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## Studies on correlation and path coefficient for growth and yield attributes in green gram (*Vigna radiata* L. Wilczek)

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### Abstract

The current study was conducted at the agriculture research farm of the Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Punjab during the *kharif* season 2022. A Randomized Block Design (RBD) with three replications were used to study variability, correlation and path including 20 Green gram germplasm for the 13 traits studied *viz.* days to 50% flowering, days to maturity, plant height, number of primary branches, number of clusters per plant, number of pods per plant, number of pods per cluster, number of seeds per pod, pod length (cm), seed index (g), biological yield per plant (g), seed yield per plant (g) and harvest index. Finding revealed that Seed yield showed significant and positively correlated with Biological yield (0.9406 and 0.9318) followed by harvest index (0.7592 and 0.7573) and number of clusters per plant (0.5264 and 0.4585) at both genotypic and phenotypic level respectively. Highest positive direct effect was noted for Biological yield per plant (0.7526) and lowest for number of clusters per plant (0.0039). Hence, selection for these characters could bring improvement in yield and yield components. Correlation was likewise noteworthy and favourable between these features. Therefore, identifying high-yielding genotypes from a population with substantial segregation would be aided by direct selection for these traits.

**Keywords:** Correlation, path coefficient, phenotypic, genotypic, direct and indirect effect, single plant yield

### Introduction

Green gram (*Vigna radiata* L. Wilczek) an important crop in the pulse category, is an annual legume belonging to Fabaceae family that is widely grown, with diploid chromosome  $2n=2x=22$  (Karpechenko, 1925) <sup>[1]</sup>. It can be grown in various cropping systems. It is commonly known as mungbean, is classified into three subgroups: one domesticated (*Vigna radiata* subsp. *radiata*) and two wild (subsp. *sublobata* and subsp. *glabra*). It is highly valued in India, particularly among the predominantly vegetarian population, as it provides a rich source of easily digestible and high-quality protein. Mungbean seeds contain approximately 59 to 65% carbohydrates, 22 to 28% total protein, 21 to 25% amino acids, 1.5 to 2.63% lipids, 1.0 to 1.5% fat, 3.5 to 4.5% fiber, and 4-5% ash, offering approximately 334 to 344 kcal of energy per serving (Srivastava and Ali, 2004) <sup>[2]</sup>. Mungbean serves as a vital protein source for India's vegetarian population. Moreover, it is recognized for its abundant folate and iron content, surpassing most other legumes (Keatinge *et al.*, 2011) <sup>[3]</sup>. Essential amino acids, such as phenylalanine, isoleucine, leucine, and lysine, are also present in significant amounts (Lambrides and Godwin, 2007) <sup>[4]</sup>.

India holds the distinction of being the largest producer of Mungbean, accounting for 65% of the global cultivation area and 54% of production (Kumari *et al.*, 2023) <sup>[23]</sup>. The crop occupies approximately 4.34 million hectares in India, resulting in a production of 2.12 million tonnes and a productivity rate of 489 kg per hectare (Anon., 2020) <sup>[5]</sup>. Greengram is a self-pollinated and short duration crop. It provides a high-quality protein supply (22-24%) and boosts the incomes of small-scale farmers (Rahim *et al.*, 2010) <sup>[6]</sup>. Mature grain has carbohydrates (62.6g), fibre (16.3g), fat (1.2g), protein (23.9g) and 347 calories per 100 grams (Majhi *et al.*, 2020) <sup>[7]</sup>.

Correlation reveals the degree and direction of association at phenotypic and genotypic levels btw the yield and its contributing traits. However, it should be noted that the correlation can sometimes fail to give accurate insights into the individual impact of each character on the dependent character. It is understandable that a path analysis would be necessary to determine which characters actually affect seed yield. So path analysis is used to measure the indirect and direct effects of traits (Dhunde *et al.*, 2022) [8].

