RESEARCH ARTICLE Legume Research- An International Journal, Volume 49 Issue 2: 228-234 (February 2026)

Genetic Variability, Correlation and Path Coefficient Analysis of Common Bean (*Phaseolus vulgaris* L.) Genotypes in the Priobia Steppe, Siberia

Nguyen Nam Thanh[1], Galeev Rinat Raifovich[2], Oksana Valerievna Parkina[2]
Zlata Valerievna Andreeva[2], Bui Manh Hung[3]

10.18805/LRF-904

ABSTRACT

Background: Common bean (*Phaseolus vulgaris* L.) is an important leguminous vegetable crop but the lack of high yielding and stable varieties is the major constraint. Exploring genetic variability is essential for crop improvement programs. Considering this, the present study focused on assessing genetic variability and associations between yield and its contributing traits to enhance production efficiency.

Methods: A two year experiment was carried out at the experimental farm of the Novosibirsk State Agrarian University during the cropping season of 2023 and 2024 to find out the genetic variability parameters, path coefficient and correlation studies in twenty six common bean genotypes.

Result: The results revealed high variability among the tested genotypes. The values of phenotypic coefficient of variation (PCV) were greater as compared to the genotypic coefficient of variation (GCV) for all the traits. High heritability along with GAM% (>20%) was observed for number of nodes per stem (NNS), number of pods per plant (NPP), number of seeds per pod (NSP), seed yield per plant (SYP), hundred seed weight (HSW) and pod width (PL). Seed yield per plant (SYP) had positive genotypic and phenotypic correlation with DF (r_g = 0.34 and r_p = 0.34), NPP (r_g = 0.64 and r_p = 0.75), HSW (r_g = 0.62 and r_p = 0.7) and PL (r_g = 0.35 and r_p = 0.4). Positive direct effect on seed yield per plant (SYP) was exhibited by traits *viz*., number of pods per plant (NPP), hundred seed weight (HSW) and days to 50% flowering (DF) in path coefficient analysis.

Key words: Correlation, Genetic variability, Path analysis, Yield.

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is one of the most important legume crops worldwide, playing a vital role in human nutrition and food security due to its high protein content and ability to fix atmospheric nitrogen in the soil (Broughton, 2003; Gepts, Aragao, Baros and Brondani, 2008). It is a diploid 2n = 22 (Broughton, 2003) and a predominantly self-pollinating crop with a low frequency of crossing (Burle *et al*., 2011). It has two distinct gene pools, namely the Mesoamerican and Andean gene pools (Musango *et al*., 2016). The Andean gene pool genotypes are uniformly large-seeded (>40 g per 100 seeds), whereas the Middle American ones are characterized as small-seeded (< 25 g) or medium-seeded (25-40 g) (Singh *et al*., 1991). Common bean is an extremely diverse crop in terms of cultivation methods, uses, the range of environments to which they have been adapted and morphological variability (Antonio *et al*., 2025; Basavaraja *et al*., 2021). *P. vulgaris* exhibits wide adaptability and is cultivated across diverse agro-ecological zones, ranging from tropical to temperate regions (Blair *et al*., 2010). Genetic diversity in common bean genotypes is a key factor determining the potential for improving yield and yield related traits for bean genotypes (Kwak and Gepts, 2009; Mamidi *et al*., 2013; Singh, 1999).

[1]Institue of Agriculture and Resources, Vinh University, 182 Le Duan Street, Vinh City, Nghean-460000, Vietnam.
[2]Institute of Fundamental and Applied Agrobiotechnologies, Novosibirsk State Agrarian University, 160 Dobrolyubov, Novosibirsk 630039, Russia.
[3]Faculty of Forestry, Vietnam National University of Forestry, Xuan Mai, Chuong My, Hanoi 100000, Vietnam.

Corresponding Author: Nguyen Nam Thanh, Institue of Agriculture and Resources, Vinh University, 182 Le Duan Street, Vinh City, Nghean-460000, Vietnam.
Email: thanhnn@vinhuni.edu.vn
ORCID: 0009-0006-7929-1016

How to cite this article: Thanh, N.N., Raifovich, G.R., Parkina, O.V., Andreeva, Z.V. and Hung, B.M. (2026). Genetic Variability, Correlation and Path Coefficient Analysis of Common Bean (*Phaseolus vulgaris* L.) Genotypes in the Priobia Steppe, Siberia. *Legume Research*. **49(2):** 228-234. doi: 10.18805/LRF-904.

