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Genetic Cause and Effect Interrelationships for Yield and Yield Components of Mungbean [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

Background: Mungbean (*Vigna radiata* L.) an exemplary protein-rich food legume, presents itself as an abundant source of various essential nutrients. Effective selection of traits and identification of genotypes is important to develop high yield potential varieties in green gram.

Methods: Twenty-seven genotypes were planted in a Randomized Block Design, with three check varieties, over the course of two consecutive summers, specifically in 2022 and 2023.

Result: AKM 96-2, IPDI-539, PRATIKSHA NEPAL, SUKETI-1 and TMB 96-2 consistently showed excellent performance. Path analysis highlighted the strong impact of the number of pods per plant on seed yield, followed by 100-seed weight, pod length, flowering days, branches and clusters per plant, with seeds per plant having the least impact. These traits possess the potential to serve as selection criteria in mungbean breeding program.

Key words: GCV, Genetic variability, Mungbean, Path analysis, PCV.

INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek], a self-pollinating leguminous crop belonging to the *Fabaceae* family with a chromosome number of 2n = 22, holds a crucial position as the predominant pulse crop in India, following chickpea, redgram and blackgram. Originating from the Indo-Burma region of the Hindustan center (Vavilov, 1926), mungbean cultivation is predominantly undertaken within the rice-based farming system due to its remarkable adaptability to short growth durations, minimal input requirements and low water consumption.

Mungbean presents a multifaceted array of benefits for sustainable agriculture. Its inherent ability to restore soil fertility through biological nitrogen fixation, coupled with its contribution to the reduction of greenhouse gas emissions and the augmentation of carbon sequestration (Alom *et al.,* 2015), renders it an invaluable asset. Furthermore, mungbean is an exemplary source of essential nutrients, boasting a staggering 26.3% raw protein content, 59.8% carbohydrates and substantial levels of iron, zinc, phosphorus, vitamin A and vitamin C (Keatinge *et al.,* 2011; Nair *et al.,* 2013). Its unique amino acid composition, rich in leucine, phenylalanine, lysine, valine and isoleucine, surpassing methionine and cysteine levels found in other legumes (Ahmad and Belwal, 2020), further enhances its nutritional value.

Despite its multifaceted advantages, mungbean cultivation faces challenges, including limited availability of suitable land, cold stress during the *rabi* season, a lack of high-yielding genotypes, a low seed replacement ratio of improved varieties and imbalanced usage of plant nutrients (Kuchanur *et al.,* 2017). Consequently, global mungbean productivity remains disappointingly low at 0.5 t/ha, significantly below the estimated yield potential of 2.5 - 3.0 t/ha (Nair *et al.,* 2019). In recognition of the nutritional significance of pulses, the 68th UN General Assembly declared 2016 as the International Year of Pulses, aiming to raise awareness among farming communities.

To address these problems, effective selection of traits and identification of genotypes are crucial for developing high-yielding mungbean varieties. Seed yield is a complex trait determined by various yield-attributing characters, either directly or indirectly (Degefa *et al.,* 2013). Effective selection can be achieved through genetic analysis by assessing genetic diversity within mungbean germplasm to identify traits associated with resilience and conducting trait association studies to select traits that contribute to

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higher yields. The research aims to elucidate the genetic variability, heritability, genetic advance, genetic interrelationships between yield and its components and path analyses which will assist and focused on developing high-yielding, stress-resistant mungbean varieties. ((Ford, 1964; Dewey and Lu, 1959, Harini *et al.,* 2022; Sawarkar *et al.,* 2015, Das *et al.,* 2024). Therefore, the present study aimed to evaluate mungbean genotypes during the summer seasons of 2022 and 2023, assessing various agronomic traits helps to identify potential and stable germplasm as a parent for future breeding program and will explore the potential of molecular markers for marker-assisted selection.