### Materials and Method

The present investigation was carried out at the research farm, Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara, Punjab during *Kharif* 2022. Three replications of a randomised block design (RBD) were used to raise twenty different mungbean genotypes tabulated in (Table 1). Using a 30 x 10 cm spacing, the seeds were planted and after tenth day following sowing, the crop was thinned out, leaving one healthy seedling per hill. Recommended agronomic practices and need based plant protection measures were taken. Each line was sown in two rows of 1.5 m. The information was gathered on thirteen traits where growth attributes *viz.* days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, clusters per plant, pods per plant and seed weight per pod. Additional yield-related characteristics *viz.* biological yield, harvesting index and seed yield per plant (g). According to Panse and Sukhatme (1967) [9] recommendations, the analysis of RBD variance and its importance for each character were carried out. Genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation coefficients were calculated by adopting the method explained by Miller *et al.* (1958) [10]. Path analysis suggested by Wright (1921) [11] and Dewey and Lu (1959) [12] was adopted for portioning the genotypic correlation between variables with seed yield into direct and indirect effects of those variables on yield.

**Table 1:** List of 20 Genotypes of Green gram used in the experiment

S. No	Genotypes	S. No	Genotypes
1	Tilak	11	KM11-587
2	KM11-586	12	COGG-1276
3	Bansi Bhoog	13	KM11-585
4	LGG-460	14	JLM-1748
5	MGG-296	15	KM11-582
6	JLM-1702	16	JLM-1754
7	MASCO-44	17	NAVYA
8	RMG-1091	18	RMG-1030
9	ML-2056	19	SAMRAT
10	MH-934	20	RMG-1004

### Estimating of correlation

Now, genotypic and phenotypic correlation coefficients were calculated using formula

$$\text{Phenotypic correlation (rp)} = \frac{\text{PCov. xy}}{\sqrt{\text{PVx. PVy}}}$$

$$\text{Genotypic correlation (rg)} = \frac{\text{GCov. xy}}{\sqrt{\text{GVx. GVy}}}$$

$$r_{xy} = \frac{\text{Cov (x, y)}}{\sqrt{V(x)} \times \sqrt{V(y)}}$$

Where,

$r_{xy}$  = Correlation coefficient between character x and y

$\text{Cov}_{x,y}$  = Co-variance of character x and y

$V_x$  = Variance of character x, and

$V_y$  = Variance of character y

$r_p$  = Phenotypic correlation

$r_g$  = Genotypic correlation.

### Path Analysis

Path analysis splits the correlation coefficient into the measures of direct and indirect effects and measures contribution of each independent variable on the dependent variable and estimates residual effects. It helps in determining the yield and yield contributing characters.

To estimate various direct and indirect effects, the following equations were used

$$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \dots + r_{1I}P_{Iy}$$

$$r_{2y} = r_{2y}P_{1y} + P_{2y} + r_{23}P_{3y} + \dots + r_{2I}P_{Iy}$$

$$r_{Iy} = r_{I1}P_{1y} + r_{I2}P_{2y} + r_{I3}P_{3y} + \dots + P_{Iy}$$

Where,

$r_{1y}$  to  $r_{Iy}$  = Coefficient of correlation between factor 1 to I and dependent character y

$r_{12}$  to  $r_{I-1,I}$  = Coefficient of correlation among causal factors themselves

$P_{1y}$  to  $P_{Iy}$  = Direct effects of characters 1 to I on character y.

### Residual effect

Residual effect, which measures the contribution of the characters not considered was obtained as:

$$(PRY) = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum_{ij} P_i^2 Y + 2 \sum_{\substack{i \neq j \\ i > j}} P_{iy} P_{jy} R_{ij}$$

### Results and Discussion

ANOVA of the thirteen traits tabulated in Table 2 exhibited significant variance at 1 percent level and 5 percent respectively, indicating a substantial range of variability among the germplasm, except for number of primary branches. These findings suggest that selection based on these traits can result in significant improvements, as there is a considerable degree of variability across all the characters Chaudhary *et al.*, (2023) [24]