Submitted: 18-09-2025 **Accepted:** 02-11-2025 **Online:** 08-11-2025

Analysis of genetic variation is essential for understanding the basic genetics of common bean (Zargar *et al.,* 2014). It would be useful for determining the morphological variation among the gene pool (Basavaraja *et al*., 2021), thereby supporting the selection of appropriate

genotypes for breeding programs (Kwak and Gepts, 2009). However, the number of studies on genetic variability and agromorphological traits of common bean genotypes in specific climatic regions such as Siberia remains limited. The Priobia steppe region of Siberia is characterized by a harsh climate with a short growing season and low temperatures, requiring common bean genotypes to possess special adaptive traits to ensure productivity (Ivanov Smolenskaya, 2017). Therefore, evaluation of genetic variation and morphological traits of local common bean genotypes in this region is essential for developing cultivars adapted to these specific environmental conditions. Therefore, this study aims to: (i) assess the genetic variability, heritability and genetic advance of key agronomic traits of common bean under these conditions; (ii) evaluate phenotypic and genotypic correlations among traits; and (iii) apply path analysis to clarify the direct and indirect effects of traits on grain yield. This study aimed to estimate the genetic variability and association of quantitative traits among genotypes.

MATERIALS AND METHODS

Treatments and experimental design

The present investigation involving 26 common bean genotypes (Table 1) was sown from May to September at the experimental farm of the Novosibirsk State Agrarian University over two seasons (2023 and 2024). The soil in the experimental field is gray forest heavy loam. It presents the following physical, chemical features: humus content 4.5%, mobile phosphorus 9.8-2.8 mg/100 g, mobile potassium 6.2-6.4 mg/100 g, nitrate nitrogen 6-10 mg/kg and ammonia nitrogen 14.2-15.9 mg/kg. The sum of absorbed bases 30.8-52.0 mg-eq. per 100 g of soil, reaction pH 6.0-6.5 (Yakubenko and Parkina, 2019). The experiment was conducted under rainfed conditions, without irrigation or fertilization throughout the growing season. Weather conditions varied greatly during the different growing seasons. During 2023, the weather was rather dry compared to the long-term average, with low average precipitation (38 to 47 mm) and average temperatures ranging from 12 to 24°C, whereas 2024 was wetter (66 mm to 113 mm) and average temperatures ranging from 10 to 22°C. During the experiment, the average temperature tended to gradually increase from May to July and gradually decrease from August to September (Fig 1). The experiment was conducted using a randomized block design with three replications. The experimental field was 80 m in length and 2 m in width. Plots were 200 cm in length, 70 cm in width and 70 cm apart. Each genotype was sown in three rows of 200 cm long, with an inter-plant spacing of 6 cm and inter-row spacing of 70 cm. Thirdty five seeds were planted in each row.

Data collection and meaasurements

Plant parameters recorded were days to 50% flowering (DF), days to maturity (PM), plant height (PH), number of nodes per stem (NNS), number of pods per plant (NPP), pod length (PL), pod width (PW), number of seeds per pod (NSP), grain yield per plant (SYP) and hundred seed weight (HSW) was recorded on five plants of each genotype which were chosen randomly, with border plants excluded. Pest and disease monitoring was conducted throughout the growing season. Weeds were removed manually and plants showing symptoms of pest or disease infestation were excluded from further measurements.

The average mean for each trait over three replications was computed for each genotype and analysed statistically to determine analysis of variance (ANOVA) was performed using IRRISTAT software version 5.0 (IRRI). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated using the approach given by Burton (1952).

$$PCV\ (\%) = \frac{\sqrt{\delta^2_p}}{x} \quad ...(1)$$

$$GCV\ (\%) = \frac{\sqrt{\delta^2_g}}{x} \quad ...(2)$$

Where
$\sigma^2 g$ = Genotypic variance.
$\sigma^2 p$ = Phenotypic variance.
x = Sample mean.

Genetic advance as per cent of mean (GAM%) were calculated using the formula given by Johnson, Robinson and Comstock (1955).

$$GAM\ (\%) = \frac{K * \delta p * H}{x} \times 100 \quad ...(3)$$

Where
K = 2.06 at 5% selection intensity.
H = Heritability.
δp = Phenotypic standard deviation.
x = Sample mean.