MATERIALS AND METHODS

Experimental location and details

The research investigation was carried out at the agricultural experimental farm, (AEM) Narendrapur, Division of genetics and plant breeding, West Bengal, over two years, encompassing the main season of summer of 2021 and 2022. The AEM, Narendrapur lies at 22°43′N latitude and 88°40′E longitude belongs to New Alluvial Zone at an elevation of 8m above mean sea level. The experimental materials comprised of 30 germplasm including three check varieties *i.e.*, SAMRAT, SIKHA and VIRAT (Table 1). All the genotypes were obtained from the ICAR-Indian Institute of Pulse Research, Kanpur. The experiment was laid out in the randomized complete block design (RCBD) with three replications. The size of unit plot was 3 m × 2.2 m. The distances of 45 cm between rows, 15 cm within the plants, 75 cm between plots and 1 m between replications. The experimental field was prepared, genotypes were sown and followed various intercultural operations for better growth of seedlings. Fertilizers were applied @ 20:40:20 kg of N: P_2O_5: K_2O along with 300 cft. of farm yard manure (FYM) per hectare. Half of nitrogenous and whole of phosphatic and potassic fertilizers were applied in lines as basal at the time of sowing. The rest amount of nitrogen was applied after 25 days of sowing as top dressing. Weeding was done before top dressing of nitrogenous fertilizer. Other management practices were followed as per recommended package of practices.

Five randomly selected plants were harvested per plot when color of almost all the pods become black or brown. Pods of each plant were kept separately in paper bags and sun dried. Threshing was done by hand and strict care was taken to avoid mechanical mixture of seeds. Data on various parameters were recorded such as days to 50% flowering (DTF) was measured as the number of days from sowing to when 50% of the plant population showed blooming, while days to maturity (DTM) were recorded from sowing to the harvesting date of the plot. Plant height (PH, cm) was measured from the base to the tip of the main shoot and the number of primary branches per plant (NPB) and branches per plant (BPP) were counted at maturity. The number of clusters per plant (NCP) and pods per plant (NPP) were counted from selected plants at maturity, while pod length (PL, cm) was determined from five randomly selected pods per plant. The number of seeds per pod (NSP) was counted from each pod and 100-seed weight (HSW, g) was obtained by weighing 100 well-dried seeds from the produce of each selected plant. Finally, seed yield per plant (SYP, g) was recorded as the total yield from selected plants in each plot. The obtained data were statistically analyzed in R software version 4.3.2 and estimated the analysis of variance (Fisher,1936), components of correlation coefficient (Burton and Devane, 1953), genetic variability parameters (Johnson *et al.,* 1955) and path analysis (Dewey and Lu, 1959).

RESULTS AND DISCUSSION

The pooled analysis of variance (ANOVA) showed in (Table 2) as a measure of variability was carried out for 30 mungbean genotypes. Significant differences among all the genotypes and interaction between genotypes and environments were revealed for all the characters studied. This indicates that genotypes were taken under the research work had present

Table 1: Thirty germplasm of mungbean evaluated for eleven quantitative traits.

Sl. no.	Germplasm
1	AKM 96-1
2	AKM-96-2
3	CO8
4	COGC-912
5	EC5200-34
6	IPDI-539
7	IPM2-17
8	IPM2-5-8
9	IPM2K-14-9
10	MH2-15
11	MH-521
12	MH-805
13	MI-1464
14	ML-1059
15	ML-2056
16	ML-5
17	NM-1
18	PDM 04-123
19	PDM-281
20	PDM-54
21	PRATIKSHA NEPAL
22	PUSA-0672
23	PUSA-0891
24	PUSA-9972
25	SML-1808
26	SUKETI-1
27	TMB 96-2
28	SAMRAT
29	SIKHA
30	VIRAT

Table 2: Pooled Analysis of variance of various quantitative traits of mungbean.

Source	DF	DTF	DTM	PH	NPB	BPP	NCP	NPP	PL	NSP	HSW	SYP
Replication	4	11.56	8.82	18.21	0.06	0.23	0.18	5.44	0.09	1.71	0.12	0.31
Treatment	29	3074.02**	29.90**	251.16**	3.14**	8.70**	6.29**	196.17**	1.17**	5.94**	1.17**	37.54**
Season	1	31.35**	204.79**	8268.49**	0.58**	4.54**	301.58**	3037.53**	6.96**	68.79**	38.92**	1886.01**
S × T	29	2881.64**	26.09**	144.53**	0.1562**	0.06**	5.08**	61.39**	0.57**	6.11**	0.81**	15.40**
Error	116	4.31	3.29	6.90	0.05	0.12	0.45	3.99	0.11	0.87	0.05	0.64

