40 genotypes of mungbean were mentioned in the Table 2.

Based on the mean performance of mungbean genotypes, under this environmental condition, the high mean value is significant for all the traits except plant height, days to 50% flowering and days to maturity. After analyzing the mean performance of these genotypes, it was found that 5 genotypes for days to 50 % flowering, 33 for days to maturity, 28 plant height, 20 number of branches per plant, 25 for clusters per plant, 5 for pods per plant, 12 for pod length, 5 for protein content, 6 for seed index, 15 for harvest index, 4 for seed yield plant and no genotypes showed more one mean performance for biological yield per plant over check SAMRAT in desirable direction, respectively. According to the mean performance of the studied genotypes, it is observed that few of them can be selected for their better performance, such as JLM 1758 and JLM 1757 for the lowest days to 50% flowering, JLM 1757, COGG 10-10, RMG 1039, JLM 1754 and KM 11 563 for protein content, RMG 1030, ML 2050, KM 11 586, BPMR 145, RMG 268, PM 9-11, COGG 10-10, NDMK 13-1. KM 11 575, KM 11 563, BM 2003-2, IGKM 05-26-3, ML 2333, RMG 1093 and NVL 641 for the high harvest index, PM 9-11, BPMR 145, RMG 1030 and RMG 268 for seed yield per plant over the check SAMRAT.

Correlation coefficient

The correlation of seed yield per plant was positive and significant at phenotypic level with days to 50% flowering, biological yield per plant, clusters per plant, pod length and seeds per plant. This character needs due consideration during any selection method. Similar results were reported by Khanpara *et al.*, (2012), Gadakh *et al.*, (2013), Bisht *et al.*, (2014), Katiyar *et al.*, (2015), Bhutia *et al.*, (2016) and Choudhary *et al.*, (2016). The correlation of biological yield per plant was positive and significant at phenotypic level with seed yield per plant, harvest index and seed index. Similar findings also agree with previous findings Gadakh *et al.*, (2013), Bisht *et al.*, (2014), Kumar *et al.*, (2018) in mungbean. The trait Days to 50% flowering showed positive and significant correlation with clusters per plant, pods per plant, pod length, seed per plant, seed yield per plant and harvest index (Table 3).

In conclusion, the information from mean performance and correlation analysis in mungbean will be helping in finding out the structural yield components that can be appropriately incorporated into an improved plant type. Being grown under marginal conditions, it requires a change in the plant type for wider adaptability. Hence, presently study reveals that days to 50% flowering, biological yield per plant, clusters per plant, pod length and seeds per plant are important agronomic traits as directly contributed towards seed yield per plant. Therefore, selection based on these component traits would results improvement in seed yield of mungbean.

S. No.	Name of	S. No.	Name of
	Genotypes		Genotypes
1	IPM 5-07	21	KM 11 563
2	PUSA 1471	22	KM 11 575
3	PUSA 1472	23	KM 11 586
4	KM 2342	24	RMG 1040
5	HUM 27	25	ML 2024
6	COGG 10-10	26	BGS 9
7	SGC 20	27	BGS 11
8	IGKM 05-26-3	28	MSJ 118
9	RMG 1030	29	RMG 1083
10	COGG 12-10	30	PUSA 871
11	NVL 641	31	RMG 1039
12	ML 2050	32	RMG 268
13	PM 9-11	33	RMG 1093
14	IPM 9901-8	34	SML 668
15	BM 2002-1	35	JLM 1751
16	BM 2003-2	36	JLM 1752
17	BPMR 145	37	JLM 1754
18	ML 2333	38	JLM 1757
19	BM 4	39	JLM 1758
20	NDMK 13-1	40	SAMARAT ©

