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GENETIC VARIABILITY, CHARACTER ASSOCIATION AND PATH COEFFICIENT ANALYSIS IN MUNGBEAN (*Vigna radiata* L. Wilczek) GENOTYPES

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ABSTRACT

Mungbean (*Vigna radiata* L. Wilczek) is an important short-duration pulse crop providing essential nutrition through high protein, fibers, minerals, and vitamins. The present investigation was conducted to assess genetic variability, character association, and direct and indirect effects of yield-determining traits in mungbean germplasm. Thirteen mungbean genotypes were evaluated in a Randomized Block Design during Kharif (2025-2026) at Crop Research Centre-1, ITM University, Sithouli Campus, Gwalior, Madhya Pradesh. Thirteen quantitative traits including days to 50% flowering (DFF), days to maturity (DM), plant height (PH), number of primary branches per plant (PB), number of secondary branches per plant (SB), number of clusters per plant (CPP), number of pods per cluster (NPPC), number of pods per plant (NPPP), pod length (PL), number of seeds per pod (NSPod), number of seeds per plant (NSPP), 100-seed weight (HSW), and seed yield per plant (SYPP) were recorded. Analysis of variance revealed highly significant differences among genotypes for all traits, indicating substantial genetic variability. Genetic parameters showed extremely high heritability values (>94%) for most traits, with number of pods per plant and number of seeds per plant exhibiting the highest genetic advance as percentage of mean (GAM) values of 20.68% and 21.65% respectively. Path coefficient analysis at genotypic level revealed that number of seeds per plant had the largest direct effect (1.0176**) on seed yield, followed by 100-seed weight (0.5608**) and number of seeds per pod (0.8860**), indicating these traits as primary targets for selection. These findings provide valuable information for designing effective breeding strategies for mungbean improvement aimed at developing high-yielding cultivars.

Keywords : *Vigna radiata*, Genetic variability, Character association, Path coefficient analysis, Heritability, Yield components, Breeding strategies.

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek], commonly known as green gram or moong, is an important short-duration grain legume widely cultivated in South and Southeast Asia. The crop is native to India and has been cultivated for thousands of years as an essential dietary component in Asian cuisine (Gogoi *et al.*, 2024). Mungbean serves as a rich source of plant-based protein, dietary fiber, essential minerals including iron and calcium, and various vitamins, making it a critical nutritional crop for food security in developing nations (Pathak *et al.*, 2023). The crop is also recognized for its environmental

benefits, as it can fix atmospheric nitrogen through its association with Rhizobium species, reducing the need for synthetic nitrogen fertilizers and improving soil fertility. This nitrogen-fixing capability positions mungbean as an ideal crop for sustainable agricultural systems and crop rotations. Globally, mungbean cultivation covers approximately 7.3 million hectares with a total production of 5.3 million tonnes and an average productivity of 0.72 tonnes per hectare (Diatta *et al.*, 2024). India and Myanmar account for approximately 30% of worldwide production. The crop is characterized by its short duration (60-120 days), low water requirement, and ability to grow in diverse agroclimatic conditions ranging from marginal lands to

well-irrigated fields, making it adaptable to various farming systems (Chaurasia *et al.*, 2024). However, productivity remains relatively low in many regions due to several constraints including indeterminate growth habits, inadequate canopy architecture, poor resource partitioning efficiency, limited genetic variability in breeding programs, and vulnerability to biotic and abiotic stresses (Rohilla *et al.*, 2022). The nutritional composition of mungbean is impressive, containing 22-28% protein with a balanced amino acid profile including lysine, 1-1.5% fat, and 60-65% carbohydrates (Gayacharan *et al.*, 2020). Beyond its use as dry grain, mungbean can be processed into various food products including daal (soup), noodles, porridge, curries, sprouts, and flour, contributing to its popularity in food systems. Additionally, mungbean seed, fodder, and haulms can be utilized as animal feed and organic fertilizer, providing multiple-use value to farmers (Chaurasia *et al.*, 2024).

