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Correlation and path analysis studies on yield and its component traits in greengram (*Vigna radiata* L.)

Jilla Divya*, Neha Thomas, G.M. Lal*** and Abhinav Dayal****

Department of Genetics and Plant Breeding, Sam Higgin bottom University of Agriculture, Technology & Science, Prayagraj, UP, 211007.
***Corresponding Author's Email: neha.thomas@shuats.edu.in*

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ABSTRACT

In the present investigation, 31 mungbean genotypes were evaluated for different quantitative traits to determine relationships among yield and some yield components using direct (variability, heritability, and genetic advance) and indirect selection parameters (correlation and path coefficient analysis). Significant genetic variations were observed among the genotypes for pods/plant, days to 50% flowering, days to maturity, plant height, 100-seed weight, and seed yield/plant. The magnitude of correlation revealed that seed yield/plant had a positive and highly significant correlation with plant height, number of primary branches, number of clusters per plant, number of pods per plant, biological yield, and 100-seed weight. Path coefficient analysis indicated that 100- seed weight, number of primary branches, plant height, and pod length had the maximum direct positive effect on seed yield/plant. Consequently, based on the genetic parameter correlation and path analysis, a number of effective branches, pods/plant, and 100-seed weight should be given significant precedence while formulating a selection strategy for effective improvement of mungbean varieties.

Keywords : Mungbean, correlation, path analysis, effective branches, pods plant^{-1}, 100-seed weight, seed yield

INTRODUCTION

Mungbean [*Vigna radiata* (L.)] also known as greengram, is one of the most important pulse crops in India. It is grown over an area of 33.41 lakh hectares with 57.07 lakh tonnes of production and a productivity of 885 kg ha^{-1} (Directorate of Pulses Development annual report, 2023). As a significant legume crop with the potential to increase soil fertility, Mung bean is self-pollinated, short-lived, broadly adaptable, extremely flexible, and drought tolerant. Green gram has a high seed protein content (27%) and the capacity to fix atmospheric nitrogen biologically to replenish soil fertility (Anita *et al.*, 2022). The lack of genetic variety for high-yield potential is the main obstacle that limits significant advancements in the production of mung beans (Sandhiya *et al.,* 2018).

It is crucial to choose superior parents who show greater heritability and genetic advancement for a range of features in any yield improvement effort.

Genetic variability, therefore, with the aid of appropriate metrics like genotypic and phenotypic coefficient of variation, and path coefficient analysis, is vitally important to begin an effective breeding program. Correlation studies are not a reliable source of information on the relationships between heritable features that could have unfavorable effects. However, path analysis divides total correlation into direct and indirect effects aids in improving the efficacy of these selections

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*M. Sc Scholar, **Assistant Professor, ***Associate Professor

(Nitesh *et al.,* 2018). The choice of a high-yielding genotype for a breeding program is based on two relationships between yield-contributing features and grain yield, as well as the direct and indirect implications of these relationships. (Prabhath *et al.,* 2019). Path coefficient analysis is a powerful statistical method specifically intended to measure how various components interact and affect seed yield both directly and indirectly (Hemavathy *et al.,* 2015). It is crucial to understand the relationships between different characters and path coefficients in order to compile the yield-contributing characters' optimal contribution. The best way to investigate certain forces causing correlation is to calculate the direct and indirect impacts of path analysis (Anil *et al.,* 2024). Genetic variability and correlation between yield and yield components in mungbean have been studied by several researchers including Kate *et al.,* (2017), Hemavathy *et al.,* (2015), and Santhi Priya *et al.,* (2021), reported who significant differences among various genotypes. With this background, the present investigation was undertaken to examine the genetic variability, heritability, genetic advance, correlation, and path analysis with respect to various desirable characters in thirty-one genotypes of mungbean. The acquired information will assist in recognizing promising lines for a hybridization program to explore mungbean varieties of high-yielding potential coupled with quality.

MATERIALS AND METHODS

The experiment was conducted during *Kharif-2023* at the field experimentation center of the Department of Genetics and Plant Breeding, SHUATS, Prayagraj, Uttar Pradesh which is nearly 5km away from Prayagraj city and is very near to Yamuna River. The site is located at 25.28N latitude, 81.54 E longitude, and 98 meters above sea level.

