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A Comprehensive Study on Variability, Heritability, Correlation and Path Coefficients in Mungbean Genotypes [Vigna radiata (L.) Wilczek] at Satna District

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ABSTRACT

A Completely Randomized block design (CRBD) was implemented at Research farm, Genetics and Plant Breeding AKS University, Satna, to cultivate fifteen diverse cultivars of Mungbean during the Kharif season from July to November 2023. The study involved collecting data for twelve quantitative traits and analyzing variance, genetic variability, correlation, and path coefficient. The results revealed significant inter-varietal variation in all twelve examined characters, indicating their suitability for breeding programs. Those genotypes demonstrating exceptional performance in desirable traits, could potentially serve as valuable donors for enhancing specific traits in future breeding programs. As per mean the performance, some varieties viz., PGRV 95016, Virat, IC 76499, PDM 04-123, PPU 911, and ML 2056 are high yielding and suitable for growing in Satna district of (M.P.). High degree of GCV, PCV were recorded for the number of pods per plants, biological yield (g.), number of pods per clusters, number of clusters per plants, total number of branches per plant, and seed yield per plant (g.) indicating simple selection for these traits will be useful for the planning of a breeding programme. High positive significant correlation with seed yield per plant (g.) were recorded for days to 50% flowering, days to first picking pods, days to second picking pods, total no. of branches per plant, number of clusters plants, biological yield (g.), number of pods per clusters, number of pods per plant, and number of seeds / pod have. Days to fifty percent blooming, days to first picking pods, number of pods per plant, biological yield (g), and harvest index (%) were shown to be significant characteristics based on path coefficient analysis that may be taken into consideration during mungbean seed yield enhancement and selection.

Keywords: Mungbean, Variance, Variability, Correlation, Path Coefficient.

INTRODUCTION

According to Sahu *et al.,* (2024) Mungbean is highly valued as a pulse crop for its short growth cycle, resilience in environments with low water and soil fertility. Mungbean, scientifically classified as Vigna radiata (L.) Wilczek, is a diploid species with a chromosome number of 2n=2x-22. Originating from South Asia, particularly India, it is believed that Vigna radiata var. sublobata is the probable ancestor of mungbean. Mungbean, a major pulse crop, is primarily cultivated in India, Bangladesh, Sri Lanka, Pakistan, Nepal, and other Southeast Asian countries (Singh *et al.,* 2015). In India, the main mungbean producing states include Maharashtra, Madhya Pradesh, Rajasthan, Bihar, and Tamil Nadu. Notably, mungbean stands out as an affordable source of dietary protein, with higher iron content compared to many other legumes (Nair *et al.,* 2012). It belongs to the Leguminosae (Fabaceae) family, specifically the sub-family Papilionaceae. India's green gram production stands at 24.48 lakh tonnes per year, making it the top producer globally with an average productivity of 531 kg per hectare Anonymous (2022).

Mungbean stands out among different pulses due to its high vitamin B content and rich essential amino acids like Arginine, Leucine, Lysine, Tryptophan, and Valine. Moreover, green gram sprouts are a good source of vitamin C and E (Engel, 1978). Mung is typically consumed in different ways like Dal, sprouts, and green pods as a vegetable. It is also utilized in the production of various food items such as Mangori, Papad, Dalbada, Namkeen, etc. Mungbean displays notable diversity in traits like flowering time, plant height, and protein content, which has been harnessed in breeding initiatives to unveil a range of improved varieties. Understanding the genetic nature of varieties,

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the role of gene action in determining yield, and the impact of enhancing component traits on yield per unit area are all crucial aspects. Therefore, before initiating any breeding program, it is essential to have a thorough understanding of the nature and extent of genetic variability, as well as the associations between yield and other parameters.

Additionally, calculating genetic advance and heritability provides valuable insight into the expected level of improvement through selection and the reliability of phenotype-based selection methods. (Falconer, 1989). Correlation coefficient measure the degree of association. the basis for selection is the genotypic or phenotypic correlation between two or more attributes. An essential method for dividing the correlation coefficient into both the direct and indirect impacts of factors on the dependent variable is path coefficients analysis (Wright, 1921).