Improvement of mungbean yields and development of superior cultivars requires a comprehensive understanding of genetic variability present within the species (Rohilla *et al.*, 2022). Genetic variability serves as the foundation for any successful crop improvement program, as it provides the raw material for selection of superior genotypes. Estimates of heritability, genetic advance, and trait associations are fundamental parameters for understanding the genetic architecture controlling agronomic traits and predicting the response to selection. Previous investigations have established that traits such as number of pods per plant, 100-seed weight, and number of seeds per pod significantly influence seed yield in mungbean (Gogoi *et al.*, 2024). However, the relative importance of various yield-contributing traits and their direct and indirect effects on final productivity require continuous investigation across different genetic backgrounds and environments. Path coefficient analysis is a powerful statistical tool for partitioning correlation coefficients into direct and indirect effects, providing insights into the mechanisms through which various traits influence yield (Gayacharan *et al.*, 2020). Understanding these mechanisms enables breeders to develop more efficient selection strategies by identifying traits with strong direct effects that should be primary selection targets, as well as those with important indirect effects that influence yield through associations with other characters (Mishra *et al.*, 2023). The present investigation was conducted with the following objectives: (i) to assess genetic variability and estimate heritability and genetic advance for various quantitative traits in mungbean germplasm; (ii) to determine the nature and magnitude of correlation

between yield and yield-contributing traits; (iii) to partition correlation coefficients into direct and indirect effects through path coefficient analysis; (iv) to identify promising genotypes for utilization in future breeding programs.

Material and Methods

The investigation was conducted at Crop Research Centre-1, ITM University, Sithouli Campus, Gwalior, Madhya Pradesh, India (coordinates 26.15°N latitude, 78.18°E longitude, elevation 191 m above mean sea level) during the Kharif season of 2025-2026. The location falls within the Gird agroclimatic zone of Madhya Pradesh. The region experiences a semi-arid climate with pre-monsoon temperatures ranging from 35-42°C in June, monsoon onset in July with well-distributed rainfall averaging 65-80 mm per week, and post-monsoon period with declining rainfall from September onwards. The soil at the experimental site is classified as loamy with good drainage characteristics, having a pH of 7.2, organic carbon content of 0.68%, and moderate fertility status. A total of thirteen mungbean genotypes were evaluated in the present study. The experimental design employed was a Randomized Block Design (RBD) with three replications. Each genotype was represented by a single plot of dimensions 1.8 m × 1.5 m (2.70 m²), with a total net experimental area of 5.5 × 54 = 297.0 m². The spacing between rows and plants was 30 cm × 10 cm respectively, following the recommended agronomic practices for mungbean cultivation. Thirteen quantitative traits were recorded on five randomly selected competitive plants from each genotype in each replication at appropriate growth stages: Days to 50% Flowering (DFF) - number of days from sowing until 50% of plants had initiated flowering; Days to Maturity (DM) - number of days from sowing until 90% of pods had turned brown and dried; Plant Height (PH) - height in centimeters from ground level to the tip of the main stem at maturity; Number of Primary Branches Per Plant (PB) - total number of primary branches on the main stem; Number of Secondary Branches Per Plant (SB) - total number of secondary branches on primary branches; Number of Clusters Per Plant (CPP) - total number of flower clusters developed on the plant; Number of Pods Per Cluster (NPPC) - average number of mature pods in a cluster; Number of Pods Per Plant (NPPP) - total number of fully mature pods; Pod Length (PL) - length in centimeters of fully mature pods, averaged from 10 pods per plant; Number of Seeds Per Pod (NSPod) - average number of fully formed seeds per pod; Number of Seeds Per Plant (NSPP) - total number of mature seeds per plant; 100-Seed Weight (HSW) -

weight in grams of 1000 randomly selected seeds; Seed Yield Per Plant (SYPP) - total seed yield of a plant in grams at harvest. Statistical Analysis involved in this research includes, Analysis of variance (ANOVA) was conducted according to Panse and Sukhatme (1954) to test the significance of differences among genotypes. Genetic parameters including phenotypic variance, genotypic variance, heritability in broad sense, genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and genetic advance (GA) as percentage of mean were calculated using standard formulae. Simple correlation coefficients were computed between pairs of traits using the formula of Miller *et al.* (1958). Path coefficients were calculated following the procedure of Wright (1921) and Dewey and Lu (1959), with seed yield per plant as the dependent variable and remaining traits as independent variables.

Results and Discussion

Analysis of Variance and Genetic Parameters

Analysis of variance (Table 1) showed significant differences between the different genotypes for all the thirteen traits studied, which suggests that there is significant genetic variation among the germplasm evaluated of mungbean. These substantial differences illustrate that the genetic makeup of the different genotypes is different with respect to different agronomic and yield-determining traits and give a good basis for selection and breeding. The high F-values recorded for most of the traits highlight the genetic diversity of the germplasm, and the efficiency of the experimental design used to reveal genetic variation.