The experimental materials comprised thirty-one genotypes of mungbean obtained from the All India Coordinated Pulse Improvement Project, Department of Genetics and Plant Breeding, Institute of Agriculture Science, Banaras Hindu University, Varanasi (Table 1). The experiment was laid out in a randomized block design with three replications during *Kharif 2023-24*. Seeds of each genotype were sown in a unit plot size of 1m^2 long with a spacing of 30 x 10 cm. Standard agronomic practices were adopted for the experiments.

Table 1. Name of the mungbean genotypes, their pedigree, and place of origin

Sl.No.	Genotypes	Origin/Source
1	IPM-2-14	IIPR, Khanpur
2	VIRAT	IIPR, Khanpur
3	IPM-205-7	IIPR, Khanpur
4	SAMRAT (CHECK)	IIPR, Khanpur
5	MGG-295	PJTSAU, Hyderabad
6	LGG-460	PJTSAU, Hyderabad
7	MGG-351	PJTSAU, Hyderabad
8	GM-3	PJTSAU, Hyderabad
9	SHAKTI	TNAU, Coimbatore
10	CO-7	TNAU, Coimbatore
11	CO-8	TNAU, Coimbatore
12	KM-2	UAS, Dharwad
13	MGG-348	UAS, Dharwad
14	MGG-385	UAS, Dharwad
15	PUSHA-105	IARI, New Delhi
16	VEENA	IARI, New Delhi
17	VBN-3	NPRC, Vamban
18	VBN-2	NPRC, Vamban
19	SML-1668	PAU, Ludhiana
20	ML-131	PAU, Ludhiana
21	R-288-8	RAU, Rajasthan
22	RM-12-11	RAU, Rajasthan
23	SIKHA	OUAT, Bhubaneshwar
24	AMULYA	NRI Agritech, Guntur
25	MH-421	CCSHAU, Hissar
26	Su-urd-113	SDAU, Gujarat
27	MGG-2	MPKV, Maharashtra
28	MGG-347	ARS, Madhira
29	SM-02-103	-
30	MGG-371	-
31	KM-11-564	-

Observations were recorded on days to 50% flowering and days to maturity (%), plant height (cm), number of primary branches, number of clusters per plant, days to 50% pod setting, number of pods per plant, pod length (cm), number of seeds per pod, biological yield (g), harvest index (%), 100-seed weight (%), seed yield per plant (g) were recorded on a plot basis.

The data were subjected to the analysis of variance (Panse and Sukhatme, 1967) and further, biometrical procedures were followed to estimate the genotypic and phenotypic coefficient of variation (Burton, 1952), heritability in a broad sense (Burton and Devane, 1953), genetic advance (Lush

1940) and correlation (Al Jibouri *et al.*, 1958), and path coefficient analysis (Dewey and Lu, 1959).

Results and Discussion

Variability studies

The analysis of variance depicting mean squares for the different thirteen characters studied is presented in Table 2. Highly significant differences were observed among genotypes for alltraits. A wide range of variability in mungbean germplasm was displayed by different characters namely; days to 50% flowering (33-49), days to maturity (57-68), plant height (73-97 cm), number of branches per plant (5-10), number of clusters per plant (3-5), days to 50% pod setting (61-68), number of pods per plant (8-24), pod length (6.53-8.53 cm), number of seeds per pod (9.20-12.47), biological yield (26.48-38.25 g), harvest index (19.48-27.49 %), 100-seed weight (3.00-5.00 g), and seed yield per plant (3.60-12.26 g). Awide range of phenotypic variation was observed (Table 3). These findings are in agreement with those of Sridhar *et al.*, (2020). In response to selection, thep henotypic variance was partitioned into its genotypic and environmental components. It was observed that for all the characters, environmental components of variation were comparatively lower than other components, indicating that the phenotypic variability might be a reliable measure of genotypic variability. Therefore, selection based on phenotype would be effective for these characters. The genotypic and phenotypic components of variability were high for seed yield per plant, number of pods per plant, and 100-seed weight which were in agreement with those of Sineka *et al.*, (2021).

The highest σ2g and σ2p (37.13 and 61.53) were observed for plant height followed by days to 50% flowering, number of pods per plant, and biological yield.