Broad sense heritability (H^2) was assessed as per the procedure given by Falconer (1989).

$$H^2 = \frac{\delta^2_g}{\delta^2_p} \quad ...(4)$$

Genotypic (r_g) and phenotypic correlation coefficient (r_p) were computed using procedure recommended by Miller *et al*. (1983). Path coefficient analysis was done according to Dewey and Lu (1959). Standard path coefficients which are the standardized partial regression coefficients were obtained using statistical software packages OPSTAT (Pal *et al*., 2017).

RESULTS AND DISCUSSION

Genetic variation of common beans

Analysis of variance (ANOVA) showed significant differences between genotypes for all traits under investigation (Table 2). This variation in genotypes may be a result of genotypic diversity, environmental effect and their interaction

(Sonali *et al*., 2025). Estimates of heritability and genetic advances are important preliminary steps in the breeding program as they provide information needed in designing the effective breeding program and the relative practicability of selection (Sadeghi *et al*., 2011). The results indicated that the phenotypic coefficient of variability (PCV) were higher than the genotypic coefficient of variability (GCV) for all the traits (Basavaraja *et al*., 2021; Madakbas and Ergin, 2011), which reflect the influence of environment on the expression of all traits.

Table 1: Origin of the common bean genotypes.

ID	Name	Site of origin	Type
1	Ruby	VNIIZBK	dwarf
2	Sunny	SibNIISR	dwarf
3	Brunot	Italy	dwarf
4	Nurse	SibNIISR	dwarf
5	Bichanka	KRIA	dwarf
6	Nika	SibNIISR	dwarf
7	Bomba	Ukraine	dwarf
8	Darina	SibNIISR	dwarf
9	Canario	Peru	dwarf
10	Viola	SibNIISR	dwarf
11	Oran	VNIIZBK	dwarf
12	Yantarnaya	VNIISSOK	dwarf
13	Mukhranula	Georgia	dwarf
14	Sunray	Canada	dwarf
15	Golden	VIPGR	dwarf
16	Elizabeth	VIPGR	dwarf
17	Nerusa	VNIIZBK	dwarf
18	Secunda	South Africa	dwarf
19	Katia	SibNIISR	dwarf
20	Maxi	France	dwarf
21	Vernoorl	SibNIISR	dwarf
22	Daria	VNIISSOK	dwarf
23	Stringless	USA	dwarf
24	Unidor	Holland	dwarf
25	Sinenikov	VIPGR	dwarf
26	Paulista	Brazil	dwarf

VNIIZBK - All-Russian research institute of grain legumes, SibNIISR - Siberian research institute of plant growing and breeding, KRIA - Kuban research and design technological institute of agriculture named after P.P. Lukyanenko, VNIISSOK - All-Russian research institute of vegetable crops breeding and seed production, VIPGR- All-Russian - All-Russian institute of plant genetic resources named after N.I. Vavilov.

According to Johnson *et al*. (1955), estimated genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are categorised as: low (<10%); medium (10-20%) and high (>20%). Both high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for NNS (27.19% and 27.74%), NPP (57.85% and 61.42%), SYP (22.32% and 27.03%), HSW (36.41% and 36.44%) and PL (21.98% and 22.09%). The remaining traits recorded moderate to low GCV estimates. The broad sense heritability is an important genetic parameter that reflects the relationship between genotype and phenotype of a trait. According to Dabholkar (1992), the broad sense heritability values are classified as high (>60%), medium (30-60%) and low (<30%). Except for DF and PH, which showed a moderate heritability (53.29% and 53.90%), all other traits exhibited high heritability. This result is consistent with previous studies, which showed that most traits of common bean possess high heritability values (Eyuel *et al*., 2022; Nigussie *et al*., 2020).

Genetic advance (GAM) serves as an important indicator for predicting the potential improvement of traits through selection, enabling breeders to identify and prioritize traits with the greatest potential for genetic gain. Genetic advance as a per cent of the mean ranged from 9.44% for PH to 112.25% for NPP (Table 3). This result indicated that selecting the top 5% of the genotypes could result in an advance of 9.44-112.25% over the respective population mean.