Table.1 List of the genotypes used for present study

Genotypes	DF	DM	PH	BPP	CPP	PPP	PL	SPP	BYP	PC	SI	HI	SYP
IPM 5-07	43.25	60.75	59.0	3.95	13.15	21.70	7.18	10.65	16.90	21.70	3.33	34.24	5.83
PUSA 1471	42.75	62.00	55.7	4.00	12.30	21.10	7.77	11.65	16.05	19.92	3.91	28.18	4.34
PUSA 1472	46.00	63.25	49.4	3.95	11.30	17.25	7.25	9.60	15.30	22.21	3.64	33.87	5.15
KM 2342	42.00	60.75	41.2	3.30	8.25	14.10	6.75	9.20	15.25	22.35	3.09	25.84	3.95
HUM 27	43.25	60.00	44.2	3.95	8.05	21.85	7.97	9.30	17.05	21.54	4.22	30.88	5.19
COGG 10-10	41.25	65.25	60.0	3.30	7.95	17.40	8.10	11.55	12.90	23.65	4.10	43.15	5.65
SGC 20	41.25	64.00	54.7	4.00	9.20	15.35	7.05	10.10	15.10	21.39	3.34	29.74	4.37
IGKM 05-26-3	44.75	62.00	56.1	4.00	8.10	17.15	7.88	11.20	15.80	22.17	3.20	36.92	5.85
RMG 1030	40.75	60.00	54.8	4.00	7.70	14.80	6.55	12.05	15.10	21.65	3.03	46.89	7.04
COGG 12-10	40.75	62.25	44.4	3.40	6.15	11.95	7.23	10.05	14.45	22.86	3.72	35.27	5.34
NVL 641	42.00	62.00	56.2	4.00	5.20	18.60	9.89	11.80	16.90	22.70	3.74	36.15	6.06
ML 2050	42.00	62.00	51.3	3.85	7.20	11.30	7.32	10.30	14.15	22.23	3.30	45.06	6.30
PM 9-11	40.75	62.00	49.9	3.25	5.95	9.10	7.30	10.10	16.35	21.30	3.35	43.78	7.11
IPM 9901-8	41.00	66.75	40.8	3.50	8.10	13.20	7.28	10.60	14.65	20.57	3.79	34.16	4.97
BM 2002-1	40.00	62.75	46.8	4.00	5.15	10.75	7.79	10.15	18.10	21.90	5.21	30.98	5.70
BM 2003-2	42.00	63.25	39.3	4.00	4.40	14.70	10.13	11.35	14.15	21.03	5.65	39.00	5.65
BPMR 145	40.75	64.00	49.9	4.00	6.40	9.35	8.02	10.20	16.05	22.20	4.88	44.28	7.05
ML 2333	43.50	61.25	47.8	4.00	8.85	16.95	7.82	11.05	15.65	20.33	3.63	36.88	5.79
BM 4	42.00	62.00	55.9	3.95	8.05	13.70	6.85	9.90	18.25	21.17	3.32	32.16	5.91
NDMK 13-1	42.00	60.00	46.9	3.95	8.00	18.95	6.22	10.35	15.30	21.95	3.13	40.13	6.10
KM 11 563	41.00	62.00	38.2	3.85	7.40	15.35	7.16	10.35	16.30	23.10	2.88	39.06	6.30
KM 11 575	42.00	60.75	44.3	3.35	5.15	18.30	7.71	12.25	14.75	21.45	3.06	39.74	5.90
KM 11 586	42.00	63.00	50.8	2.95	6.00	17.05	7.30	11.75	9.65	22.35	3.11	44.94	4.32
RMG 1040	42.00	63.75	52.4	3.10	4.10	18.20	6.36	10.00	14.45	21.75	2.07	29.26	4.21
ML 2024	42.00	62.50	45.9	3.05	4.30	21.80	7.06	10.95	17.00	22.35	2.66	24.75	4.13
BGS 9	40.75	61.25	44.4	3.30	4.70	17.20	7.89	9.80	19.10	22.08	2.35	25.26	4.89
BGS 11	40.00	60.00	43.4	3.70	5.30	18.05	6.60	10.80	12.10	22.20	2.64	31.18	3.84
MSJ 118	42.00	62.00	53.1	3.60	5.35	12.80	6.80	9.60	16.80	21.60	3.03	24.99	4.11
RMG 1083	41.50	61.25	46.3	3.20	6.35	18.75	6.43	10.45	14.90	21.90	3.00	31.08	4.72
PUSA 871	40.75	60.00	42.3	3.00	4.15	12.20	6.13	10.20	14.15	22.00	3.12	31.98	4.65