(DF= Degree of freedom; DTF= Days to 50% flowering; DTM=Days to maturity; PH=Plant height (cm); NPB= Number of primary branches per plant; BPP= Number of branches per plant; NCP= Number of clusters per plant; NPP=Number of pods per plant; PL= Length of pod; NSP= Number of seeds per pod; HSW= 100 seed weight; SYP= Seed yield per plant)
(*and ** indicate significant at 0.05 and 0.01 levels of Probability).

the characters. Salman *et al.,* (2021) and Dhoot *et al.,* (2017) also reported significant differences for all the characters studied. Over two years of study, some genotypes consistently had good performance than the other genotypes (Table 3). Early flowering was observed in SIKHA, IPM2K-14-9, MH2-15, PRATIKSHA NEPAL and IPDI-539. These genotypes could be considered for the development of early maturity lines of mungbean. Among the genotypes, ML-1059, PUSA-9972, PDM04-123, SML-1808 and PDM-281 were recorded for more days to mature. The genotypes such as VIRAT, SIKHA, SAMRAT, AKM-96-2, SUKETI-1, IPM-2-17 were consistently showing the significantly good performance for most of the characters like plant height, number of primary branches per plant, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per plant and 100 seed weight. Highest seed yield per plant was recorded in VIRAT and it was followed by SIKHA, SAMRAT, IPDI-539 and SUKETI-1. This indicates great scope for the effective selection.

Table 4 showed various genetic variability parameters of the characters like mean values, range having minimum and maximum values, phenotypic (PV) and genotypic variance (GV) and its coefficients, heritability in broad sense (%), genetic Advance (GA) and genetic advance as percent of mean. The mean and range of the characters revealed the large variation had recorded of the genotypes due to the interaction between genotypes and environment. A comparison of genotypic variance and phenotypic variance was performed to determine the magnitude of the genotypic contribution to the mungbean improvement. The highest genotypic variance and phenotypic variance was observed for plant height, number of pods per plant and days to 50% flowering. The phenotypic variance was higher than the genotypic variance due to the combination of genotypic variance and environmental factors. Similarly, the phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV) for all the traits, suggesting a significant influence of environmental factors on the observed traits. The GCV and PCV value between above 20%, between 10% and 20% and below 10% as interpretated high, moderate and low respectively. High GCV and PCV (<20) was observed for seed yield per plant and it was followed by number of primary branches per plant and number of pods per plant. similar results were reported Ramakrishnan *et al.,* (2018), Parimala *et al.,* (2020). The highest values of GCV and PCV indicates that presence of high variability in these characters suggested reasonable scope for the improvement through selection. Moderate GCV and PCV (10 -20) was recorded for number of branches per plant and it was followed by number of clusters per plant, 100 seed weight and plant height. The above results were corroborated with Salman *et al.* (2021). Similar results were observed by Pandey *et al.,* (2007) and Nand and Anuradha (2013) for number of branches per plant and Rao *et al.,*

Table 3: Mean performance of thirty genotypes of various quantitative traits over two years (2022 and 2023).