According to Johnson *et al*. (1955), the genetic advance values are classified as high (>20%), medium (10-20%) and low (<10%). High GAM values indicate additive gene effect, whereas low GAM values indicate non-additive gene effect (Singh and Narayanan, 1993). Except for DF, PM and PH, which showed low to moderate genetic advance, all other traits exhibited high genetic advance, ranging from 28.47 to 112.25%.

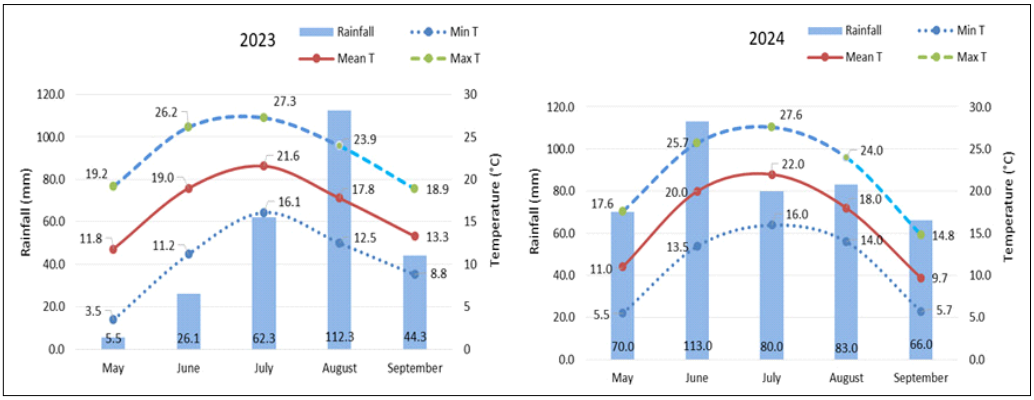


Fig 1: Climatic conditions during the two cultivation periods.

The results indicated relatively high broad-sense heritability and genetic advance for traits such as NNS, NPP, NSP, SYP, HSW and PL. These findings suggest that a considerable proportion of the phenotypic variation in these traits is genetically controlled, possibly with some contribution from additive effects and that selection could be effective for improving these traits. The present results concur with the findings of Simon and Mebede (2020).

The high heritability (68.07) associated with moderate genetic advance (11.94) for PM and PW. This suggests that both additive and non-additive gene effects contribute to the genetic control of these traits. The moderate broad-sense heritability (53.29) associated with low genetic advance (9.44) for DF. This indicates the predominance of non-additive gene effects in the genetic control of this trait. Out of all the traits under study, five traits *viz*., NNS, NPP, SYP, HSW and PL recorded maximum values for heritability (h^2), GCV and GAM% thus, depicting the effect of additive gene action on these traits and therefore, may be helpful for efficient selection.

Correlation coefficients

In plant genetics and breeding studies, correlated traits are important because of genetic causes of correlations

Table 2: Analysis of variance for traits in common bean.

Source of variation	df	DF	PM	PH	NNS	NPP	NSP	SYP	HSW	PL	PW
Treatment	25	69.63*	343.15*	244.54*	6.47*	1028.77*	3.49*	134.51*	2497.07*	58.13*	0.25*
Replication	2	290.12*	613.21*	1218.64*	0.07	208.77*	1.06*	556.85*	35.27*	0.33	0.02
Error	103	8.28	25.99	6.62	0.03	15.23	0.05	1.75	2.96	0.58	0.08

*Indicates significant differences at 5% level, DF - Days to 50% flowering, PM - Physiological maturity, PH - Plant height, NNS - Number of nodes per stem, NPP - Number of pods per plant, NSP - Number of seeds per pod, SYP - Seed yield per plant, HSW - Hundred seed weight, PL - Pod length, PW - Pod width.

Table 3: Genetic parameters of common bean genotypes.