**Table 2:** Analysis of Variance (ANOVA) for thirteen traits in green gram

Source of variation	df	Mean sum of squares												
		DDF	DM	PH	NPB	NCP	NPP	NPC	NSP	PL	SI	BY	SYP	HI
Replications	2	5.02	0.71	56.34	0.08	1.43	1.14	0.76	0.10	1.85	0.00	4.45	0.13	0.87
Treatment	19	5.08**	4.11**	48.76**	0.30 <sup>ns</sup>	1.71**	15.57**	1.36**	2.66*	1.40*	0.13**	76.95**	2.58**	2.60**
Error	38	1.77	0.82	14.42	0.03	0.29	1.45	0.09	0.99	0.39	0.02	4.46	0.21	0.45
CV		3.41	1.41	5.58	5.93	8.49	7.27	11.20	9.45	8.13	4.79	4.95	8.02	4.99

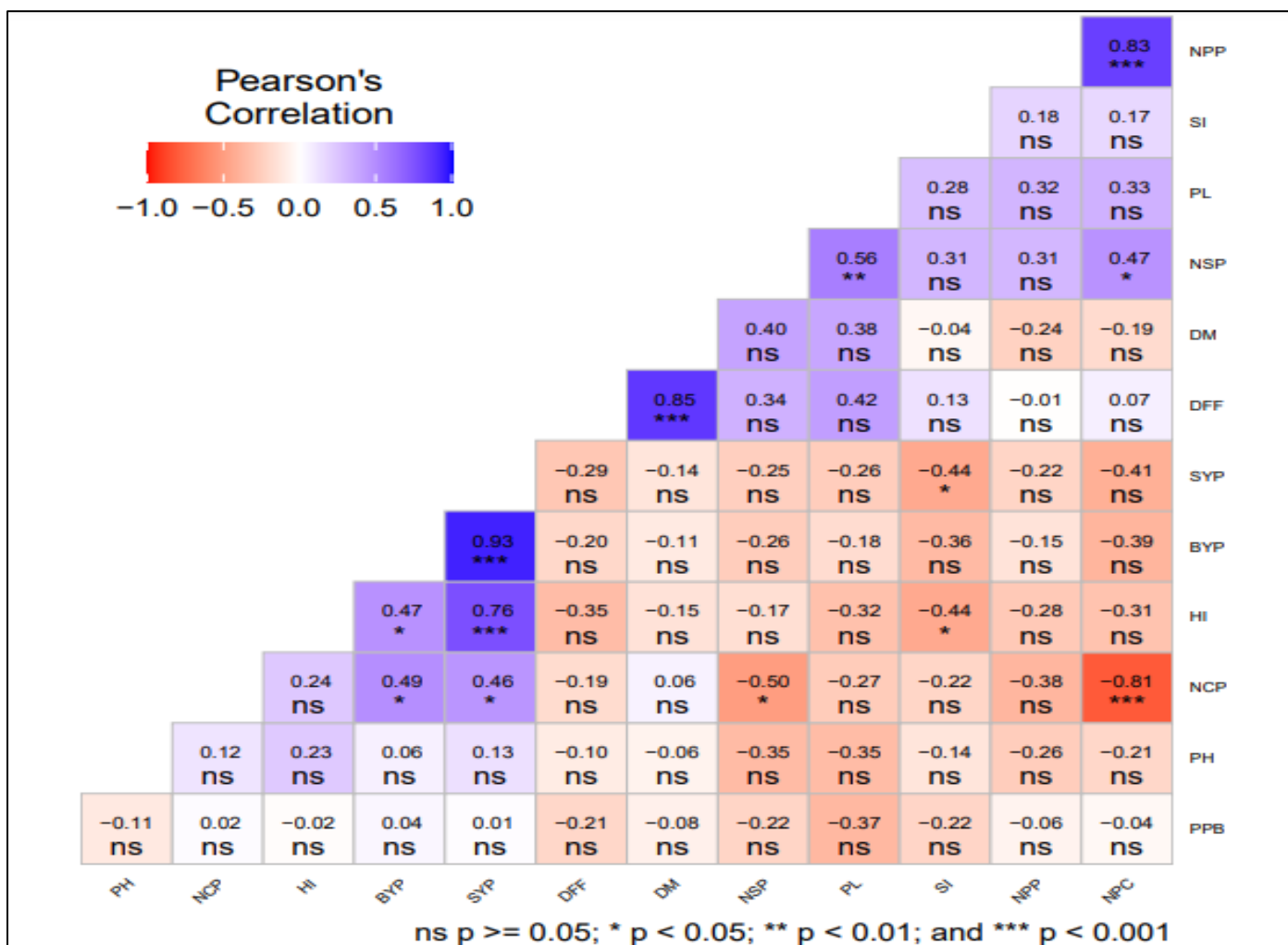
### Correlation

Table 3 and Figure 1 shows the assessment of the correlation between various characteristics. Seed yield showed positively significantly correlated with Biological yield (0.9406 and 0.9318) followed by harvest index (0.7592 and 0.7573) and No of clusters per plant (0.5264 and 0.4585) at both the level viz., genotypically and phenotypically, Similar findings reported by (Saikumar *et al.*, 2022) [13] and (Shakeer *et al.*, 2022) [14]. SYP is negatively significantly associated with Seed index (-0.5104 and -0.4441) and No. of pods per cluster (-0.4582 and 0.4123) at both genotypic and phenotypic levels respectively. SYP associated negatively at genotypic level with No. of seeds per pod (-0.4151), Days to 50% flowering (-0.3979) and Pod length (-0.3892). Harvest index is positively and significantly correlated with biological yield per plant at genotypic (0.4916) and phenotypic (0.4726) levels, and negatively associated with Seed index (-0.5663 and -0.444) at both levels, and few characters are genotypically negatively correlated with HI such as Pod length (-0.519) and Days to 50% flowering (-0.4877). Biological