Germplasm	DTF	DTM	PH	NPB	BPP	NCP	NPP	PL	NSP	HSW	SYP
AKM 96-1	44.67 d	68.33 d-h	54.16 ijkl	2.11 ghi	8.22 def	6.17 f-m	21.73 efg	7.25 f-j	9.65 gh	3.22 hij	5.26 nop
AKM-96-2	44.83 d	68.00 d-i	63.54 c	3.13 c	6.46 mn	7.22 cde	27.92 cd	7.11 g-k	11.67 bcd	3.76 def	8.40 fg
CO8	41.18 f	69.17 b-g	52.35 k-n	2.50 def	7.57 ghij	6.77 e-h	27.13 d	7.80 b-e	10.96 c-g	3.27 hij	9.50 de
COGC-912	38.00 ghi	68.17 d-i	53.15 j-m	1.88 ij	6.49 mn	6.00 h-m	17.65 h	7.42 e-h	12.36 bc	2.69 k	4.33 p
EC5200-34	40.00 fgh	64.50 kl	52.20 lmn	1.77 ijk	7.70 ghi	6.66 e-i	23.53 ef	8.23 b	14.12 a	3.14 hij	8.80 ef
IPDI-539	37.50 hi	63.50 l	54.82 h-l	3.05 c	7.18 jkl	6.57 e-j	29.75 c	6.99 h-k	10.10 e-h	3.64 efg	10.82 c
IPM2-17	46.00 cd	67.50 e-j	59.72 d-g	3.05 c	7.06 kl	6.97 d-g	24.04 e	7.97 bc	12.38 b	3.88 cde	6.82 j-m
IPM2-5-8	45.00 cd	67.83 d-i	63.12 c	1.88 ij	7.76 fgh	6.12 f-m	21.74 efg	7.97 bc	11.23 b-f	2.56 k	6.29 klm
IPM2K-14-9	36.83 i	65.67 i-l	56.70 ghi	2.10 ghi	8.78 bc	5.78 i-m	20.83 g	7.40 e-h	11.60 bcd	3.81 de	7.15 h-k
MH2-15	37.00 i	65.33 jkl	52.85 klm	2.00 hij	7.93 efg	5.37 m	21.86 efg	6.78 jk	9.55 gh	3.32 hij	5.99 lmn
MH-521	45.29 cd	71.50 ab	50.10 mn	2.66 de	7.98 efg	8.23 b	20.65 g	7.21 f-k	9.33 h	3.09 ij	6.91 jkl
MH-805	45.48 cd	70.33 a-d	54.83 h-l	1.48 k	6.20 no	6.53 e-k	21.10 fg	7.20 f-k	10.56 d-h	3.22 hij	6.47 klm
MI-1464	45.71 cd	66.67 g-k	56.20 hij	2.36 efg	7.44 h-k	6.17 f-m	18.02 h	7.61 c-f	10.79 d-g	3.02 j	4.76 p
ML-1059	53.17 a	71.83 a	62.45 cd	1.80 ijk	5.65 p	6.12 f-m	17.60 h	7.44 d-h	11.71 bcd	3.11 ij	5.02 op
ML-2056	41.17 f	65.33 jkl	57.15 f-i	2.82 cd	7.54 g-j	5.58 lm	16.20 h	7.54 c-g	11.63 bcd	3.64 efg	7.68 g-j
ML-5	41.40 f	69.83 a-e	43.12 o	2.10 ghi	5.87 op	5.62 klm	21.44 efg	7.44 d-h	11.34 b-f	3.20 hij	6.80 j-m
NM-1	45.83 cd	69.33 b-f	57.35 e-i	1.72 jk	7.13 jkl	6.13 f-m	17.95 h	7.36 e-h	10.90 d-g	3.15 hij	5.03 op
PDM 04-123	48.83 b	71.50 ab	60.38 c-f	1.70 jk	9.02 b	6.17 f-m	22.12 efg	6.77 k	10.14 e-h	3. hij	5.86 mno
PDM-281	46.17 cd	66.67 g-k	58.02 e-h	2.59 def	7.15 jkl	6.25 f-m	17.80 h	7.28 f-i	11.18 b-f	3.46 fgh	4.88 p
PDM-54	44.00 de	66.67 g-k	57.22 e-i	1.91 ij	8.57 cd	6.06 g-m	17.07 h	7.17 f-k	9.93 fgh	3.03 j	4.59 p
PRATIKHA NEPAL	37.00 i	67.00 f-j	55.48 h-l	3.00 c	5.47 p	7.01 def	26.93 d	8.23 b	10.79 d-g	3.75 def	7.91 f-i
PUSA-0672	40.17 fg	69.00 c-g	56.97 ghi	2.00 hij	9.53 a	6.52 e-l	.70 efg	7.59 c-g	10.77 d-g	3.31 hij	7.00 ijk
PUSA-0891	41.83 ef	68.00 d-i	50.32 mn	2.29 fgh	9.92 a	6.33 e-l	21.07 fg	7.64 c-f	10.60 d-h	3.22 hij	6.88 jkl
PUSA-9972	49.24 b	70.83 abc	57.76 e-h	1.82 ij	6.84 lm	5.69 j-m	21.26 fg	7.37 e-h	10.57 d-h	3.38 ghi	8.05 fgh
SML-1808	47.73 bc	68.00 d-i	49.40 n	2.27 fgh	8.35 cde	6.13 f-m	21.95 efg	7.48 d-g	10.58 d-h	3.65 dg	7.70 g-j
SUKETI-1	45.17 cd	64.33 kl	55.62 h-k	3.63 b	6.93 l	6.80 e-h	20.95 fg	8.73 a	11.75 bcd	4.14 bc	9.98 cd
TMB 96-2	45.66 cd	70.83 abc	56.77 ghi	4.34 a	9.80 a	7.77 bcd	26.66 d	6.88 ijk	10.88 d-g	4.50 a	8.41 fg
SAMRAT (cv)	41.00 f	68.83 c-g	60.49 cde	3.64 b	7.26 i-l	10.65 a	33.32 b	7.41 e-h	12.50 b	4.21 b	11.88 b
SIKHA (cv)	36.50 i	66.17 h-k	73.13 b	3.70 b	7.92 efg	6.49 e-l	42.19 a	7.25 f-j	11.38 be	3.80 de	13.69 a
VIRAT (cv)	45.83 cd	68.00 d-i	76.07 a	3.13 c	9.75 a	7.98 bc	33.38 b	7.90 bcd	11.57 bcd	3.96 bcd	13.77 a
CD at 5%	2.34	2.05	2.79	0.26	0.40	0.76	2.26	0.37	1.05	0.25	0.91
CV (%)	4.79	2.67	4.60	9.49	4.63	10.18	8.61	4.43	8.43	6.61	10.67
SE (d)	1.19	1.04	1.51	0.13	0.20	0.38	1.15	0.19	0.53	0.13	0.46