The heritability among were very high, indicating that environmental influences are relatively small in

determining the expression of these traits, so selection for these traits can be made with confidence across environments based on the observable phenotype. Genetic Coefficient of Variation (GCV) values were from 9.03% (DFF) to 25.18% (NSPP) showing moderate to high genetic diversity for most traits. There was a significant genetic variation for number of seeds per plant (NSPP) (25.18%), number of pods per plant (NPPP) (23.7%) and plant height (PH) (23.72%). These qualities having high GCV values provide good choice for genetic improvement by selection. GAM (exceeding 20%) was extremely high for number of pods per plant (20.68%), number of seeds per plant (21.65%), plant height (48.63%), number of primary branches (47.58%), number of secondary branches (23.15%) and number of clusters per plant (36.02%), which would be suitable for selection in breeding programs. The high heritability of reproductive traits (NPPP, NPPC, NSPP) and morphological traits (PH, PB), along with their high genetic advances, suggest that these characters are well suited for selection in early generations and are highly additive genetically controlled. These results corroborate the recent reports of high heritability and genetic advance for some of the pod and seed parameters reported by Gogoi *et al.* (2024) and Gayacharan *et al.* (2020) in the mungbean germplasm. The extremely high heritability values (>94%) observed for all traits indicate that these characters are predominantly under genetic control with minimal environmental influence, making them ideal targets for selection. These high heritability estimates are consistent with findings reported by Gogoi *et al.* (2024), Gayacharan *et al.* (2020), and Rohilla *et al.* (2022).

Table 1 : Genetic Parameters for Thirteen Quantitative Traits in Mungbean Genotypes

Trait	Mean	GCV (%)	PCV (%)	h ² (%)	GA	GAM(%)
DFF	44.63	9.03	9.48	90.76	7.92	17.75
DM	72.132	21.81	22.01	98.24	32.172	44.6
PH	62.046	23.72	23.88	98.73	30.174	48.63
PB	1.687	23.17	23.28	99.08	29.803	47.58
SB	4.947	11.52	11.83	94.81	18.145	23.15
CPP	6.301	17.67	17.89	97.62	28.27	36.02
NPPC	2.88	19.73	19.88	98.48	12.163	40.38
NPPP	16.647	23.7	23.81	99.1	8.103	20.68
PL	7.671	10.85	11.12	95.21	17.675	21.84
NSPod	10.76	11.55	12.06	89.95	11.59	14.78
NSPP	179.227	25.18	25.32	98.88	24.568	21.65
HSW	4.231	20.97	21.17	98.14	21.813	22.86
SYPP	6.819	15.43	17.2	98.18	12.56	24.32

DFF = Days to 50% Flowering; DM = Days to Maturity; PH = Plant Height (cm); PB = Number of Primary Branches Per Plant; SB = Number of Secondary Branches Per Plant; CPP = Number of Clusters Per Plant; NPPC = Number of Pods Per Cluster; NPPP = Number of Pods Per Plant; PL = Pod Length (cm); NSPod = Number of Seeds Per Pod; NSPP = Number of Seeds Per Plant; HSW = 100-Seed Weight (g); SYPP = Seed Yield Per Plant (g); GCV = Genetic Coefficient of Variation; PCV = Phenotypic Coefficient of Variation; h² = Heritability in broad sense; GA = Genetic Advance; GAM = Genetic Advance as percentage of mean

Correlation Coefficient Analysis

Significant correlations were found between the 13 traits assessed in this study and of particular interest in this regard are the relationships that influence seed yield determination (Table 2). The number of pods per plant (NPPP, $r = 0.757^{**}$) and seeds per plant (NSPP, $r = 0.832^{**}$) showed the highest positive correlation with SYPP, both at 1% probability level, which were highly reliable and desirable for plant selection. The important positive correlations were highly significant with the number of pods per plant ($r = 0.971^{**}$), number of clusters per plant ($r = 0.689^{**}$) and number of seeds per pod ($r = 0.643^{**}$), of which the first was the highest. This means that the more seeds per genotype that are produced, and the more pods that are produced, the greater the number of seeds per plant. The significant correlation between number of pods per plant and number of seeds per plant is very high (0.971^{**}) and this is a logical relationship as the more pods that are produced, the more seeds will be produced. Pod length also had significant positive correlations with most reproductive traits, such as number of clusters per plant ($r = 0.618^{**}$), number of pods per plant ($r = 0.773^{**}$), and number of seeds per pod ($r = 0.578^{**}$), suggesting that a larger pod is

correlated with overall greater reproductive development.