yield per plant shows positive (0.5483 and 0.4885) and negative (-0.4185 and -0.3865) with No. of clusters per plant and number of pods per cluster respectively at genotypic and phenotypic levels, whereas BYP is genotypically and negatively associated with No. of seeds per pod (-0.3983) and Seed index (0.3922). Seed index is genotypically positively significant with pod length (0.4191). Days to 50% flowering (0.7545 and 0.4195), Number of seeds per pod (0.6495 and 0.558), Days to maturity ((0.5634 and 0.3845) are positively significantly correlated with pod length at genotypic and phenotypic levels but number of pods per cluster (0.4125) and number of pods per plant (0.3919) are only genotypically significantly associated. No. of seeds per pod shown genotypically, phenotypically positively significance with number of pods per cluster (0.5739 and 0.4683), days to maturity (0.521 and 0.3962) and genotypically significant with Days to 50% flowering (0.5145), which also genotypically negatively associated with plant height (-0.6891) and number of clusters per plant (0.6317). Number of pods per cluster is positively correlated with Number of pods per plant (0.8433 and 0.8269) and negatively correlated with number of clusters per plant (-0.8266 and -0.8059) at both levels. Number of pods per plant negatively associated with number of clusters per plant (-

0.4269 and -0.378) meanwhile Days to 50% flowering is positively associated with days to maturity (0.9021 and 0.8548) genotypically and phenotypically. Related research has yielded comparable results, as shown by (Tejaswini *et al.*, 2022) [15], (Reshmi *et al.*, 2022) [16], (Kurandale *et al.*, 2020) [17] and (Gajanan and Lal 2022) [18].