(DF= Degree of freedom; DTF= Days to 50% flowering; DTM= Days to maturity; PH= Plant height (cm); NPB= Number of primary branches per plant; BPP= Number of branches per plant; NCP= Number of clusters per plant; NPP= Number of pods per plant; PL= Length of pod; NSP= Number of seeds per pod; HSW= 100 seed weight; SYP= Seed yield per plant).

(2006); Makeen *et al.,* (2007) and Kumhar and Choudhary (2007) for 100 seed weight. Low GCV and moderate PCV was exhibited for days to 50% flowering and number of seeds per pod. Similar results were also recorded by Harini *et al.,* (2022). This indicates that traits have more influenced of environment. Low GCV and low PCV was showed for days to maturity and pod length. Similar findings were revealed by Shiv *et al.,* (2017). It indicates less variability present in these characters, provides the selection may not be effective.

Heritability is the ratio of genotypic variance to the total phenotypic variance of the character. It provides the information of the transmission of the characters from parents to the offsprings. It is crucial parameter in the plant breeding where plant breeders could rely on it. The heritability values show the possible and extent of improvement could occur through selection. (Sawarkar, *et al.,* 2023) On the basis of diverse genotypes, the variation in the heritability was recorded. It is usually classified as high (above 60%), medium (30-60%) and low (0 to 30%). The high heritability helps in the effective selection of the genotypes. The broad sense of heritability of the characters was observed from (60.83%) to (95.75%). All the characters were showed as high heritability. The highest broad sense of heritability was recorded for number of branches per plant (95.75%) which was followed by seed yield per plant (95.58%), number of pods per plant (94.54%) and number of primary branches per plant (94.06%). Similar results were obtained by Salman *et al.* (2021) for number of branches per plant, Garg *et al.* (2017) for seed yield per plant and number of pods per plant. It indicates that the environment had little influence on the expression of these traits and it would be reasonable to select easily. Katiyar *et al.* (1974) noted that relying solely on heritability values does not provide any insight into the extent of genetic advancement that could be achieved through the selection of the most superior individuals. Nevertheless, Johnson *et al.,* (1955) proposed that incorporating heritability estimates together with genetic advance would yield greater utility in forecasting yield outcomes under phenotypic selection, compared to relying solely on heritability estimates. In the present study, high genetic advance was observed for plant height and number of pods per plant. The comparison of heritability in relation to genetic advancement, expressed as a percentage of the means across various traits revealed that seed yield per plant, 100 seed weight, number of pods per plant, number of clusters per plant, number of branches per plant, number of primary branches per plant and plant height had high heritability and high genetic advance as a percentage of mean indicated genetic variation. The prevalence of the additive gene action can be ascribed to the influence of activity and it would be advantageous to employ selection in order to enhance the seed yield in relation to these particular traits. Similar findings were obtained by Reshmi *et al.,* (2020) for these characters except number of clusters per plant, number of branches per plant, Choudary *et al.,* (2017) for number of primary branches per plant, Talukdar *et al.,* (2020) for number of pods per plant, Rahim *et al.,* (2010)) and Ghimire. (2017) for seed yield per plant. Moreover, high heritability along with moderate genetic advance as a percentage of mean was observed for days to 50% flowering and number of seeds per pod. Similar results were reported by Hemavathy *et al.,* (2015). It indicates that these traits were predominantly regulated by the additive genes and that direct targeting of these attributes could be effective. Nevertheless, pod length and days to maturity had high heritability and low genetic advance as a percentage of mean. Hence, these characters were regulated by nonadditive genes *i.e.* dominance and epistasis, thereby enabling environmental regulation over