Character	Range		Mean	SE	CV (%)	GCV (%)	PCV (%)	H^2 (%)	GAM (%)
	Minimum	Maximum							
DF	43.40	43.96	43.68	0.28	9.07	6.28	8.60	53.29	9.44
PM	85.21	91.16	88.19	2.97	4.77	7.02	8.51	68.07	11.94
PH	47.02	55.29	51.16	4.13	11.43	10.10	13.76	53.90	15.28
NNS	3.16	3.18	3.17	0.01	5.05	27.19	27.74	96.07	54.90
NPP	19.24	22.21	20.73	1.49	10.15	57.85	61.42	88.72	112.25
NSP	4.64	4.66	4.65	0.01	2.94	14.04	14.27	96.88	28.47
SYP	15.28	18.75	17.01	1.73	14.42	22.32	27.03	68.17	37.96
HSW	41.75	43.32	42.53	0.78	2.60	36.41	36.44	99.85	74.95
PL	11.74	11.82	11.78	0.04	4.51	21.98	22.09	99.00	45.05
PW	1.08	1.09	1.09	0.01	1.86	15.76	16.09	95.84	18.77

DF- Day to 50% flowering, PM- Physiological maturity, PH- Plant height, NNS- Number of nodes per stem, NPP- Number of pods per plant, NSP- Number of seeds per pod, SYP- Seed yield per plant, HSW- Hundred seed weight, PL- Pod length, PW- Pod width, PCV- Phenotypic coefficient of variation, GCV- Genotypic coefficient of variation, H^2- Broad sense heritability, GAM- Genetic advance.

Table 4: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for growth and yield components.

Character	DF	PM	PH	NNS	NPP	NSP	SYP	HSW	PL	PW
DF		-0.23	0.22	-0.51*	0.2	0.85*	0.34*	0.69*	0.67*	-0.22
PM	0.72*		-0.68*	-0.15	-0.54*	-0.19	-0.44*	-0.56*	-0.63*	-0.04
PH	0.01	0.36*		0.27	0.50*	0.38*	0.17	0.42*	0.61*	-0.33
NNS	0.26	-0.14	0.02		0.52*	-0.17	-0.02	-0.15	-0.29	0.14
NPP	0.53*	0.42*	0.42*	0.65*		0.17	0.64*	0.71*	0.47*	-0.08
NSP	0.62*	0.28	-0.26	-0.08	-0.26		0.07	0.51*	0.54*	-0.24
SYP	0.34*	0.39*	0.38*	0.24	0.75*	-0.41*		0.62*	0.35*	-0.33
HSW	0.65*	0.82*	0.35*	-0.04	0.63*	-0.05	0.70*		0.89*	-0.05
PL	0.41*	0.52*	0.34*	-0.23	0.28	0.02	0.40*	0.8*		-0.01
PW	-0.2	-0.29	-0.50*	0.17	-0.03	-0.29	-0.3	-0.05	0.05	

* indicates significant differences at 5% level.

Table 5: Partitioning of genotypic correlation (r_g) into direct and indirect effects for seed yield.

	DF	PM	PH	NNS	NPP	NSP	HSW	PL	PW	Direct effect	Pearson correlation	VIF
DF		-0.16	0.02	-0.11	0.16	0.19	0.1	0.01	-0.14	0.27	0.34*	1.44
PM	-0.45		-0.48	-0.19	0.22	0.52	-0.15	0.16	-0.03	-0.04	-0.44*	1.21
PH	0.14	-0.18		0.02	0.16	0.01	0.11	-0.13	-0.02	0.07	0.17	2.7
NNS	-0.51	-0.04	0.11		-0.11	0.47	-0.53	0.42	0.09	0.09	-0.02	1.41
NPP	0.14	-0.14	0.48	0.37		-0.45	0.49	-0.77	-0.05	0.58	0.64*	2.32
NSP	0.07	-0.05	0.06	0.01	0.03		0.06	0.05	-0.16	0.06	0.07	1.42
HSW	0.15	-0.15	-0.36	-0.13	0.09	0.01		0.09	-0.04	0.54	0.62*	2.54
PL	0.11	-0.16	0.09	-0.05	0.12	0.15	0.05		-0.01	0.04	0.35*	2.61
PW	-0.43	-0.01	-0.61	0.17	-0.08	0.67	-0.05	0.1		-0.09	-0.33	1.8

* indicates significant differences at 5% level, Residual effect = 0.151.

through pleiotropic action or developmental interactions of genes and changes can be brought in correlated traits either by natural or artificial selection (Belay *et al.*, 2024; Sharma, 1998). Crop improvement programs can be more effective through understanding the relationships between yield and its component traits. Indirect improvement of a target trait may occur through the enhancement of another trait if they are positively correlated (Remzeena and Anitha, 2021).