GCV described by Burton (1952) is a better index for measuring genotypic variability present in the population. The highest GCV was observed for seed yield per plant, followed by the number of pods per plant, and 100-seed weight. These results were in conformity with earlier reports for

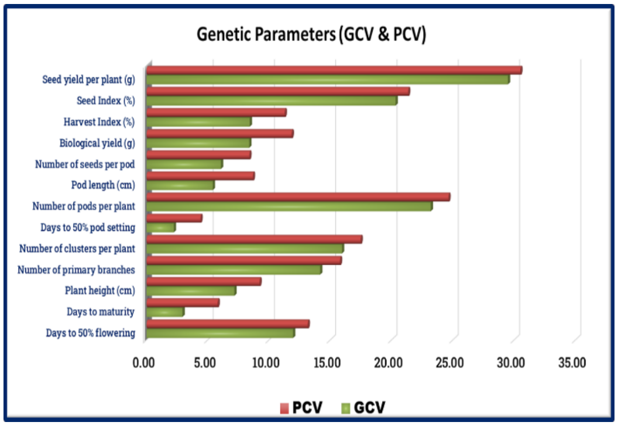

Fig. 1. Estimates of genotypic and phenotypic coefficient of variation.

Table 2. Analysis of variance for different characters in mungbean

Sr. No.	Source	Mean sum of squares (MSS) Replication	Treatment	Error
	Degree of Freedom	2	30	60
1	Days to 50% flowering	7.6240	69.762**	4.597
2	Days to maturity	19.5670	19.94**	9.828
3	Plant height	73.10	135.787**	24.406
4	Number of primary branches	0.8090	3.615**	0.27
5	Number of clusters per plant	0.2450	1.308**	0.082
6	Days to 50% pod setting	12.1480	12.358**	6.092
7	Number of pods per plant	1.9150	36.379**	1.495
8	Pod length	0.5230	0.771**	0.266
9	Number of seeds per pod	0.4770	1.741**	0.405
10	Biological yield	22.3550	29.829**	7.453
11	Harvest index	8.540	13.623**	2.848
12	100-seed weight	0.2110	2.22**	0.074
13	Seed yield per plant	0.9830	15.244**	0.35

**Significant at 1% level of significance seed yield per plant and number of pods plant-1 (Anil *et al.,* 2024) and for 100-seed weight (Samita *et al.*, 2022). Moderate GCV was observed for number of clusters per plant (15.95 %), number of primary branches (14.17 %), and days to 50% flowering (11.96 %). These results were in conformity with earlier reports for a number of clusters per plant (Chalapati *et al.,* 2020). The heritability was observed highest for seed yield per plant (93.42 %) followed by 100-seed weight (90.59%), number of pods per plant (88.60 %), and days to 50% flowering (82.53 %). The higher estimates of heritability indicated that these characters were less affected by the environment and under the control of the additive gene effect. These findings were in conformity with Devendra *et al.,* (2015) for most characters, and Zuge *et al.,* (2019) for the remaining characters. The lowest value of heritability was observed for days to 50% pod setting, indicating that this trait is more affected by the environment and governed by polygenes. Genetic advance (GA) as percent of means was the highest for plant height (9.75%). Higher values of heritability estimates coupled with high genetic advance as a percent of mean were observed for seed yield per plant, number of pods per plant, 100-seed weight, number of primary branches, and days to 50% flowering. These results were in support with those of Bhanu *et al.,* (2017). High heritability and high genetic advance may be attributed to additive gene action (Panse, 1957).

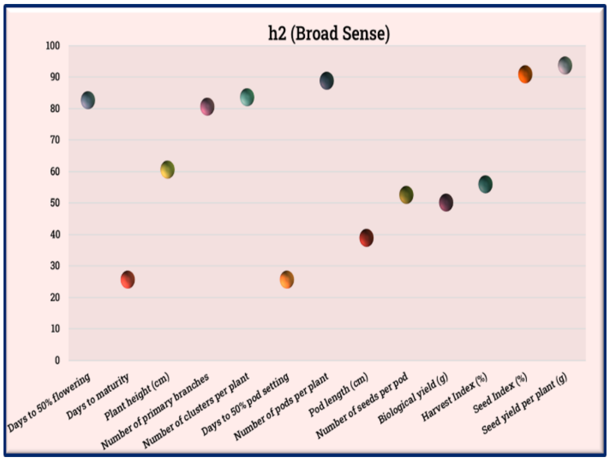

Fig. 2. Estimates of broad sense heritability.

Therefore, direct selection for characters viz., seed yield per plant, number of pods per, number of primary branches, and 100-seed weight would be effective and therefore, considered to be of prime importance in formulating the selection program.