Table 4: Pooled analysis on variability and different genetic parameters for different yield attributing characters of mungbean.

Characters	Mean	Range		PV	GV	GCV	PCV	Heritability% (Broad Sense)	Genetic advance	Genetic advance as % of mean
		Min.	Max.							
DTF	43.27	36.50	53.17	19.14	16.93	9.51	10.11	88.46	7.97	18.42
DTM	67.96	63.50	71.83	6.13	4.41	3.09	3.64	72.09	3.68	5.41
PH	57.05	43.12	76.07	43.73	40.62	11.17	11.59	92.88	12.65	22.18
NPB	2.48	1.48	4.34	0.55	0.51	28.86	29.76	94.06	1.43	57.65
BPP	7.65	5.48	9.92	1.49	1.43	15.64	15.98	95.75	2.41	31.52
NCP	6.60	5.37	10.65	1.20	0.98	14.98	16.60	81.42	1.84	27.84
NPP	23.22	16.20	42.19	33.93	32.08	24.39	25.09	94.54	11.34	48.86
PL	7.48	6.77	8.73	0.24	0.18	5.60	6.49	74.39	0.74	9.94
NSP	11.08	9.33	14.12	1.34	0.82	8.15	10.45	60.83	1.45	13.09
HSW	3.45	2.56	4.50	0.21	0.19	12.56	13.45	87.13	0.83	24.14
SYP	7.55	4.33	13.77	6.45	6.16	32.87	33.62	95.58	5.00	66.20

DTF = Days to 50% flowering, DTM=Days to maturity, PH=Plant height(cm), NPB=Number of primary branches per plant, BPP= Number of branches per plant, NCP=Number of clusters per plant, NPP=Number of pods per plant, PL= Length of pod, NSP= Number of seeds per pod, HSW= 100 seed weight, SYP= Seed yield per plant, PV= Phenotypic Variance, GV= Genetic variance, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation.

the manifestation of these traits and their improvement could be achieved through the utilization of heterosis breeding.

Correlation coefficient analysis is usually do to study the relationships between the seed yield and other attributes. Table 5 represent the phenotypic and genotypic correlation coefficient of the seed yield and its attributing traits. Overall basis, the genotypic correlation exhibited a higher magnitude compared to the corresponding phenotypic correlation across all pairs of characters. This suggests that the presence of environmental effects has a dampening effect on the association observed at the phenotypic level. This finding indicates that both the environmental and genotypic correlations in those specific cases operate in a similar direction, ultimately leading to the maximization of their expression at the phenotypic level. Seed yield per plant highly significant and positively correlated with plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod and 100 seed weight at phenotypic and genotypic level except pod length at genotypic level only. These results are in accordance with Baisakh *et al.,* (2016) for plant height, Ghimire *et al.,* (2017) for number of primary branches per plant, Sandhiya and Saravanan (2018) for the number of clusters per plant, Reshmi *et al.,* (2020), Ramakrishnan *et al.,* (2018) for number of pods per plant, Das and Barua (2015) for the number of seeds per pod; Kate *et al.,* (2017) for 100 seed weight. These traits could be directly selected in the development of high yielding varieties of mungbean. Days to 50% flowering was observed non-significant and negative correlation between most of the characters but exhibited significant positive correlation with days to maturity and significant negative correlation with number of pods per plant and seed yield per plant at phenotypic and genotypic level. Similarly, days to maturity had negative and non-significant correlation all the characters except pod length, number of seeds per plant and 100 seed weight had negative correlation at genotypic level only and seed yield per plant at both levels. Plant height showed the significant and positive correlation with number of primary branches per plant, number of clusters per plant, number of pods per plant and 100 seed weight at both levels. However, it had negative significant correlation with number of seeds per plant at genotypic level only. Number of primary branches per plant exhibited significantly high and positive correlation with number of clusters per plant, number of pods per plant and 100 seed weight. In case of number of branches per plant significant and negative correlation with number of seeds per plant while number of clusters per plant significant and positively correlation with the number of pods per plant and 100 seed weight at both levels. Likewise, characters like number of pods per plant had positive correlation with the 100 seed weight and pod