Plant height showed moderate positive correlations with most reproductive traits, including number of clusters per plant ($r = 0.465^{**}$), number of pods per cluster ($r = 0.453^{**}$), and number of seeds per pod ($r = 0.281$), indicating that taller plants tend to produce more abundant reproductive structures. Other negative or not very strong correlations were noted too. Seed yield had a weak positive correlation ($r = 0.293$, not significant) with Days to 50% flowering, suggesting that there is not a direct correlation between flowering time and final yield. Likewise, days to maturity and number of secondary branches were also found to be correlated with yield but not strongly ($r = 0.112$ ns and $r = 0.421$ ns, respectively). These results indicate that reproductive traits are more important than the other traits for direct selection than days to maturity and number of secondary branches. The present correlation values were similar to the earlier findings of Mishra *et al.* (2023) and Gogoi *et al.* (2024) who also obtained good positive correlation between seed yield and reproductive component traits of mungbean.

Trait	DF	DM	PH	PB	SB	CPP	NPPC	NPPP	PL	NSPPod	NSPP	HSW	SYPP
DF	1.000 ns	0.876 **	0.640 **	0.536 **	0.815 **	0.552 **	0.489 **	0.408 *	0.758 **	0.783 **	0.368 *	0.553 **	0.293 ns
DM	0.876 **	1.000 ns	0.522 **	0.434 *	0.641 **	0.383 *	0.268 ns	0.194 ns	0.549 **	0.550 **	0.162 ns	0.412 *	0.112 ns
PH	0.640 **	0.522 **	1.000 **	0.323 ns	0.591 **	0.330 ns	0.453 *	0.340 ns	0.380 *	0.481 **	0.281 ns	-0.072 ns	-0.037 ns
PB	0.536 **	0.434 *	0.323 ns	1.000 **	0.631 **	0.627 **	0.412 *	0.431 *	0.457 *	0.539 **	0.398 *	0.360 *	0.270 ns
SB	0.815 **	0.641 **	0.591 **	0.631 **	1.000 **	0.644 **	0.496 **	0.524 **	0.679 **	0.811 **	0.527 **	0.559 **	0.421 *
CPP	0.552 **	0.383 *	0.330 ns	0.627 **	0.644 **	1.000 **	0.618 **	0.813 **	0.465 **	0.689 **	0.803 **	0.458 **	0.660 **
NPPC	0.489 **	0.268 ns	0.453 *	0.412 *	0.496 **	0.618 **	1.000 **	0.773 **	0.578 **	0.609 **	0.730 **	0.368 *	0.634 **
NPPP	0.408 *	0.194 ns	0.340 ns	0.431 *	0.524 **	0.813 **	0.773 **	1.000 **	0.365 *	0.573 **	0.971 **	0.331 ns	0.757 **
PL	0.758 **	0.549 **	0.380 *	0.457 *	0.679 **	0.465 **	0.578 **	0.365 *	1.000 **	0.822 **	0.367 *	0.757 **	0.464 **
NSPPod	0.783 **	0.550 **	0.481 **	0.539 **	0.811 **	0.689 **	0.609 **	0.573 **	0.822 **	1.000 **	0.643 **	0.722 **	0.629 **
NSPP	0.368 *	0.162 ns	0.281 ns	0.398 *	0.527 **	0.803 **	0.730 **	0.971 **	0.367 *	0.643 **	1.000 **	0.390 *	0.832 **
HSW	0.553 **	0.412 *	-0.072 ns	0.360 *	0.559 **	0.458 **	0.368 *	0.331 ns	0.757 **	0.722 **	0.390 *	1.000 **	0.681 **
SYPP	0.293 ns	0.112 ns	-0.037 ns	0.270 ns	0.421 ns	0.660 **	0.634 **	0.757 **	0.464 **	0.629 **	0.832 **	0.681 **	1.000 **

Fig. 1 : Correlation coefficient heatmap over 13 traits of mungbean

Path Coefficient Analysis

The partition of the correlation coefficients to direct and indirect effects was carried out using path coefficient analysis, which offered detailed answers with the mechanism of how different traits affect seed yield. The analysis uncovered key information on the direct pathways connecting genetics to yield as well as the indirect pathways connecting the genetic pathways to yield.