MATERIALS AND METHODS

The current study was carried out in Kharif 2023 at the Genetics and Plant Breeding Research Farm of AKS University in Sherganj, Satna, M.P. The climate of district Satna is semi-arid and sub tropical type with hot dry summer and cold dry winter. The annual rainfall is around 950 mm. The experiment materials utilized during this work were collections of 15 mungbean (Vigna radiata L.) varieties/strains with indigenous native genotypes. These genotypes show a broad range of variability in terms of different morphological and agronomic traits. The experiment used a completely randomized block design to assess fifteen mungbean germplasm samples in an irrigated environment. To produce a high-quality crop, suggested cultural techniques were implemented. Five competitive plants were chosen at random from each plot to record observations for all qualitative and quantitative characters. These observations were made based on the plot.

The data were recorded for the following 12 quantitative characters from randomly selected plant of mungbean trial. The experiment's design analysis of variance was conducted in accordance with Panse and Sukhatme's (1967) protocol. The formula proposed by Burton and de Vane (1953) was used to assess the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and environmental coefficient of variation (ECV). Burton and de Vane's (1953) formula was used to assess heritability in the broad sense (h2b). The genetic advancement was computed using the Johnson *et al.,* (1955) approach. As formula proposed by Searle (1961), the basic interactions between various features at the genotypic and phenotypic levels were determined. Path coefficient analysis was performed using the Dewey & Lu (1959) formula.

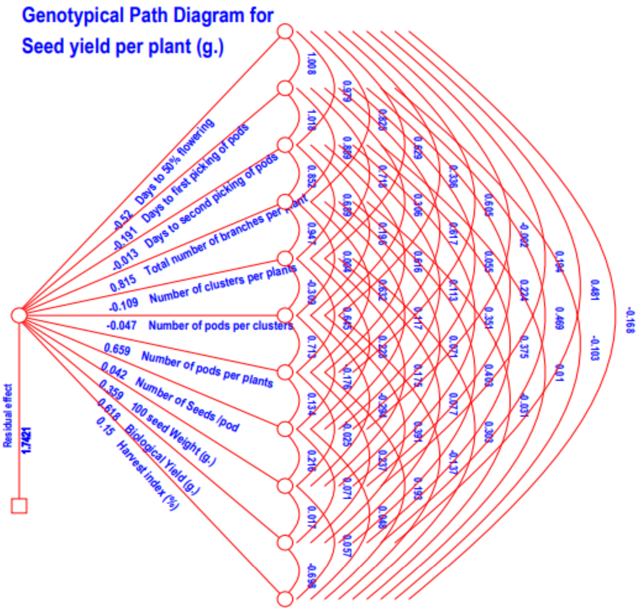

Figure 1: Diagram of the genotypic path

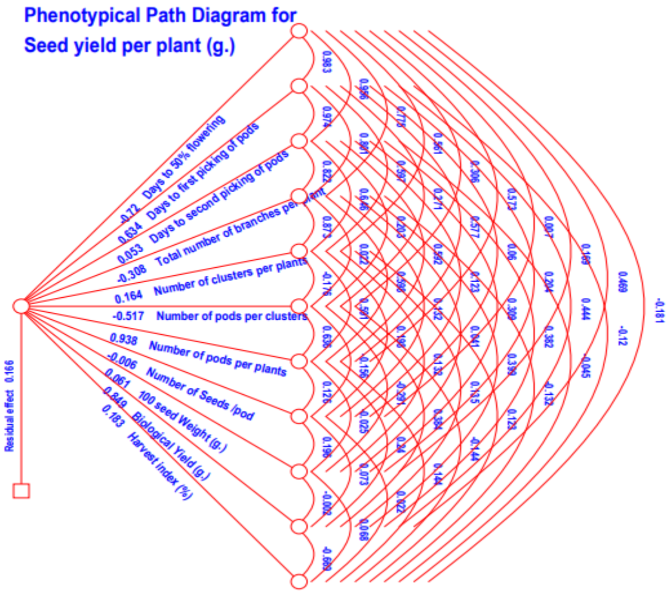

Figure 2: Diagram of phenotypic path

RESULTS AND DISCUSSION

Variance

For the trial design, which comprised 15 mungbean strains/varieties for the twelve quantitative features, an analysis of variance was carried out. The results indicated in Table 1, showing significant differences for all the characters. The maximum variances due to replication and treatment were found for number of pods per plants (64.969) and (1226.528**), respectively. The highest environmental, genotypical, and phenotypical variance observed for number of pods per plants (44.025, 364.817, and 408.843), respectively. These results are corroborates with earlier results of Jeberson *et al.,* (2017); Azam *et al.,* (2018); Ghimire *et al.,* (2018); Govardhan *et al.,* (2018); Mehandi *et al.,* (2018); Sushmitharaj *et al.* (2018); Muthuswamy *et al.,* (2019); Kumar *et al.,* (2019); Joshi *et al.,* (2021); Salman *et al.,* (2021); and Kadam *et al.,* (2023) indicating the presence of sufficient variability among the evaluated genotype for the traits under consideration.