### Path analysis

Studying correlations alone, however, does not provide a whole picture of how each individual trait contributes to the whole. Because of its ability to distinguish between partially indirect and direct effect sources of association, path analysis is useful for comparing variables based on the magnitude of their contributions. Table 4 reveals the path analysis through direct and indirect effect of each trait on selected variable i.e., seed yield. Negative direct effect is noted for following traits such as Pod length and followed by Number of primary branches, days to 50% flowering, plant height, number of pods per cluster and seed index. Highest direct negative effect is noted for pod length (-0.019) and lowest is noted for seed index (0.0008) and moderate negative direct effect is noted for Days to 50% flowering (-0.0129) and plant height (-0.0077). Positive direct effect is noted for Biological yield per plant followed by harvest index, days to maturity, number of seeds per pod, number of pods per plant and number of clusters per plant. Highest positive direct effect is noted for Biological yield per plant (0.7526) and lowest is noted for number of clusters per plant (0.0039). Moderate positive direct effect is noted for days to maturity (0.0153), showing that these were significant yield-adding characteristics in greengram. Number of seeds per pod (0.022). number of seeds per pod noted highest positive indirect effect on seed yield through pod length (0.0143), (Manivelan *et al.*, 2019) [19] also reported similar results for indirect positive effect and days to 50% flowering showed highest negative indirect effect on seed yield through days to maturity (-0.0116). Other studies have produced analogous findings, as reported by (Yajavathi *et al.*, 2022) [20] for the traits viz, BYP, HI, NSP, PH, NPB; (Mohan *et al.*, 2021) [21] also registered same results for positive direct effect (NPP and NSP) and negative direct effect (PH and NSP). (Dawane *et al.*, 2022) [22] Observed parallel data for NPP, NSP, DM and HI.



DFE- Days to 50% flowering, DM- Days to maturity, PH- Plant height, NPB- Number of primary branches, NCP- Number of clusters per plant, NPP- Number of pods per plant, NPC- Number of pods per cluster, NSP- Number of seeds per pod, PL- Pod length (cm), SI- Seed Index (g), BYP- Biological yield per plant(g), SYP- Seed yield per plant(g), HI- Harvest index.

**Fig 1:** Correlation Studies in yield and its component characters in Green gram

**Table 3:** Correlation Studies for thirteen characters in Green gram

		DFE	DM	PH	NPB	NCP	NPP	NPC	NSP	PL	SI	BYP	HI	SYP
DFE	P	1	0.8548	-0.1019	-0.2101	-0.1853	-0.0059	0.0662	0.3351	0.4195	0.1266	-0.2045	-0.3464	-0.2914
	G	1	0.9021	-0.2357	-0.2011	-0.2567	-0.0299	0.0801	0.5145	0.7545	0.136	-0.2826	-0.4877	-0.3979
DM	P		1	-0.0649	-0.0763	0.0565	-0.2361	-0.1865	0.3962	0.3845	-0.0429	-0.1098	-0.1511	-0.1386
	G		1	-0.1395	-0.0213	0.105	-0.3059	-0.2458	0.521	0.5634	-0.1074	-0.1417	-0.2023	-0.1787
PH	P			1	-0.1139	0.1157	-0.2591	-0.2107	-0.3528	-0.3491	-0.1382	0.0629	0.2305	0.1312
	G			1	-0.1505	0.1822	-0.3095	-0.2531	-0.6891	-0.5963	-0.1814	0.059	0.2238	0.1215
NPB	P				1	0.0155	-0.0604	-0.0367	-0.222	-0.37	-0.2183	0.0365	-0.0155	0.0111
	G				1	-0.0116	-0.0711	-0.0228	-0.2965	-0.5163	-0.2657	0.0177	-0.0509	-0.0162
NCP	P					1	-0.3779	-0.8059	-0.5046	-0.2688	-0.2159	0.4885	0.2364	0.4585
	G					1	-0.4269	-0.8266	-0.6317	-0.3625	-0.2547	0.5483	0.2929	0.5264
NPP	P						1	0.8269	0.3094	0.3169	0.1834	-0.1476	-0.2822	-0.2221
	G						1	0.8433	0.372	0.3919	0.1859	-0.1852	-0.3644	-0.277
NPC	P							1	0.4683	0.334	0.1676	-0.3865	-0.3127	-0.4123
	G							1	0.5739	0.4125	0.1806	-0.4185	-0.3756	-0.4582
NSP	P								1	0.558	0.3136	-0.2622	-0.1684	-0.2498
	G								1	0.6495	0.3646	-0.3983	-0.3498	-0.4151
PL	P									1	0.2798	-0.1834	-0.3231	-0.2599
	G									1	0.4191	-0.2621	-0.519	-0.3892
SI	P										1	-0.357	-0.444	-0.4441
	G										1	-0.3922	-0.5663	-0.5104
BYP	P											1	0.4726	0.9318
	G											1	0.4916	0.9406
HI	P												1	0.7592
	G												1	0.7573