DF (r_g = 0.34), NPP (r_g = 0.64), NSP (r_g = 0.51), HSW (r_g = 0.62) and PL (r_g = 0.35) exhibited significant and positive genotypic association with grain yield where the highest genotypic correlation coefficient was recorded for NPP. This indicates that the genotypes with high number of pods per plant, number of seeds per pod, hundred seed weight, pod length and days to 50% flowering were producing higher grain yield. The results are in line with previous research, in which Sadeghi *et al*. (2011) reported highly significant correlations of seed yield with number of seeds per pod, number of pods per plant, days to flowering and hundred seed weight. Number of pods per plant showed a significant positive association with plant height (r_g = 0.5), number of nodes per stem (r_g = 0.52), hundred-seed weight (r_g = 0.71) and pod length (r_g = 0.47). Pod length with DF (r_g = 0.67), PH (r_g = 0.61), NPP (r_g = 0.47) and NSP (r_g = 0.54) had significant positive association.

Phenotypic correlation coefficients for agronomic traits ranged from -0.5 to 0.82 (Table 4). Seed yield per plant had significant positive phenotypic correlation with DF (r_p = 0.34), PM (r_p = 0.39), PH (r_p = 0.38), NPP (0.75), HSW (r_p = 0.7) and PL (r_p = 0.8). Number of pods per plant showed a significant positive association with DF (r_p = 0.53), PM (r_p = 0.42), PH (r_p = 0.42), NNS (r_p = 0.65) and HSW (r_p = 0.63). Pod length with DF (r_p = 0.41), PM (r_p = 0.52), PH (0.34) and HSW (r_p = 0.8) had significant positive association.

Path co-efficient analysis

Path co-efficient analysis is an efficient approach to separate correlation coefficients into direct and indirect component effects since it assesses the direct impact of one variable on the other (Sonali *et al.*, 2025). Correlation studies give a greater understanding of the causes and effects of relationships between different pairs of component traits and the main trait when paired with path coefficient analysis (Verma *et al.*, 2021). In our study, we considered seed yield per plant (SYP) as the dependent variable and the other traits as independent ones. Multicollinearity among independent traits was tested using the Variance Inflation Factor (VIF). All VIF values were below 5, indicating no multicollinearity problem among the independent variables in the path analysis model (Table 5).

The results revealed that NPP had maximum positive (0.58) and direct effect on SYP followed by HSW (0.54), DF (0.27), NNS (0.09), PH (0.07), NSP (0.06) and PL (0.04) suggesting that they are the major contributors to seed yield per plant. Daniel (2015) had reported that path coefficient at genotypic level showed that number of pods per plant had positive direct influence on grain yield.

NPP showed a significant positive correlation with SYP (r = 0.64) and had a direct effect coefficient of 0.58; this result indicates that the number of pods per plant directly influences seed yield of common bean genotypes. Similarly, HSW and DF showed significant positive correlations with SYP (r = 0.62 and r = 0.34) and had direct effect coefficients of 0.54 and 0.27, respectively. Therefore, seed yield per plant is directly influenced by hundred seed weight and days to 50% flowering.

Pod length showed a significant positive correlation with SYP (r = 0.35) but had a low direct effect coefficient (0.04) and it indirectly influenced seed yield per plant via DF (0.11), NPP (0.12) and NSP (0.15). Similarly, plant height influenced seed yield mainly through indirect effects via the traits DF (0.14), NPP (0.16) and HSW (0.11). The residual effect shows how much the explanatory variables represent the variability of the dependent variable (R. K. Singh and Chaudhary, 1985). The residual effect was 0.151, indicating that the independent traits accounted for 97.7% (R^2 = 0.977) of the total variation in seed yield, while a small proportion (2.3%) remained unexplained by the model.

CONCLUSION

This study analyzed the genetic variation and evaluated the correlations among quantitative traits related to yield of 26 common bean genotypes collected from the Priobia

steppe, Siberia, by estimation of genetic parameters and path coefficient analysis. The results revealed significant genetic variation among genotypes. The high broad-sense heritability and genetic advance observed for traits such as NNS, NPP, NSP, SYP, HSW and PL indicate that these traits are mainly controlled by additive gene effects, offering opportunities for effective selection and genetic improvement.