Table.2 Mean performances of forty genotypes for thirteen traits

Int.J.Curr.Microbiol.App.Sci (2020) Special Issue-11: 1479-1486

RMG 1039	42.00	62.00	43.4	3.95	8.00	12.15	6.37	10.50	15.25	23.30	3.29	34.01	5.14
RMG 268	43.25	67.25	33.3	2.85	6.70	16.00	7.65	10.65	15.82	22.35	3.10	44.22	6.97
RMG 1093	40.75	67.25	29.4	3.05	8.15	14.65	6.65	10.95	16.34	21.45	3.05	36.71	5.74
SML 668	42.00	66.75	30.6	2.80	8.30	17.92	6.18	11.20	16.89	22.20	3.22	31.26	5.16
JLM 1751	39.00	63.75	52.3	5.65	5.22	14.06	5.93	5.93	16.95	22.48	3.04	13.98	2.27
JLM 1752	39.00	59.25	41.0	5.65	4.18	9.17	6.35	6.07	16.45	20.92	2.96	22.81	3.83
JLM 1754	40.25	64.25	44.4	5.65	5.03	15.05	7.30	6.18	14.35	23.10	3.09	29.60	4.23
JLM 1757	37.75	63.25	45.9	5.65	4.55	14.05	6.27	6.07	15.60	23.75	3.11	29.24	4.72
JLM 1758	35.75	61.25	43.9	5.00	4.05	9.90	7.27	6.22	17.60	20.58	3.08	12.03	2.11
SAMARAT ©	40.00	64.00	51.3	3.90	5.30	18.75	7.45	12.73	22.78	23.08	3.88	35.42	6.95
Mean	41.39	62.54	47.0	3.84	6.79	15.52	7.23	10.09	15.77	21.97	3.38	33.48	5.19
Range Min	35.75	59.25	29.4	2.80	4.05	9.10	5.93	5.93	9.65	19.92	2.07	12.03	2.11
Range Max	46.00	67.25	60.0	5.65	13.15	21.85	10.13	12.73	22.78	23.75	5.65	46.89	7.11
C.V.	2.68	1.14	4.4	7.01	6.71	6.14	3.79	4.47	6.02	2.78	6.57	8.97	4.62
S.E.	0.56	0.36	1.0	0.13	0.23	0.48	0.14	0.23	0.47	0.31	0.11	1.50	0.12
C.D. (5%)	1.56	1.00	2.9	0.38	0.64	1.33	0.38	0.63	1.33	0.85	0.31	4.20	0.34

Table.3 Phenotypic (lower diagonal) and Genotypic (upper diagonal) correlation coefficient for thirteen characters in mungbean

Character	DF	DM	PH	BPP	CPP	PPP	PL	SPP	BYP	SYP	SI	HI	PC
DF	1.0000	0.0391	0.1800	-0.5141	0.6302	0.5424	0.2730	0.5828	-0.1719	0.4108	0.1058	0.4538	-0.0893
DM	0.0216	1.0000	-0.3015	-0.2162	0.0764	-0.0393	0.0786	0.0993	0.0156	0.1339	0.1667	0.1588	0.2031
PH	0.1470	-0.2783**	1.0000	0.1856	0.2394	0.1803	0.1682	0.1311	0.0123	0.0507	0.0726	0.0706	0.0192
BPP	-0.3611**	-0.1732*	0.1671*	1.0000	-0.1486	-0.2808	-0.0709	-0.7715	0.1876	-0.3562	0.0865	-0.4589	0.0531
CPP	0.5224**	0.0700	0.2321**	-0.1259	1.0000	0.3621	-0.0190	0.3094	-0.0301	0.2428	0.1367	0.2394	-0.2332
PPP	0.4035**	-0.0266	0.1683*	-0.2611**	0.3454**	1.0000	0.1423	0.4383	0.0250	0.0236	-0.1671	0.0360	0.0475
PL	0.2145**	0.0791	0.1498	-0.0627	-0.0069	0.1342	1.0000	0.3643	0.0464	0.3535	0.6511	0.3250	-0.1189
SPP	0.4602**	0.0946	0.1243	-0.6967**	0.2970**	0.4063**	0.3545**	1.0000	-0.0734	0.6173	0.2085	0.6710	-0.0696
BYP	-0.1142	0.0188	0.0074	0.1481	-0.0181	0.0259	0.0598	-0.0782	1.0000	0.1712	0.0870	-0.3404	-0.0773
SYP	0.3358**	0.1275	0.0573	-0.3324**	0.2324**	0.0147	0.3223**	0.5871**	0.1362	1.0000	0.3451	0.8675	0.1471
SI	0.0815	0.1525	0.0691	0.0699	0.1203	-0.1604*	0.5833**	0.2087**	0.0689	0.3237**	1.0000	0.2830	-0.1322
HI	0.3684**	0.1439	0.0664	-0.3782**	0.2214**	0.0248	0.2601**	0.6113**	-0.3579**	0.8208**	0.2516**	1.0000	0.1958
PC	-0.0644	0.1296	-0.0046	0.0084	-0.1840*	0.0341	-0.0832	-0.0462	-0.0492	0.1068	-0.0858	0.1236	1.0000