Table 1 Analysis of variance (mean sum of squares) for 12 quantitative characters in mongbean

Characters	Source of Variation			Variance		
	Replication	Treatments	Error	Environmental	Genotypical	Phenotypical
	Df= 2	Df= 14	Df= 28			
D50PF	4.108	153.432**	5.788	1.929	49.215	51.144
D1stPP	11.646	167.344**	8.533	2.844	52.937	55.781
D2ndPP	9.074	148.052**	9.254	3.085	46.266	49.351
TNBPP	1.917	35.343**	5.648	1.883	9.898	11.781
NCPP	4.319	50.804**	12.483	4.161	12.774	16.935
NPPC	0.622	12.339**	1.532	0.511	3.603	4.113
NPPP	64.969	1226.528**	132.076	44.025	364.817	408.843
NSPP	0.115	8.073**	0.152	0.051	2.641	2.691
SI (g.)	0.127	3.042*	0.127	0.042	0.972	1.014
BYPP (g.)	0.625	377.445**	17.201	5.733	120.082	125.815
HI (%)	60.685	184.377**	29.549	9.850	51.609	61.459
SYPP(g)	29.954	71.569**	9.247	3.082	20.774	23.856

**Significant at 5% probability level. **Significant at 1% probability level, D50PF Days to 50% flowering, D1stPP Days to first picking of pods, D2ndPP Days to second picking of pods, TNBPP Total number of branches per plant, NCPP Number of clusters per plants, NPPC Number of pods per clusters, NPPP Number of pods per plants, NSPP Number of seeds /pod, SI 100 grain weight (g), BYPP Biological Yield (g), HI Harvest index (%), SYPP Seed yield per plant (g)*

GCV and PCV

The comparison of mean performance among 15 varieties/genotypes for 12 characters of mungbean highlighted a significant level of variability within the evaluated collections, as shown in Table 2. Those genotypes demonstrating exceptional performance in desirable traits, as outlined in Table 3, could potentially serve as valuable donors for enhancing specific traits in future breeding programs. GCV and PCV were estimated for all the 12 characters and have been presented in Table 4.

Number of pods/plant (41.69) showed the highest genotypic coefficient variation, followed by biological yield (g.) (40.838), number of pods/clusters (37.397), number of plants/clusters (32.562), total number of branches/plant (31.741), and seed yield/plant (g.) (29.44). This suggests that certain characteristics are less susceptible to changes in their surroundings, hence these qualities should be prioritized more. The magnitude of GCV ranged from highest number of pods per plants (41.69) to lowest days to second picking of pods (8.224).

The high PCV were recorded for number of pods per plants (44.134), followed by biological yield (g.) (41.802), number of pods per clusters (39.96), number of clusters per plants (37.492), total number of branches per plant (34.628), and seed yield per plant (g.) (31.549). The magnitude of PCV ranged from lowest, days to second picking of pods (8.494) to highest, number of pods per plants (44.134).