Character association

Correlation coefficient analysis

The estimation of the correlation coefficient has been done at both phenotypic and genotypic levels. The results indicated that the values of genotypic correlation were higher than their phe-

Table 3. Estimates of genetic parameters for seed yield and its components in mungbean

Parameters		DF50	DM	PH (cm)	NPB	NCPP	DP50	NPPP	PL (cm)	NSPP	BY (g)	HI (%)	100-Seed weight (g)	SYPP
Range	Min.	33.33	57.27	73.33	5.40	3.00	68.13	7.93	6.53	9.20	26.48	19.48	3.00	3.60
	Max.	49.47	68.40	97.20	10.33	5.67	61.47	24.53	8.51	12.47	38.25	27.49	5.00	12.26
Mean		38.98	62.53	84.99	7.45	4.01	64.84	14.70	7.59	10.98	32.58	22.49	4.16	7.56
Vg		21.72	3.37	37.13	1.12	0.41	2.09	11.63	0.17	0.45	7.46	3.59	0.72	4.97
Vp		26.32	13.20	61.53	1.39	0.49	8.18	13.12	0.43	0.85	14.91	6.44	0.79	5.31
GCV%		11.96	2.94	7.17	14.17	15.95	2.23	23.20	5.41	6.08	8.38	8.43	20.32	29.49
PCV%		13.16	5.81	9.23	15.79	17.47	4.41	24.64	8.69	8.40	11.85	11.28	21.35	30.51
ECV		5.50	5.01	5.81	6.97	7.14	3.81	8.32	6.80	5.80	8.38	7.50	6.55	7.82
Broad sense heritability (h^2) %		82.533	25.538	60.336	80.496	83.31	25.532	88.606	38.776	52.35	50.02	55.771	90.599	93.423
GA (as % of mean)		22.38	3.06	11.47	26.18	29.99	2.32	44.98	6.94	9.06	12.21	12.96	39.85	58.71

* DF50: Days to 50% flowering, DP50: Days to 50% pod setting, PH: Plant height (cm), NPB: Number of primary branches per plant, NCPP: Number of clusters per plant, DM: Days to maturity, NPPP: Number of pods per plant, PL: Pod length NSP: Number of seeds per pod, BY: Biological Yield (g), SI: Seed Index (g), HI: Harvest index (%), SYPP: Seed yield per plant (g).

* Vg: Genotypic variance; Vp: Phenotypic variance; Ve: Environmental variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; GA: Genetic Advance

notypic counterparts (Table 4). This indicated that though there was a high degree of association between the two variables at the genotypic level, its phenotypic expression was deflated by the influence of the environment. This indicated a greater role of non-genic factors in determining these associations, which reflected that the environment may deviate from the expression of genotypic association. Seed yield plant-1 showed a significant and positive correlation with all characters except for days to maturity, pod length, and number of seeds per pod at both genotypic and phenotypic levels. Hence these traits, except days to maturity, pod length, and number of seeds per pod, could be utilized in indirect selection so as to improve seed yield per plant. Days to 50% flowering had no significant correlation but it shows a positive correlation with biological yield and days to maturity and a negative correlation with the number of primary branches, number of pods per plant, and harvest index. Days to 50% pod setting has no significant correlation but it shows a positive correlation with pod length and a negative

Table 4. Genotypic and phenotypic correlation coefficients among thirteen yield and yield attributing characters studied in mungbean