Seed yield per plant showed a significant positive correlation with DF (r_g = 0.34 and r_p = 0.34), NPP (r_g = 0.64 and r_p = 0.75), HSW (r_g = 0.62 and r_p = 0.70) and PL (r_g = 0.35 and r_p = 0.40). The number of pods per plant, 100-seed weight and days to flowering had a direct influence on seed yield per plant. Pod length and plant height influenced seed yield mainly through indirect effects via days to flowering, number of pods per plant, number of seeds per pod and 100-seed weight. These results may help enhance the effectiveness of conservation and improvement of common bean genetic resources in the Priobia steppe, Siberia.

ACKNOWLEDGEMENT

The authors sincerely thank the Ministry of Education and Training of Vietnam and the Ministry of Science and Higher Education of the Russian Federation for granting scholarships for postgraduate studies in the Russian Federation. The authors are also grateful to the Institute of Fundamental and Applied Agrobiotechnologies, Novosibirsk State Agrarian University, for their encouragement and support.

Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsor- ship influenced the design of the study, data collection, analysis, decision to publish, or preparation of the manuscript.

REFERENCES

Antonio, M., Maurizio, R., Monica, B. and Giovanni, P. (2025). Pheno-morphological, agronomic and genetic diversity in a common bean core collection from Calabria (Italy). *Italian Journal of Agronomy.* **20(2025):**100038. doi:10.1016/j.ijagro.2025.100038.

Basavaraja, T., Manjunatha, L., Rahul, C., Gurumurthy, S. and Singh, N.P. (2021). Assessment of genetic variability, diversity and trait correlation analysis in common bean (*Phaseolus vulgaris* L.) genotypes. *Legume Research.* **44(3):** 252-260. doi: 10.18805/LR-4208.

Belay, A., Wassu, M. and Dagnachew, L. (2024). Correlations and path coefficient analysis of grain yield and grain yield related traits in small seeded common bean geno types (*Phaseolus vulgaris* L.) at Goroand Gimir, Southeast Ethiopia. *Journal of Forestry and Natural Resources.* **3(2):** 12-22.

Blair, M.W., Díaz, L.M., Buendía, H.F. and Duque, M.C. (2010). Genetic diversity, seed size associations and population structure of a core collection of common beans (*Phaseolus vulgaris* L.). *Theoretical and Applied Genetics.* **119(6):** 955-972. doi: 10.1007/s00122-009-1097-5.

Broughton, W.J. (2003). Beans (*Phaseolus* Spp.) - Model food legumes. *Plant and Soild.* **252(1):** 55-128.

Burle, M.L., Fonseca, J.R., Peloso, M.J., Melo, L.C., Temple, S.R. and Gepts, P. (2011). Integrating phenotypic evaluations with a molecular diversity assessment of a Brazilian collection of common bean landraces. *Crop Science.* **51:** 2668-2680.

Burton, G.W. (1952). Quantitative Inheritance in Grasses. Paper Presented at the 6th International Grassland Congress.

Dabholkar, A.R. (1992). Elements of Biometrical Genetics. New Delhi, India: Concept Publishing Company.

Daniel, A. (2015). Trait associations in common bean genotypes grown under drought stress and field infestation by BSMbean fly. *The Crop Journal.* **3(4):** 305-316.

Dewey, J.R. and Lu, K.H. (1959). Correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal.* **51:** 515-518.

Eyuel, M., Garome, S., Sentayehu, A. and Birhanu, A. (2022). Genetic variability analysis and association of traits in common bean (*Phaseolus vulgaris* L.) landraces collected from Ethiopia at Jimma. *Advances in Agriculture.* **2022:** 4400711. doi:10.1155/2022/4400711.

Falconer, D.S. (1989). Introduction to Quantitative Genetics. Harlow, Essex, UK/New York: Longmans Green/John Wiley and Sons.

Gepts, P., Aragao, F.J.L., Baros, E. and Brondani, M.W. (2008). Genomics of Phasejlus beans, a major source of dietary protein and micronutrients in the tropics. *Springer New York*. 113-143.

Ivanov, I.G., Shvachkin, S.M. and Smolenskaya, N.E. (2017). Adaptability and productivity of bean (*Phaseolus vulgaris* L.) varieties in the south of Western Siberia. *Siberian Bulletin of Agricultural Science.* **47(2):** 33-38.

Johnson, H.W., Robinson, H.E. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal.* **47:** 314-318.