Table 2: Mean performance of 12 quantitative characters of mungbean genotypes

Genotypes	D50PF	D1stPP	D2ndPP	TNBPP	NCPP	NPPC	NPPP	NSPP	SI (g.)	BYPP (g.)	HI (%)	SYPP(g)
Virat	58.5667	73.5367	88.1633	15.2667	18.3333	3.4333	51.5133	7.4067	5.2300	43.7467	33.6733	22.9933
Sikha	49.8000	65.1833	79.8900	9.4700	7.7433	4.6400	24.6767	8.5733	5.7867	36.5567	16.7333	11.3267
PDM 139	57.5000	71.9300	87.3533	10.3633	10.5233	4.3167	44.8400	8.2300	5.7967	17.8833	43.9133	12.4233
IC 76499	51.7333	68.3167	83.8900	9.4533	12.4667	8.8200	86.3833	7.2167	5.7167	24.3767	43.7767	20.1533
PDM 04-123	56.5000	70.3133	85.1167	9.1633	7.1700	9.9267	61.3900	9.4067	4.0900	51.6467	28.4167	18.7400
ML 2056	45.2000	61.6367	77.0633	11.0667	14.4433	4.0900	54.1667	12.3333	3.5000	21.8900	40.2867	16.4533
MH 521	51.5667	67.6533	82.0700	10.5700	8.8533	7.5900	57.3733	7.2600	3.3833	19.2167	43.5333	12.2467
IPM 99-125	36.1333	49.1967	70.2500	5.2267	7.6933	3.4200	29.4467	8.6467	5.4100	11.3133	43.5533	9.2500
TGM 37	55.0000	71.2833	87.5567	11.1700	10.2467	4.5567	37.5767	9.4433	5.2033	28.5767	33.7700	13.2867
PS 16	53.2333	70.1733	87.1067	13.6667	16.6100	3.6033	45.7800	7.8633	4.7667	19.1000	41.0600	14.7533
NDU 16	41.4667	57.5000	72.4933	4.9433	7.7633	4.1367	29.2333	9.6467	5.6533	18.6433	42.3233	12.2333
PUSA 9072	56.7333	72.5567	89.0400	8.8333	11.8500	4.5867	47.0767	10.7933	6.4433	17.3567	42.7400	14.6933
PPU 911	41.6667	58.3233	74.9733	6.1967	6.5033	4.1767	23.1733	9.4667	5.5767	31.0800	37.7467	16.6400
PGRV 95016	59.5667	77.8433	96.1100	16.6467	17.7800	5.2233	79.0933	12.3333	7.1200	37.2700	41.9100	26.6400
Mean	45.9667	63.5767	79.5100	6.6433	6.6600	3.6100	15.4933	8.2667	5.4900	23.8400	47.3000	10.3933

D50PF Days to 50% flowering, D1stPP Days to first picking of pods, D2ndPP Days to second picking of pods, TNBPP Total number of branches per plant, NCPP Number of clusters per plants, NPPC Number of pods per clusters, NPPP Number of pods per plants, NSPP Number of seeds /pod, SI 100 grain weight (g), BYPP Biological Yield (g), HI Harvest index (%), SYPP Seed yield per plant (g)

High genotypic and phenotypic coefficients of variation were found in the traits, and an environmental coefficient of variation suggested that environmental influences had a greater influence. Because of this, care must be taken during the selection process because environmental fluctuations have an unpredictable nature and could cause results to be misinterpreted. Because of the influence of the environment, the phenotypic coefficients of variation (PCV) for all the seed quantity characteristics were slightly larger in magnitude than the corresponding genotypic coefficients of variation.

Table 3: Most desirable genotypes of mungbean identified for 12 quantitative

Traits	Genotypes
D50PF	IPM 99-125, NDU 16, PPU 911, ML 2056, and Sikha.
D1stPP	IPM 99-125, NDU 16, PPU 911, ML 2056, Sikha, and MH 521.
D2ndPP	IPM 99-125, NDU 16, PPU 911, ML 2056, Sikha, and MH 521.
TNBPP	PGRV 95016, Virat, PS 16, TGM 37, ML 2056, MH 521, and PDM 139.
NCPP	Virat, PGRV 95016, PS 16, ML 2056, IC 76499, and PUSA 9072.
NPPC	PDM 04-123, IC 76499, MH 521, PGRV 95016, Sikha, and PUSA 9072.
NPPP	IC 76499, PGRV 95016, PDM 04-123, MH 521, ML 2056, and Virat.
NSPP	ML 2056, PGRV 95016, PUSA 9072, NDU 16, PPU 911, TGM 37.
SI (g.)	PGRV 95016, PUSA 9072, PDM 139, Sikha, IC 76499, NDU 16.
BYPP (g.)	PDM 04-123, Virat, PGRV 95016, Sikha, PPU 911, TGM 37.
HI (%)	PDM 139, IC 76499, IPM 99-125, MH 521, PUSA 9072, and NDU 16.
SYPP(g)	PGRV 95016, Virat, IC 76499, PDM 04-123, PPU 911, and ML 2056.

High degree of GCV, PCV were recorded for the number of pods per plants, biological yield (g.), number of pods per clusters, number of clusters per plants, total number of branches per plant, and seed yield per plant (g.) indicating simple selection for these traits will be useful for the planning of a breeding programme. Similar results were observed by Muthuswamy *et al.,* (2019); Azam *et al.,* (2018); Govardhan *et al.,* (2018); Ghimire *et al.,* (2018); Sushmitharaj *et al.,* (2018); Joshi *et al.,* (2021); Asari *et al.,* (2019); Salman *et al.,* (2021); Singh *et al.,* (2022); and Parsaniya *et al.,* (2022a).