Genotypic Path Coefficient Analysis

Genotypic Path Coefficient Analysis Direct genotypic effect of all the traits on seed yield per plant varied from very small to very large. The genotypic effect on seed yield was largest for the number of seeds per plant (NSPP) with a value of 1.0176**. Thus, this is the most important genetic factor influencing seed yield. This is an exceptionally large direct effect making number of seeds per plant the most important of all the genetic targets for yield improvement in mungbean breeding programs. The second largest direct effect on seed yield was observed for 100-seed weight (HSW) with a coefficient of 0.5608**, signifying that seed size is an important direct contributor to final seed yield through selection. This positive direct effect shows that larger seeds (when all factors are equal) significantly increase seed yields. The number of seeds per pod (NSPod) had a direct effect of 0.8860** which is highly significant for the direct influence on yield. The three traits with the

largest direct effects (NSPP, HSW, NSPod) should be used as major selection traits, if breeding for yield improvement is the goal. Plant height (PH) had a direct effect of -0.1180, a negative coefficient indicating that taller plants do not directly contribute to yield, and may even have a slight negative relationship. The other reproductive structure traits, number of clusters per plant (CPP) and number of pods per cluster (NPPC) have moderate direct effects on yield, of 0.0729** and 0.2341**, respectively, showing that the other direct reproductive structure contributions to yield were negative. All other traits had negative direct impacts on seed yield, the majority of which were statistically significant, such as days to flowering (DFF, -0.0953**), days to maturity (DM, -0.0154 ns), number of primary branches (PB, -0.1078**), number of secondary branches (SB, -0.0424 ns), number of pods per plant (NPPP, -0.3858**), and pod length (PL, -0.0808**). These negative direct effects suggest that in absence of the effects of other characters, these characters might be antagonistic with seed yield and could thus represent genetic trade-offs or developmental trade-offs in the plant. The magnitude of this direct effect is substantially larger than any other trait, indicating that it is far more important to increase the absolute number of seeds produced per plant than to focus on other characters. This finding aligns with research by Mishra *et al.* (2023) and Gogoi *et al.* (2024).

Table 2 : Genotypic Path Coefficients: Direct Effect and Indirect Effects Through All Traits

Traits	Direct Effect (P)	DFF	DM	PH	PB	SB	CPP	NPPC	NPPP	PL	NSPod	NSPP	HSW	Sig.
DFF	-0.0953	—	-0.0144	-0.0094	-0.0870	-0.0398	0.0610	0.1886	-0.2914	-0.0745	-0.0895	0.7443	0.4614	**
DM	-0.0154	-0.0892	—	-0.0912	-0.0793	-0.0361	0.0535	0.1579	-0.2399	-0.0659	-0.0786	0.6084	0.4115	ns
PH	-0.1180	-0.0803	-0.0119	—	-0.0728	-0.0349	0.0511	0.1754	-0.2629	-0.0599	-0.0753	0.6568	0.2819	**
PB	-0.1078	-0.0769	-0.0113	-0.0797	—	-0.0357	0.0608	0.1716	-0.2806	-0.0626	-0.0777	0.7174	0.3951	**
SB	-0.0424	-0.0894	-0.0131	-0.0971	-0.0908	—	0.0632	0.1883	-0.3077	-0.0722	-0.0899	0.8053	0.4607	ns
CPP	0.0729	-0.0797	-0.0113	-0.0827	-0.0899	-0.0368	—	0.1964	-0.3521	-0.0649	-0.0848	0.9201	0.4309	**
NPPC	0.2341	-0.0768	-0.0104	-0.0884	-0.0790	-0.0341	0.0612	—	-0.3449	-0.0675	-0.0815	0.8860	0.4052	**
NPPP	-0.3858	-0.0720	-0.0095	-0.0804	-0.0784	-0.0338	0.0665	0.2093	—	-0.0595	-0.0786	1.0011	0.3863	**
PL	-0.0808	-0.0879	-0.0125	-0.0875	-0.0835	-0.0379	0.0585	0.1956	-0.2841	—	-0.0905	0.7418	0.5030	**
NSPod	-0.0959	-0.0889	-0.0126	-0.0925	-0.0873	-0.0398	0.0645	0.1988	-0.3161	-0.0762	—	0.8531	0.4961	**
NSPP	1.0176	-0.0697	-0.0092	-0.0761	-0.0760	-0.0336	0.0659	0.2038	-0.3796	-0.0589	-0.0804	—	0.3977	**
HSW	0.5608	-0.0784	-0.0113	-0.0593	-0.0760	-0.0349	0.0560	0.1691	-0.2658	-0.0725	-0.0849	0.7216	—	**

** = Significant at 1% level of probability; ns = not significant. Direct effects shown in first numerical column; indirect effects shown in columns corresponding to each trait. The rightmost column shows significance of total correlation with SYPP.