Characters	Σ	DM	PH (cm)	NPB	NCPP	DP50	NPPP	PL (cm)	NSPP	BY (g)	HI (%)	100-Seed weight(g)	SYPP
DF50	rp	0.250*	0.0591	-0.204*	-0.0032	0.197	-0.245*	0.1002	0.1386	0.1391	-0.1681	0.0545	0.0192
	rg	0.299*	0.0317	-0.235*	0.0031	0.573**	-0.270*	0.1995	0.1909	0.217*	-0.221*	0.0725	0.0142
DM	rp		0.1915	-0.1935	0.1092	0.0995	-0.268*	0.0738	0.219*	0.1519	-0.2004	-0.1774	-0.1931
	rg		0.542**	-0.425**	0.333*	0.651**	-0.490**	-0.1576	0.586**	0.518**	-0.541**	-0.309*	-0.0861
PH (cm)	rp			-0.0025	0.445**	-0.1287	0.204*	-0.1803	0.0843	0.1476	-0.1398	-0.032	0.0028
	rg			-0.0316	0.497**	-0.419**	0.245*	-0.1596	0.109	0.0609	-0.0914	-0.0355	0.321*
NPB	rp				-0.334*	-0.077	0.0007	-0.252*	-0.1273	-0.14	0.1636	-0.1646	0.1991
	rg				-0.377**	-0.1919	0.0217	-0.522**	-0.239*	-0.257*	0.222*	-0.1983	0.219*
NCPP	rp					-0.1629	0.331*	-0.0166	-0.0233	0.260*	-0.256*	-0.220*	0.2125
	rg					-0.331*	0.381**	0.1119	0.0085	0.374**	-0.374**	-0.251*	0.440**
DP50	rp						-0.210*	0.0416	-0.1129	0.0676	-0.1148	-0.1666	0.0452
	rg						-0.382**	0.657**	0.0495	0.1531	-0.1909	-0.229*	0.112
NPPP	rp							-0.0812	-0.1767	-0.0258	0.0557	0.0721	0.1732*
	rg							-0.0844	-0.246*	-0.1232	0.1537	0.0661	0.394**
PL (cm)	rp								0.226*	-0.0098	-0.007	-0.0555	-0.0261
	rg								0.0959	-0.042	-0.0007	-0.1603	-0.0445
NSPP	rp									0.0424	-0.03	0.269*	-0.0132
	rg									0.092	-0.1281	0.375**	-0.0312
BY (g)	rp										-0.944**	-0.0919	-0.206*
	rg										-0.990**	-0.1398	0.852*
HI (%)	rp											0.1019	0.19
	rg											0.1135	0.268*
100-Seed weight (g)	rp												0.250*
	rg												0.264*

*Significant at 5% level of significance; **Significant at 1% level of significance rp: Phenotypic coefficient of variation; rg: Genotypic coefficient of variation DF50: Days to 50% flowering, DP50: Days to 50% pod setting, PH: Plant height (cm), NPB: Number of primary branches per plant, NCPP: Number of clusters per plant, DM: Days to maturity, NPPP: Number ofpods per plant, PL: Pod length NSP: Number of seeds per pod, BY: Biological Yield (g), SI: Seed Index (g), HI: Harvest index (%), SYPP: Seed yield per plant (g).

Table 5. Genotypic and phenotypic path coefficient analysis showing direct and indirect effects among thirteen yield and yield attributing characters studied in mungbean