Table 4: Mean, Range, GCV, PCV, and ECV for 12 quantitative characters in mungbean

S.N.	Characters	Grand mean	Range		GCV	PCV	ECV	CV @ 5%
			Min.	Max.				
1	D50PF	50.7089	36.1333	59.5667	13.834	14.103	4.744	4.7445
2	D1stPP	66.6016	49.1967	77.8433	10.924	11.214	4.386	4.3860
3	D2ndPP	82.7058	70.2500	96.1100	8.224	8.494	3.678	3.6782
4	TNBPP	9.9120	4.9433	16.6467	31.741	34.628	23.977	9.9768
5	NCPP	10.9760	6.5033	18.3333	32.562	37.492	32.190	12.1895
6	NPPC	5.0753	3.4200	9.9267	37.397	39.960	24.389	8.3895
7	NPPP	45.8144	15.4933	86.3833	41.690	44.134	25.085	9.0848
8	NSPP	9.1258	7.2167	12.3333	17.806	17.976	4.268	4.2677
9	SI (g.)	5.2778	3.3833	7.1200	18.678	19.079	6.741	6.7412
10	BYPP (g.)	26.8331	11.3133	51.6467	40.838	41.802	15.456	8.4559
11	HI (%)	38.7158	16.7333	47.3000	18.556	20.249	14.041	7.0406
12	SYPP(g)	15.4818	9.2500	26.6400	29.440	31.549	19.642	9.6416

Heritability in Broad Sense

Heritability in broad sense and Genetic advancement was estimated for all the 12 characters and has been presented in Table 5. In general, higher estimates (h2b) >80% were observed for all the characters except number of clusters per plants (75.4%). The heritability value ranged from highest number of seeds/pod (98.1%) and lowest number of clusters per plants (75.4%). High heritability estimates were found for number of seeds /pod (98.1%), days to 50% flowering (96.2%), 100 seed weight (g.) (95.8%), biological yield (g.) (95.4%), days to first picking of pods (94.9%), days to second picking of pods (93.7%), number of pods per plants (89.2%), number of pods per clusters (87.6%), seed yield per plant (g.) (87.1%), total number of branches per plant (84.0%), and harvest index (%) (84.0%) suggested that the characters are least influenced by the environmental factors and also indicates the dependency of phenotypic expression which reflect the genotypic ability of strains to transmit the gene to their progenies. However, moderate heritability (>40 % to <80%) observed for number of clusters per plants (75.4%) and low Heritability (<40%) was not observed for any studied character.

Table 5: Heritability (%) in broad sense, Genetic advancement (1% and 5%) and genetic advance as percent of mean (1% and 5%) for 12 quantitative characters in mungbean

Characters	Heritability (h^2b)	Heritability (h^2b %)	Genetic Advance 5%	Genetic Advance 1%	Gen. Adv. as 5% of Mean	Gen. Adv. as 1% of Mean
D50PF	0.962	96.2	14.176	18.168	27.956	35.828
D1stPP	0.949	94.9	14.601	18.712	21.923	28.095
D2ndPP	0.937	93.7	13.567	17.387	16.404	21.022
TNBPP	0.840	84.0	5.941	7.613	59.935	76.809
NCPP	0.754	75.4	6.394	8.195	58.257	74.659
NPPC	0.876	87.6	3.659	4.689	72.097	92.396
NPPP	0.892	89.2	37.168	47.632	81.126	103.968
NSPP	0.981	98.1	3.316	4.249	36.335	46.565
SI (g.)	0.958	95.8	1.988	2.548	37.667	48.273
BYPP (g.)	0.954	95.4	22.054	28.263	82.188	105.328
HI (%)	0.840	84.0	13.561	17.380	35.028	44.890
SYPP(g)	0.871	87.1	8.762	11.229	56.593	72.528

Conflicting results on high heritability for number of branches per plant have been given by Garg *et al.,* (2017); Pulagampalli and Lavanya (2017); Ghimire *et al.,* (2018); Malli *et al.,* (2018); Mehandi *et al.,* (2018); Varma *et al.,* (2018); Manivelan *et al.,* (2019); Muthuswamy *et al.,* (2019); Asari *et al.,* (2019); Talukdar *et al.,* (2020); Wesly *et al.,* (2020); Joshi *et al.,* (2021); and Salman *et al.,* (2021).