Int.J.Curr.Microbiol.App.Sci (2020) Special Issue-11: 1479-1486

Figure.1 Illustration of experimental research trial Kharif-2017



Acknowledgement

This research did not receive any specific funding. This research was conducted as a corresponding author's Master's degree programme submitted to Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad-211007 (Uttar Pradesh) India under the guidance of Dr. (Mrs.) G. Roopa Lavanya, Associate Professor, Department of Genetics and Plant Breeding. Authors are thankful to the staff of Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad-211007 (Uttar Pradesh) India for providing necessary research facilities. The authors are thankful to the reviewers for their careful reading of the manuscript and for providing insightful suggestions.

Conflicts of Interest

The authors declare no conflict of interest.

References

- Bhutia P, Lal GM and Thomas N. 2016.Studies on genetic variability, correlation and path analysis in green gram [*Vigna radiata* (L.) Wilczek] germplasm. International Journal of Agriculture Science. 8(51): 2267-2272.
- Bisht N, Singh DP, Khulbe RK. 2014. Genetic variability and correlation studies in advance inter-specific and inter-varietal lines and cultivars of mungbean [*Vigna radiata* (L.) Wilczek]. Journal of Food Legume. 27(2):155-157.
- Choudhary P, Payasi SK, Urmaliya K. 2016. Genetic association and path analysis for yield contributing traits in mungbean [*Vigna radiata* (L.) Wilczek]. International Journal of

Agriculture Sciences. 8(52): 2465-2468.

- Gadakh SS, Dethe AM and Kathale MN. 2013. Genetic variability, correlations and path analysis studies on yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]. Bioinfolet. 10(2a): 441-447.
- Johnson HW, Robinson HF and Comstock RE. 1955. Genotypic and phenotypic correlation in soybean and their implications in selection. Agronomy Journal. 47: 477-483.
- Katiyar M, Vishwakarma RK and Singh SK.
 2015. Character association and genetic variability in mungbean [*Vigna radiata* (L.) Wilczek]. Trends in Biosciences. 8(1): 268-270.
- Khanpara MD, Vachhani JH, Jivani LL, Jethava AS and Vaghasia PM. 2012.
 Correlation and path coefficient analysis in green gram [*Vigna radiata* (L.) Wilczek]. Asian Journal of Bio Science. 7(1): 34-38.
- Kumar, A., Sharma, N.K., Kumar, R., Sanadya, S.K. and Sahoo, S., 2018. Correlation and path analysis for seed yield and components traits in mungbean under arid environment. International Journal of Chemical Studies, 6(4): 1679-1681.
- Kumar, A., Sharma, N.K., Kumar, R., Sanadya, S.K., Sahoo, S. and Yadav, M.K. 2020. Study of genetic variability parameters for seed yield and its components traits in mungbean under arid environment. International Journal of Chemical Studies, 8(4): 2308-2311.
- Sahoo, S., Sanadya, S.K., Kumari, N. and Baranda, B. 2019. Estimation of the various genetic variability parameters for seed yield and its component traits in mothbean germplasm [*Vigna aconitifolia* (Jacq.) Marechal]. Journal

of Pharmacognosy and Phytochemistry SP3: 49-52.

- Sahoo, S., Sharma, A.K., Sanadya, S.K., and Kumar, A. 2018. Character association and path coefficient analysis in mothbean germplasm. International Journal of Current Microbiology and Applied Sciences, 7(8): 833-839.
- Sharma NK. 2016. Mungbean production strategy. Swami Keshwanand Rajasthan Agricultural University, Bikaner. DOR/SKRAU/2016/NFSM Publication-1, 21.
- Singh C, Singh P, Singh R. 2015. Modern Techniques of Raising Field Crops. Oxford & IBH Publishing Co. Pvt. Ltd., New Delhi, 386.