Table 5: Pooled analysis for Phenotypic (P) and Genotypic (G) correlation co-efficient among different yield attributing characters of mungbean.

Characters		DTM	PH	NPB	BPP	NCP	NPP	PL	NSP	HSW	SYP
DTF	P	0.559**	0.170	-0.163	-0.013	0.028	-0.323**	0.014	-0.064	-0.066	-0.275**
	G	0.621**	0.124	-0.185	-0.051	0.002	-0.369**	-0.078	-0.150	-0.112	-0.299**
DTM	P		0.007	-0.192	0.027	0.193	-0.096	-0.201	-0.166	-0.117	-0.217*
	G		-0.050	-0.236*	-0.029	0.181	-0.137	-0.414**	-0.309**	-0.223*	-0.269*
PH	P			0.324**	0.181	0.243*	0.533**	0.060	0.180	0.285**	0.469**
	G			0.339**	0.164	0.272**	0.551**	-0.001	0.213*	0.290**	0.494**
NPB	P				0.122	0.577**	0.612**	0.119	0.143	0.781**	0.645**
	G				0.123	0.614**	0.635**	0.119	0.171	0.859**	0.673**
BPP	P					0.099	0.145	-0.140	-0.195	0.164	0.159
	G					0.098	0.138	-0.212*	-0.263*	0.161	0.173
NCP	P						0.513**	0.109	0.189	0.456**	0.496**
	G						0.547**	0.081	0.246*	0.544**	0.555**
NPP	P							0.029	0.157	0.517**	0.846**
	G							-0.023	0.158	0.556**	0.889**
PL	P								0.510**	0.110	0.206
	G								0.555**	0.051	0.233*
NSP	P									0.189	0.237*
	G									0.193	0.296**
HSW	P										0.611**
	G										0.665**

(DTF= Days to 50% flowering; DTM= Days to maturity; PH= Plant height (cm); NPB= Number of primary branches per plant; BPP= Number of branches per plant; NCP= Number of clusters per plant; NPP= Number of pods per plant; PL= Length of pod; NSP= Number of seeds per pod; HSW= 100 seed weight; SYP= Seed yield per plant) (* and ** indicate significant at 0.05 and 0.01 levels of Probability).

length had significant positive correlation with the number of seeds per pod at phenotypic and genotypic level and with seed yield per plant at genotypic level only.