Genetic Advancement

From the maximum biological yield (g) (82.188%) to the lowest days to second picking of pods (16.404%), the range of expected genetic advance was expressed as a percentage of mean. For biological yield (g.) (82.188%), number of pods per plant (81.126%), number of pods per cluster (72.097%), total number of branches/plant (59.935%), number of clusters per plant (58.257%), and seed yield per plant (g.) (56.593%), a high estimate of expected genetic advance as a percent of mean (5%) was found. However, moderate expected genetic advance observed for 100 seed weight (g.) (37.667%), number of seeds /pod (36.335%), and harvest index (%) (35.028%). Days to 50% blooming (27.956%), days to first pod picking (21.923%), and days to second pod picking (16.404%) all had low estimates of expected genetic advance.

Table 6: Genotypic and phenotypic correlation coefficient for 12 quantitative traits in mungbean

Traits		D50PF	D1stPP	D2ndPP	TNBPP	NCPP	NPPC	NPPP	NSPP	SI (g.)	BYPP (g.)	HI (%)	SYPP(g)
D50 PF	Gen	1.0000	0.9081**	0.9788**	0.8246**	0.6289**	0.3357	0.6051**	-0.0019	0.1943	0.4813*	-0.1680	0.6020**
	Phe	1.0000	0.9830**	0.9562**	0.7749**	0.5614*	0.3061	0.5732**	0.0067	0.1691	0.4685*	-0.1808	0.5621**
D1st PP	Gen		1.0000	0.9181**	0.8888**	0.7182**	0.3058	0.6168**	0.0552	0.2240	0.4693*	-0.1034	0.6659**
	Phe		1.0000	0.9736**	0.8012**	0.5974*	0.2709	0.5772**	0.0601	0.2045	0.4436*	-0.1199	0.5977**
D2nd PP	Gen			1.0000	0.8525**	0.6893**	0.1958	0.6160**	0.1132	0.3511	0.3751	0.0100	0.6631**
	Phe			1.0000	0.8224**	0.6464**	0.2033	0.5915**	0.1228	0.3090	0.3816	-0.0449	0.6188**
TNB PP	Gen				1.0000	0.9470**	0.0035	0.6323**	0.1173	0.0715	0.4026	-0.0307	0.7928**
	Phe				1.0000	0.8727**	0.0217	0.5979**	0.1324	0.0411	0.3991	-0.1324	0.6956**
NCPP	Gen					1.0000	-0.3092	0.6446**	0.2279	0.1751	0.0771	0.3026	0.7940**
	Phe					1.0000	-0.1755	0.5913**	0.1982	0.1316	0.1347	0.1228	0.6940**
NPPC	Gen						1.0000	0.7130**	-0.1764	-0.2935	0.3908	-0.1374	0.3311
	Phe						1.0000	0.6357**	-0.1564	-0.2912	0.3840	-0.1439	0.2886
NPPP	Gen							1.0000	0.1341	-0.0251	0.2367	0.1931	0.3311
	Phe							1.0000	0.1264	-0.0251	0.2402	0.1439	0.2886
NSPP	Gen								1.0000	0.2160	0.0706	0.0475	0.3273
	Phe								1.0000	0.1956	0.0728	0.0219	0.3034
SI (g.)	Gen									1.0000	0.0168	0.0571	0.2749
	Phe									1.0000	-0.0021	0.0684	0.2312
BYPP (g.)	Gen										1.0000	-0.6977**	0.6348**
	Phe										1.0000	-0.6693**	0.6159**
HI (%)	Gen											1.0000	-0.0763
	Phe											1.0000	-0.0587
SYPP (g)	Gen												1.000
	Phe												1.000

**Significant at 5% probability level. **Significant at 1% probability level*

For biological yield (g.), number of pods per plant, number of pods per cluster, total number of branches per plant, seed yield per plant (g.), 100 seed weight (g.), and number of seeds/pod, high heritability combined with high genetic advance was observed, suggesting that these characters could be primarily governed by additive gene action. Therefore, adopting these attributes could have a greater impact on the intended genetic improvement. Low genetic advancement and low heritability show that selection would be ineffective because the trait is greatly influenced by the environment.

This finding is substantiated by similar results of high genetic advance as a per cent of mean reported by Katiyar *et al.,* (2015); Garg *et al.,* (2017); Ghimire *et al.,* (2018); Malli *et al.,* (2018); Sharma *et al.,* (2018); Mehandi *et al.,* (2018); Varma *et al.,* (2018); Manivelan *et al.,* (2019); Muthuswamy *et al.,* (2019); Asari *et al.,* (2019); Wesly *et al.,* (2020); Salman *et al.,* (2021); Joshi *et al.,* (2021); and Dandale *et al.,* (2022).