Characters	Σ	DF50	DM	PH (cm)	NPB	NCPP	DP50	NPPP	PL (cm)	NSPP	BY (g)	HI (%)	100-Seed weight(g)	SYPP
DF50	P	-0.0311	-0.0078	-0.0018	0.0064	0.0001	-0.0061	0.0076	-0.0031	-0.0043	-0.0043	0.0052	-0.0017	0.0192
	G	-0.4055	-0.1212	-0.0128	0.0951	-0.0013	-0.2322	0.1096	-0.0809	-0.0774	-0.0881	0.0895	-0.0294	0.0142
DM	P	-0.0577	-0.2308	-0.0442	0.0447	-0.0252	-0.023	0.0619	-0.017	-0.0505	-0.035	0.0462	0.0409	-0.1931
	G	0.0443	0.1483	0.0803	-0.063	0.0494	0.0966	-0.0727	-0.0234	0.0869	0.0768	-0.0802	-0.0458	0.420**
PH (cm)	P	0.0052	0.0169	0.0881	-0.0002	0.0392	-0.0113	0.018	-0.0159	0.0074	0.013	-0.0123	-0.0028	0.2151
	G	0.0062	0.1056	0.1949	-0.0062	0.0968	-0.0816	0.0477	-0.0311	0.0212	0.0119	-0.0178	-0.0069	-0.321*
NPB	P	-0.0186	-0.0176	-0.0002	0.0912	-0.0304	-0.007	0.0001	-0.023	-0.0116	-0.0128	0.0149	-0.015	0.1991
	G	-0.317	-0.574	-0.0427	1.3516	-0.509	-0.2594	0.0293	-0.7052	-0.3235	-0.3475	0.3006	-0.2681	0.219*
NCPP	P	0.0007	-0.0243	-0.0991	0.0744	-0.2228	0.0363	-0.0737	0.0037	0.0052	-0.058	0.057	0.0489	0.496**
	G	0.0022	0.237	0.3537	-0.2682	0.7122	-0.2359	0.2712	0.0797	0.006	0.2665	-0.2666	-0.1789	-0.568**
DP50	P	-0.0074	-0.0037	0.0048	0.0029	0.0061	-0.0376	0.0079	-0.0016	0.0042	-0.0025	0.0043	0.0063	0.0452
	G	0.2695	0.3064	-0.1969	-0.0903	-0.1559	0.4705	-0.1799	0.3092	0.0233	0.072	-0.0898	-0.1077	0.112
NPPP	P	0.1401	0.1533	-0.1167	-0.0004	-0.1891	0.1203	-0.5719	0.0464	0.1011	0.0147	-0.0318	-0.0413	0.512**
	G	0.2943	0.5338	-0.2666	-0.0236	-0.4147	0.4164	-1.0891	0.092	0.2674	0.1341	-0.1674	-0.0719	0.375**
PL (cm)	P	0.0025	0.0019	-0.0045	-0.0063	-0.0004	0.001	-0.002	0.0251	0.0057	-0.0002	-0.0002	-0.0014	-0.0261
	G	0.1663	-0.1314	-0.1331	-0.435	0.0933	0.5478	-0.0704	0.8338	0.08	-0.035	-0.0006	-0.1336	-0.0445
NSPP	P	-0.0182	-0.0287	-0.0111	0.0167	0.0031	0.0148	0.0232	-0.0296	-0.1311	-0.0056	0.0039	-0.0353	-0.0132
	G	-0.0735	-0.2255	-0.0419	0.0921	-0.0033	-0.019	0.0945	-0.0369	-0.3849	-0.0354	0.0493	-0.1444	-0.0312
BY (g)	P	-0.0251	-0.0274	-0.0266	0.0253	-0.047	-0.0122	0.0047	0.0018	-0.0076	-0.1806	0.1704	0.0166	0.2123*
	G	1.3207	3.1495	0.3701	-1.5628	2.2746	0.9305	-0.7488	-0.2555	0.5595	6.0792	-6.0193	-0.8499	-0.320*
HI (%)	P	0.0156	0.0186	0.0129	-0.0151	0.0237	0.0106	-0.0052	0.0006	0.0028	0.0874	-0.0926	-0.0094	0.19
	G	-1.3938	-3.4124	-0.5773	1.4041	-2.363	-1.2049	0.9703	-0.0043	-0.809	-6.2508	6.313	0.7166	0.852*
100-Seed	P	0.0133	-0.0433	-0.0078	-0.0402	-0.0536	-0.0407	0.0176	-0.0135	0.0656	-0.0224	0.0249	0.244	0.250*
weight (g)	G	0.1004	-0.4271	-0.0492	-0.2745	-0.3477	-0.3168	0.0914	-0.2219	0.5192	-0.1935	0.1571	1.384	0.264*
SYPP	P	0.0192	-0.1931	0.2151	0.1991	0.496**	0.0452	0.512**	-0.0261	-0.0132	0.2123*	0.19	0.250*	
	G	0.0142	0.420**	-0.321*	0.219*	-0.568**	0.112	0.375**	-0.0445	-0.0312	-0.320*	0.268*	0.264*	

*Significant at 5% level of significance; **Significant at 1% level of significance

Residua l(G) = 0.639 Residual (P)=0.679 Bold diagonal figures are the direct effects

DF50: Days to 50% flowering, DP50: Days to 50% pod setting, PH: Plant height (cm), NPB: Number of primary branches per plant, NCPP: Number of clusters per plant, DM: Days to maturity, NPPP: Number of pods per plant, PL: Pod length NSP: Number of seeds per pod, BY: Biological Yield (g), SI: Seed Index (g), HI: Harvest index (%), SYPP: Seed yield per plant (g).

correlation with the number of pods per plant and 100-seed weight. The negative and significant correlation of seed yield per plant with biological yield, and positive and significant correlation with plant height, number of primary branches, number of clusters per plant, number of pods per plant, biological yield, harvest index, and 100-seed weight at both genotypic and phenotypic level were in agreement with Reshmi *et al.,* (2022). These results propound that any positive increase in such traits will improve the seed yield of mungbean. As the seed yield per plant is influenced mutually by genetic and environmental effects, even a small scale of fluctuation in environmental conditions might cause variation in the final yield. Thus, it is advisable to select the varieties as per the recommendations.