**Table 4:** Path analysis for thirteen characters in Green gram

	DDF	DM	PH	NPB	NCP	NPP	NPC	NSP	PL	SI	BYP	HI	SYP
DDF	-0.0129	-0.0116	0.003	0.0026	0.0033	0.0004	-0.001	-0.0066	-0.0097	-0.0018	0.0036	0.0063	-0.3979
DM	0.0138	0.0153	-0.0021	-0.0003	0.0016	-0.0047	-0.0038	0.008	0.0086	-0.0016	-0.0022	-0.0031	-0.1787
PH	0.0018	0.0011	-0.0077	0.0012	-0.0014	0.0024	0.002	0.0053	0.0046	0.0014	-0.0005	-0.0017	0.1215
NPB	0.0033	0.0004	0.0025	-0.0165	0.0002	0.0012	0.0004	0.0049	0.0085	0.0044	-0.0003	0.0008	-0.0162
NCP	-0.001	0.0004	0.0007	0	0.0039	-0.0017	-0.0032	-0.0025	-0.0014	-0.001	0.0021	0.0011	0.5264
NPP	-0.0002	-0.0024	-0.0025	-0.0006	-0.0034	0.008	0.0067	0.003	0.0031	0.0015	-0.0015	-0.0029	-0.277
NPC	-0.0004	0.0013	0.0013	0.0001	0.0044	-0.0045	-0.0053	-0.003	-0.0022	-0.001	0.0022	0.002	-0.4582
NSP	0.0113	0.0114	-0.0151	-0.0065	-0.0139	0.0082	0.0126	0.022	0.0143	0.008	-0.0087	-0.0077	-0.4151
PL	-0.0143	-0.0107	0.0113	0.0098	0.0069	-0.0074	-0.0078	-0.0123	-0.019	-0.008	0.005	0.0099	-0.3892
SI	-0.0001	0.0001	0.0001	0.0002	0.0002	-0.0002	-0.0001	-0.0003	-0.0003	-0.0008	0.0003	0.0005	-0.5104
BYP	-0.2127	-0.1066	0.0444	0.0133	0.4127	-0.1394	-0.315	-0.2997	-0.1973	-0.2951	0.7526	0.37	0.9406
HI	-0.1864	-0.0773	0.0855	-0.0195	0.1119	-0.1393	-0.1436	-0.1337	-0.1984	-0.2164	0.1879	0.3822	0.7573

DDF- Days to 50% flowering, DM- Days to maturity, PH- Plant height, NPB- Number of primary branches, NCP- Number of clusters per plant, NPP- Number of pods per plant, NPC- Number of pods per cluster, NSP- Number of seeds per pod, PL- Pod length (cm), SI- Seed Index (g), BYP- Biological yield per plant(g), SYP- Seed yield per plant(g), HI- Harvest index.

### Conclusion

In the majority of cases, genotypic correlation coefficient values were higher than phenotypic correlation coefficient values for the related traits. Seed yield showed positively significantly correlated with Biological yield followed by harvest index and Number of clusters per plant at both genotypic and phenotypic levels indicating that these attributes were mainly influencing the seed yield in mungbean. Positive direct effect was noted for Biological yield per plant followed by harvest index, days to maturity, number of seeds per pod, number of pods per plant and number of clusters per plant. Highest positive direct effect is noted for Biological yield per plant and lowest noted for number of clusters per plant.

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