The significance of the correlation coefficient is greatly enhanced when the correlation coefficients are divided into distinct parts that represent the direct and indirect effects through the utilization of path analysis. This is crucial as correlation coefficients merely illustrate the interrelationship between various variables without taking into consideration the cause and effect aspect. This approach, as suggested by Dewey and Lu (1959), allows for a more comprehensive understanding of the underlying factors influencing the correlation coefficients. The path analysis ultimately results in the identification of crucial component traits that can be effectively utilized in the process of indirect selection for complex traits, such as yield. This is due to the fact that a character like seed yield is intricately dependent on numerous component characters that are mutually associated with one another. Therefore, if there is any alteration or modification in any one of these characters, it is highly likely to have a significant impact on the cause and effect relationships that exist within the system. Table 6 represent the direct and indirect effect of various characters of mungbean on seed yield. The values appearing in the diagonal are the direct effect of the traits *via* positive or negative direction on seed yield. Out of 10 yield attributing characters, seven characters were recorded positive direct effects on seed yield while two were negative indirect effect on seed yield. Highest direct effect was observed by number of pods per plant and it was followed by 100 seed weight, pod length, days to 50% flowering, number of branches per plant, number of clusters per plant and lowest had number of seeds per plant. Similar findings were obtained by Reshmi *et al.,* (2020) for number of pods per plant, Thippani *et al.,* (2013) for pod length and 100 seed weight. While, highest negative indirect effect was noticed for number primary branches per plant and it was followed by days to maturity and plant height on seed yield. Characters like number of pods per plant, in addition to the 100 seed weight and the pod length, not only exhibit a higher magnitude of positive direct effect but also demonstrate a significant and positive correlation with the seed yield per plant. This implies that by directly selection of these traits, can effectively improve the seed yield of mungbean. On the other hand, the days to 50% flowering exhibited a positive direct effect, yet its correlation with the yield was negative. This indicates that the cause of this correlation lies in the indirect effects. Consequently, in order to fully utilize the high positive direct effect of the days to 50% flowering, it is recommended to adopt a restricted selection model that can eliminate the undesirable indirect effects. By doing so, it could ensure that the use of this particular trait positively contribute to the mungbean improvement program. The positive direct effect of the number of branches per plant on seed yield, though significant, was found to have a non-significant association with the seed yield. Consequently, it can be concluded that indirect selection, specifically through the consideration of the number of clusters per plant, the number of pods per plant and 100 seed weight, would prove to be more effective in increasing the yield in the mungbean. Similarly, number of primary branches per plant showed high and significant positive correlation with the seed yield but unfortunately it had negative direct effect on seed yield. Therefore, indirect effect were mainly responsible for the production of such correlation. Hence indirect selection through number of pods per plant, 100 seed weight, pod length could be helpful in enhancing the seed yield of mungbean. The residual effect observed in the current study, with a value of 0.092, serves as a significant indication of the amount of variability that occurred in seed yield. This variability can be attributed to the various traits that were studied in the path analysis, thereby highlighting their potential influence on the final outcome. It is important to note that the residual

Table 6: Path coefficient (genotypic) analysis showing direct (bold) and indirect effects of various traits of mungbean over two years (2022 and 2023).

Traits	DTF	DTM	PH	NPB	BPP	NCP	NPP	PL	NSP	HSW	SYP(rg)
DTF	0.123	-0.063	-0.008	0.031	-0.005	0.000	-0.325	-0.018	-0.003	-0.032	-0.299**
DTM	0.077	-0.102	0.003	0.039	-0.003	0.004	-0.121	-0.097	-0.006	-0.064	-0.269*
PH	0.015	0.005	-0.063	-0.056	0.015	0.006	0.485	0.000	0.004	0.083	0.494**
NPB	-0.023	0.024	-0.021	-0.166	0.011	0.014	0.559	0.028	0.004	0.244	0.673**
BPP	-0.006	0.003	-0.010	-0.020	0.092	0.002	0.121	-0.049	-0.005	0.046	0.173
NCP	0.000	-0.018	-0.017	-0.102	0.009	0.022	0.482	0.019	0.005	0.155	0.555**
NPP	-0.046	0.014	-0.035	-0.105	0.013	0.012	0.880	-0.005	0.003	0.158	0.889**
PL	-0.010	0.042	0.000	-0.020	-0.020	0.002	-0.021	0.233	0.011	0.014	0.233*
NSP	-0.018	0.031	-0.013	-0.028	-0.024	0.005	0.139	0.129	0.020	0.055	0.296**
HSW	-0.014	0.023	-0.018	-0.142	0.015	0.012	0.489	0.012	0.004	0.285	0.665**

(DTF = Days to 50% flowering; DTM= Days to maturity; PH= Plant height(cm); NPB= Number of primary branches per plant; BPP= Number of branches per plant; NCP= Number of clusters per plant; NPP= Number of pods per plant; PL= Length of pod; NSP= Number of seeds per pod; HSW= 100 seed weight; SYP(rg)= Genotypic correlation of seed yield per plant).

effects observed in this particular study can be attributed to a multitude of factors, including environmental conditions and cultural practices, which have been known to significantly impact the seed yield.

CONCLUSION

The present investigation of research revealed the genotypes namely, AKM 96-2, IPDI-539, PRATIKSHA NEPAL, SUKETI-1, TMB 96-2 had performed well in comparison with the check varieties against most of characters. Characters like seed yield per plant, number of pods per plant, number of clusters per plant, number of seeds per plant, 100 seed weight and number of primary branches per plant can be used selection criteria in future breeding program.

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Conflict of interest

All authors declared that there is no conflict of interest.

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