Path coefficient analysis

The information on the correlation coefficient determines only the nature and degree of association existing between pairs of characters. Seed yield is dependent on several mutually associated component characters. Thus, a change in anyone of the components may possibly affect the whole network of cause and effect of the relationship tending to vitiate association of yield and yield components. Path analysis (Dewey and Lu, 1959) is valuable in partitioning the phenotypic correlation of component characters into direct and indirect effects which might provide the true association of component characters, both in magnitude and direction (Biradar *et al*., 2007). In the present study, all the characters except a number of primary branches and 100-seed weight showed a highly significant and positive correlation with seed yield (Table 5). The highest positive direct effect on yield plant^{-1} was exhibited by 100-seed weight (1.38) followed by a number of primary branches (1.35), pod length (0.83), and plant height (0.19). These findings are in agreement with the results of Juhie *et al.,* (2017). The number of pods per plant showed a moderate negative direct effect on yield at both phenotypic and genotypic levels. Days to maturity showed the lowest negative direct effect on yield at the phenotypic level and the lowest positive direct effect at the genotypic level. Path coefficient analysis revealed that 100-seed weight had a positive direct effect on seed yield. This trait also recorded a strong positive genotypic correlation with seed yield per plant. This indicated the selection of the genotypes having a greater 100-seed weight along with an optimum number of primary branches would be rewarding for isolating high-yielding genotypes in this crop.

Conclusion

The correlation study indicated the relationships among various agronomic characters and the direct and indirect effects of each character on the seed yield of mungbean under warmand dry conditions. The findings revealed that selection programs based on plant height, number of primary branches/plant, number of clusters per plant, number of pods per plant, biological yield, harvest index, and 100-seed weight should be given adequate importance in improving the seed yield of mungbean. Correlation coefficients give only partial information while path analysis allows the partitioning of correlation coefficients into direct and indirect effects. The present investigation on correlation and path analysis reveals that the selection of the genotypes having a greater 100-seed weight along with an optimum number of primary branches should be given more emphasis for the improvement of seed yield in mungbean.

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References

Anand, G., Anandhi, K. and Paulpandi,V. K. 2016. Genetic variability, correlation, and path analysis for yield and yield components in F6 families of Greengram (*Vigna radiate* (L.) Wilczek) under rainfed conditions. *Electronic J. Pl. Breed.,* **7**(1): 434-437.

Anil, A., Sharma, N.K., Kumar, R., Sanadya, S.K. and Sahoo, S. 2024. Correlation and Path Analysis

Studies in Mungbean [*Vigna radiata* (L.) Wilczek] under Arid Environment of Western Rajasthan. *Indian Journal of Agricultural Research.* doi: 10.18805/IJARe.A-6195.

Anita, S.R. Kumhar, Anil Kumar, Suchitra, Anil Kulheri, Pooja Kanwar Shekhawat, Giradhari Lal Yada, 2022. Correlation and path analysis studies of pod yield and its component traits in mungbean (*Vigna radiata* L.) genotypes. *Legume Research.* DOI: 10.18805/LR-4906.

Anuhya Jayaprada, G. Roopa Lavanya 2019. Correlation and path analysis of yield contributing traits and seed yield in green gram (*Vigna radiata* L.). *Indian Journal of Agricultural Research*, **53**(6): 753-755.

Aparna Raturi, S.K. Singh, Vinay Sharma1 and Rakesh Pathak. 2014. Genetic variability, heritability, genetic advance, and path analysis in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research,* **38** (2) 2015: 157-163.

Al- jibouri, H., Miller, P.A. and Robinson, H.F. 1958. Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. *Agronomy Journal,* **50**(10): 633-636.

Bhanu, Mn Singh and Manish Singh. 2016. Genetic variability, correlation, and path coefficient analysis for quantitative traits in mungbean genotypes. *Journal of Food Legumes,* **29**(3&4): 199-205, 2016.

Burton, G.W. 1952. Qualitative inheritance in grasses. *In Proceedings of the 6th International Grassland Congress, Pennsylvania State College*, 17-23 August 1952, **1:** 277-283.

Burton, G.W. and Devane, E. H. 1953. Estimating heritability in tall (*Fecue arundinacea*) from replicated clonal material. *Agronomy Journal*, **45**: 478-481.

Chalapati Naga Sai Krishna, Sanjay Kumar, Suresh Bg and Anand Kumar, 2020. Effect of seasonal variations on yield and its attributes in mungbean [*Vigna radiata* (L.) Wilczek]. *Journal of Food Legumes,* **33**(1): 17-22, 2020.

Dewey, D.R. and Lu, K.I. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal.* **51:** 515-518.