Correlation Coefficient Analysis

The genotypic and phenotypic correlation coefficient presented in Table 6. Days to 50% flowering (0.6020** and 0.5621**), Days to first picking pods (0.6659** and 0.5977**), Days to second picking pods (0.6631** and 0.6188**), Total no. of branches per plant (0.7928** and 0.6956**), Number of clusters plants (0.7940** and 0.6940**), Biological Yield (g.) (0.6348** and 0.6159**), Number of pods per clusters (0.3311** and 0.2886*), Number of pods per plant (0.3311** and 0.2886*), Number of Seeds / pod (0.3273** and 0.3034**) have high positive significant correlation with seed yield per plant (g.). Thus the present study supports the earlier findings that selection for days to 50% flowering, number of clusters per plants, number of seed per pods and seed yield per plant may bring about simultaneous improvement in seed yield.

Grain yield of a crop is the result of interaction of a number of inter-related characters. Therefore, selection should be based on these component characters after assessing their correlation with grain yield. Similar finding of positive and significantly correlation between seed yield per plant with their component traits was earlier reported by Garje *et al.,* (2014); Kapadia *et al.,* (2015); Katiyar *et al.,* (2015); Raturi *et al.,* (2015); Baisakh *et al.,* (2016); Garg *et al.,* (2017); Azam *et al.,* (2018); Ghimire *et al.,* (2018); Kumar *et al.,* (2018); Asari *et al.,* (2019); Muthuswamy *et al.,* (2019); Ahmad and Belwal (2020); Dhunde *et al.,* (2021); Khatik *et al.,* (2022); and Nalajala *et al.,* (2022).

Path Coefficient Analysis

In Table 7, the genotypic and phenotypic correlation coefficient of seed yield with the remaining traits under investigation are further divided into direct and indirect impacts by the use of route coefficient analysis at the genotypic and phenotypic levels.

Table 7: Direct and indirect effect for different characters on seed yield per plant at genotypic level in Mungbean

Trait		D50PF	D1stPP	D2ndPP	TNBPP	NCPP	NPPC	NPPP	NSPP	SI (g.)	BYPP (g.)	HI (%)	SYPP(g)
D50PF	Gen	-0.5204	-0.5246	-0.5093	-0.4291	-0.3272	-0.1747	-0.3149	0.001	-0.1011	-0.2505	0.0874	0.602
	Phe	-0.7197	-0.7074	-0.6881	-0.5576	-0.404	-0.2203	-0.4125	-0.0048	-0.1217	-0.3372	0.1301	0.5621
D1stPP	Gen	-0.193	-0.1915	-0.1949	-0.1702	-0.1375	-0.0586	-0.1181	-0.0106	-0.0429	-0.0899	0.0198	0.6659
	Phe	0.6229	0.6336	0.6169	0.5077	0.3785	0.1717	0.3657	0.0381	0.1296	0.2811	-0.076	0.5977
D2ndPP	Gen	-0.0132	-0.0137	-0.0134	-0.0115	-0.0093	-0.0026	-0.0083	-0.0015	-0.0047	-0.005	-0.0001	0.6631
	Phe	0.0505	0.0514	0.0528	0.0434	0.0341	0.0107	0.0313	0.0065	0.0163	0.0202	-0.0024	0.6188
TNBPP	Gen	0.6723	0.7246	0.695	0.8153	0.7721	0.0029	0.5155	0.0957	0.0583	0.3283	-0.025	0.7928
	Phe	-0.2383	-0.2464	-0.2529	-0.3075	-0.2684	-0.0067	-0.1839	-0.0407	-0.0126	-0.1227	0.0407	0.6956
NCPP	Gen	-0.0684	-0.0781	-0.075	-0.103	-0.1088	0.0336	-0.0701	-0.0248	-0.019	-0.0084	-0.0329	0.794
	Phe	0.0922	0.0982	0.1062	0.1434	0.1643	-0.0288	0.0972	0.0326	0.0216	0.0221	0.0202	0.694
NPPC	Gen	-0.0159	-0.0145	-0.0093	-0.0002	0.0147	-0.0474	-0.0338	0.0084	0.0139	-0.0185	0.0065	0.3311
	Phe	-0.1583	-0.1401	-0.1051	-0.0112	0.0907	-0.517	-0.3287	0.0809	0.1505	-0.1985	0.0744	0.2886
NPPP	Gen	0.3986	0.4063	0.4058	0.4165	0.4246	0.4697	0.6587	0.0883	-0.0165	0.1559	0.1272	0.801
	Phe	0.5378	0.5416	0.5551	0.5611	0.5548	0.5965	0.9384	0.1186	-0.0236	0.2254	0.135	0.7355
NSPP	Gen	-0.0001	0.0023	0.0048	0.005	0.0097	-0.0075	0.0057	0.0425	0.0092	0.003	0.002	0.3273
	Phe	0	-0.0003	-0.0007	-0.0007	-0.0011	0.0009	-0.0007	-0.0056	-0.0011	-0.0004	-0.0001	0.3034
SI (g.)	Gen	0.0697	0.0804	0.126	0.0257	0.0629	-0.1053	-0.009	0.0775	0.3588	0.006	0.0205	0.2749
	Phe	0.0104	0.0125	0.0189	0.0025	0.0081	-0.0178	-0.0015	0.012	0.0613	-0.0001	0.0042	0.2312
BYPP (g.)	Gen	0.2976	0.2902	0.2319	0.2489	0.0477	0.2416	0.1464	0.0437	0.0104	0.6183	-0.4314	0.6348
	Phe	0.3977	0.3765	0.3239	0.3388	0.1144	0.3259	0.2039	0.0618	-0.0018	0.8489	-0.5682	0.6159
HI (%)	Gen	-0.0251	-0.0155	0.0015	-0.0046	0.0453	-0.0206	0.0289	0.0071	0.0086	-0.1044	0.1496	-0.0763
	Phe	-0.0332	-0.022	-0.0082	-0.0243	0.0225	-0.0264	0.0264	0.004	0.0125	-0.1228	0.1834	-0.0587
D50PF	Gen	-0.3133	-0.1275	-0.0089	0.6464	-0.0864	-0.0157	0.5276	0.0139	0.0987	0.3925	-0.0114	
	Phe	-0.4045	0.3787	0.0327	-0.2139	0.114	-0.1492	0.6902	-0.0017	0.0142	0.5229	-0.0108	