Kwak, M. and Gepts, P. (2009). Structure of genetic diversity in the two major gene pools of common bean (*Phaseolus vulgaris* L., Fabaceae). *Theoretical and Applied Genetics.* **118(5):** 979-992.

Madakbas, S.Y. and Ergin, M. (2011). Morphological and phenological characterization of Turkish bean (*Phaseolus vulgaris* L.) genotypes and their present variation states. *Afr. J. Agric. Res.* **1(6):** 6155-6166. doi:10.5897/AJAR11.1361.

Mamidi, S., Rossi, M., Annam, D. and Moghaddam, S.M. (2013). Demographic factors shaped diversity in the two gene pools of wild common bean *Phaseolus vulgaris* L. *Heredity.* **110(3):** 267-276.

Miller, J.D., Kang, M.S. and Tai, P.Y.P. (1983). Genetic and phenotypic path analyses and heritability in sugarcane. *Crop Science.* **23:** 643-647.

Musango, R., Kudzai, K., Vhungu, S. and Tibugar, H. (2016). Phenotypic characterization of common bean (*Phaseolus vulgaris* L.) accessions conserved at the genetic resources and biotechnology institute. *Bio. Env. Sci.* **8(6):** 26-36.

Nigussie, K., Frew, M. and Yigzaw, D. (2020). Genetic advancement and variability of released common bean (*Phaseolus vulgaris* L.) varieties from 1974-2009 GC in Ethiopia. *Advances in Agriculture.* **13(15):** 43-50.

Pal, S., Sharma, H. R., Das, A. and Pandav, A. K. (2017). Character association and path analysis for fruit yield and it's contributing traits in cucumber (*Cucumis sativus* L.). *Int. J. Agric. Environ. Biotech.* **10(2):** 163-170. doi:10. 5958/2230-732X.2017.00019.5.

Remzeena, A. and Anitha, P. (2021). Correlation and path coefficient analysis in cluster bean (*Cyamopsis tetragonoloba* L.) genotypes. *Agricultural Science Digest.* **44(5):** 898-901. doi: 10.18805/ag.D-5385.

Sadeghi, A., Cheghamirza, K. and Dorri, H.R. (2011). The study of morpho agronomic traits relationship in common bean (*Phaseolus vulgaris* L.). *Biharean Biologist.* **5(2):** 102-108.

Sharma, J.R. (1998). Statistical and Biometrical Techniques in Plant Breeding. New Delhi: New Age International (P) Limited.

Simon, Y., Gobeze, L. and Mebede, K.G. (2020). Performance evaluation of common bean (*Phaseolus vulgaris* L.) genotypes for yield and related traits at Areka, Southern Ethiopia. *Advances in Agriculture* (2020). 1-8. doi: 10. 1155/2020/1497530.

Singh, P. and Narayanan, S.S. (1993). Biometrical Techniques in Plant Breeding. New Delhi, India: Kalyani Publishers.

Singh, R.K. and Chaudhary, B.D. (1985). Biometrical Methods in Quantitative Analysis. New Delhi: Kalyani Publishers.

Singh, S.P. (1999). In Common Bean Improvement in the Twenty-First Century. S.P. Singh (Ed.), Springer. (pp. 1-24):

Singh, S.P., Gepts, P. and Debouck, D.G. (1991). Races of common bean (*Phaseolus vulgaris,* Fabaceae). *Economic Botany.* **45(3):** 379-396.

Sonali, S., Anil, B. and Samnotra, R.K. (2025). Genetic variability, correlation and path coefficient analysis in advanced matromorphic generations of garden Pea (*Pisum sativum* L.). *Legume Research.* **48(8):** 1274-1280. doi: 10.18805/ LR-5128.

Verma, A.K., Yadav, P.K. and Lai, B. (2021). Estimation of correlation and path coefficient for yield and yield attributing traits in vegetable pea (*Pisum sativum* L.). *International Journal of Current Microbiology and Applied Sciences.* **10:** 336-344.

Yakubenko, O.E. and Parkina, O.V. (2019). A new promising variety of beans of the siberian vegetable sekection nurse. *Bulletin of NSAU.* **1(54):** 42-47.

Zargar, S.M., Sharma, A., Sadhu, A., Agrawa, G.K. and Rakwal, R. (2014). Exploring genetic diversity in common bean from unexploited regions of Jammu and Kashmir-India. *Molecular Plant Breeding.* **5:** 5-9.