Devendra K. Payasi 2015. Genetic variability analysis for seed yield and its components in mungbean (*Vigna radiata* L. Wilczek). *International Journal of Plant Breeding and Genetics.* **9** (3): 177-188, 2015.

Directorate of Pulses Development 2023-2024. Ministry of Agriculture and Farmers Welfare, Department of Agriculture and Farmers Welfare DPD Vindhyachal Bhavan, Bhopal, Madhya Pradesh.

Hemavathy, N. Shunmugavalli and Anand, G. 2015. Genetic variability, correlation and path co-efficient studies on yield and its components in mungbean [*Vigna radiata* (L.) Wilezek]. *Legume Research,* **38** (4): 2015: 442-446.

Juhie Koknal Marak, 2017. Correlation and path analysis. Study on some morphological and yield parameters of mungbean (*Vigna radiata* L. Wilezek). *Journal of Agricultural Engineering and Food Technology,* p-ISSN: 2350-0085; e-ISSN: 2350-0263; **4**(1): pp. 60-65.

Kate, A. M., Dahat, D. V. and Chavan, B. H. 2017. Genetic variability, heritability, correlation and path analysis studies in green gram (*Vigna radiata* L. Wilczek). *International Journal of Development Research*. 07, Issue, 11, pp.16704-16707, November, 2017.

Khatik, S. R., Dhaka, A., Uddin, K., Chandra, M. A., Khan, S. K., Attar, H. S., Jatav, M. Nitharwal and Kumawat, S. 2022. Estimates of genetic variability for seed yield and its component characters in green gram (*Vigna radiate*, Fabaceae). *Asian Journal of Agricultural Extension, Economics & Sociology*, **40**(10): 992-997.

Lush, J. L. 1940. Inter-size correlation regression of offspring on dairy as a method of estimating heritability of characters. *Proceedings American Society of Animal Production*, **33**: 293-301.

Nitesh, S.D., Talwade, A.C. and Gopal Katna 2018. Correlation and path analysis studies in chickpea (*Cicer arietinum* L.) for seed yield and its attributes in the Himalayan region. *Journal of Food Legumes,* **31**(4): 258-260, 2018.

Panse, V.G. 1957. Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics and Plant Breeding,* **17(2):** 318-328.

Panse, V.G. and Sukhatme, P.G. 1967. Statistical methods for agricultural workers. 2ndEd. ICAR, New Delhi. Pp. 381.

Prabhat Singh and Manoj Katiyar 2019. Path coefficient analysis of yield attributes in mungbean {*Vigna radiata* (L.) Wilezek}. *Journal of Food Legumes,* **32(3):** 189-190, 2019.

Reshmi Raj, K.R., B. Baisakh, S.K., Tripathy, D. Lenka, Salini, K. and Mohanty, M.R. 2022. Studies on correlation and path analysis for yield and yield-related characters in green gram (*Vigna radiata* L.). *The Pharma Innovation Journal,* **11**(6): 2392-2395.

Samita, Rajesh Yadav and Ravika 2022. Assessment of genetic variability and trait association in mungbean (*Vigna radiata* L.) genotypes during summer season. *Journal of Food Legumes,* **35**(3): 170-174, 2022.

Santhi Priya, D. Ratna Babu. 2024. Genetic parameters of variation and character association for seed yield and its attributes in mungbean (*Vigna radiata* L. Wilczek). *Legume Research - An International Journal*, **47**(3): 343-351 (March 2024).

Sandhiya V. and Saravanam, S. 2018. Genetic variability and correlation studies in green gram (*Vigna radiata* L.). *Electronic Journal of Plant Breeding*, **9**(3): 1094-1099.

Sineka, E., Murugan, A., Sheeba, G., Hemalatha, and Vanniarajan, C. 2021. Genetic relatedness and variability studies in green gram (*Vigna radiata* (L.) Wilczek). *Electronic Journal of Plant Breeding,* **12**(4): 1157 – 1162.

Sridhar, E. Ram Babu, SNCVL Pushpavalli. 2023. Genetic variability for yield and its related traits in green gram [*Vigna radiata* (L.) Wilczek]. *Legume Research - An International Journal*, **46**(6): 700-704.

Zuge Sopan S., Abhinav Sao and Neeraj Ankur Toppo. 2019 Genetic variability of yield and yield related traits in mungbean (*Vigna radiata* L. Wilczek) genotypes. *Agric Res J*. **56** (1): 163-165.