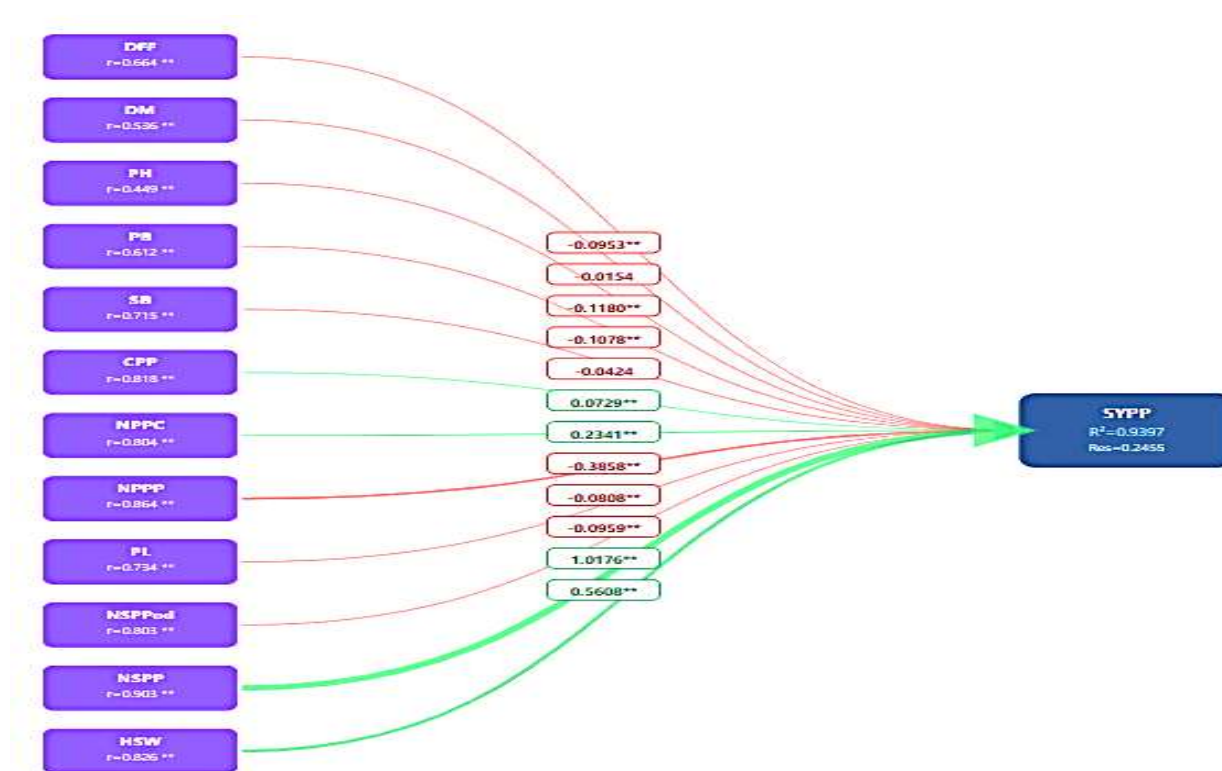


Fig. 2: Path diagram for direct effect

Conclusion

The present investigation on genetic variability, character association, and path coefficient analysis in mungbean germplasm has provided comprehensive insights into the genetic control of yield-determining traits and has important implications for breeding strategy development. The concluded the substantial genetic variability exists in the thirteen mungbean genotypes evaluated, with all traits showing highly significant differences. Number of seeds per plant is established as the paramount genetic determinant of seed yield with a direct genotypic effect of 1.0176, making this the primary target for selection in all mungbean breeding programs. 100-seed weight (0.5608) and number of seeds per pod (0.8860) are identified as secondary selection targets with substantial direct effects on yield. Significant positive phenotypic correlations between seed yield and number of seeds per plant (0.832), 100-seed weight (0.681) and number of pods per plant (0.757) provide field-reliable selection criteria that breeding programs.

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