R Square = 9.9158 for genotypic, 0.9726 for phenotypic, Residual effect = 1.7421 for genotypic, 0.1656 for phenotypic
Note: Diagonal Bold =Direct path & Red Color = Correlation Coefficient

Direct Effect on Seed Yield at Genotypic Level

Path coefficient analysis revealed that total no. of branches per plant (0.8153), followed by number of pods per plants (0.6587), biological yield (g.) (0.6183), 100 seed weight (g.) (0.3588), harvest index (%) (0.1496), and number of seeds/pod (0.0425) had exerted maximum direct effect on seed yield at genotypic level. days to 50% flowering (-0.5204), followed by days to first picking pods (-0.1915), number of clusters plants (-0.1088), days to second picking pods (-0.0134), and number of pods per clusters (-0.0474) had exhibited negative direct effect on seed yield at genotypic level.

Direct Effect on Seed Yield at Phenotypic Level

Number of pods per plants (0.9384), followed by biological yield (g.) (0.8489) days to first picking pods (0.6336), harvest index (%) (0.1834), number of clusters plants (0.1643), 100 seed weight (g.) (0.0613), and days to second picking pods (0.0528) had exerted maximum direct effect on seed yield. While days to 50% flowering (-0.7197), followed by number of pods per clusters (-0.517), total no. of branches per plant (-0.3075), and number of seeds/pod (-0.0056) had exhibited negative direct effect on seed yield at phenotypic level.

The early reports on genotypic level positive direct effect was recorded for different traits by Garje *et al.,* (2014); Kapadia *et al.,* (2015); Garg *et al.,* (2017); Varma *et al.,* (2018); Muthuswamy *et al.,* (2019); Asari *et al.,* (2019); Ahmad and Belwal (2020); Dhunde *et al.,* (2021); Parsaniya *et al.,* (2022b); Nalajala *et al.,* (2022); Shakeer *et al.,* (2022).

CONCLUSION

As per mean the performance, some varieties viz., PGRV 95016, Virat, IC 76499, PDM 04-123, PPU 911, and ML 2056 are high yielding and suitable for growing in Satna district of (M.P.). The design of the experiment indicated highly significant differences for all the characters among treatments. Wide range of variation was found for all the studied characters of paddy. High degree of GCV, PCV were indicating simple selection for these traits will be useful for the planning of a breeding programme. High positive significant correlation with seed yield per plant (g.) was indicating that the selection for these traits could be improving seed yield in mungbean crop. On the basis of path coefficient analysis showed high direct and indirect effect with seed yield were important characters that could be taken into consideration for selection and improvement of seed yield in mungbean.

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