



original scientific paper
 Ratar. Povrt. 2026, 63(2): 69-78
 doi: 10.5937/ratpov63-60663
 Manuscript submitted: 5 August 2025
 Manuscript accepted: 18 February 2026
 Published online: 13 May 2026

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Agro-morphological traits and genetic diversity of common bean (*Phaseolus vulgaris* L.) genotypes from the Priobia steppe, Siberia

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Summary: Common bean (*Phaseolus vulgaris* L.) is an important legume crop with high nutritional value and is widely cultivated across diverse ecological zones. This study aimed to evaluate the genetic diversity based on morphological markers of 16 common bean accessions collected from the Priobia steppe, Siberia. The field experiment was conducted using a randomized complete block design (RCBD) with three replications during the 2023 and 2024 growing seasons at the National Agrarian University of Novosibirsk. Analysis of variance revealed significant differences ($p < 0.05$) among genotypes for most studied traits. A dendrogram based on genetic similarity coefficients ranging from 0.22 to 0.78 classified the genotypes into four distinct genetic groups, indicating high genetic diversity among the collected common bean accessions. Correlation analyses showed positive associations between seed yield and days to flowering ($r_g = 0.34$ and $r_p = 0.34$), number of pods per plant ($r_g = 0.64$ and $r_p = 0.75$) as well as hundred seed weight ($r_g = 0.62$ and $r_p = 0.7$), suggesting that selecting genotypes with higher mean values for these traits could enhance common bean yield. The findings provide a scientific basis for breeding programs and contribute to the conservation and effective utilization of common bean genetic resources within the Siberian agroecosystem.

Keywords: common bean, genetic diversity, germplasm, morphological markers, Siberia

Introduction

As a widely cultivated legume, the common bean (*Phaseolus vulgaris* L.) plays a crucial role in human nutrition and sustainable agriculture. Its high protein value and ability to fix atmospheric nitrogen make it essential for both human consumption and soil improvement (Broughton, 2003). *P. vulgaris* is primarily a self-pollinated species with only a low rate of cross-pollination (Burle et al., 2011). It is structured into two major gene pools: the Mesoamerican and the Andean. The Andean gene pool is typically associated with large-seeded genotypes, generally exceeding 40 g per 100 seeds, whereas the Mesoamerican gene pool includes genotypes with small to intermediate seed sizes, with seed weights ranging from less than 25 g to 40 g per 100 seeds (Singh, Gepts, & Debouck, 1991). The common bean shows substantial variation in cultivation, utilization, environmental adaptation, and

morphological traits ([Antonio, Maurizio, Monica, & Giovanni, 2025](#); [Basavaraja, Manjunatha, Rahul, Gurumurthy, & Singh, 2021](#)). The common bean is highly adaptable and cultivated across both tropical and temperate regions ([Blair, Díaz, Buendía, & Duque, 2010](#)). Genetic variation in common bean genotypes underpins improvements in productivity, biotic stress resistance, and adaptation to changing climates ([Kwak & Gepts, 2009](#); [Mamidi, Rossi, Annam, & Moghaddam, 2013](#); [Singh, 1999](#)). Genetic diversity analysis using morphological markers is essential for understanding the basic genetics of common bean ([Zargar, Sharma, Sadhu, Agrawa, & Rakwal, 2014](#)). It enables the assessment of morphological variation across gene pools and reveals patterns of genetic differentiation ([Basavaraja et al., 2021](#)), supporting the identification of suitable genotypes for breeding. ([Kwak & Gepts, 2009](#)). However, the amount of research on the genetic and agro-morphological variability of common bean in Siberian regions remains limited. The Priobias steppe, with its short growing season and low temperatures, demands genotypes with adaptive traits to sustain productivity ([Ivanov, Shvachkin, & Smolenskaya, 2017](#)). Therefore, assessing the genetic diversity and morphological traits of common bean in the Priobias steppe of Siberia is essential for developing cultivars adapted to local environmental conditions. This study was conducted to: (i) evaluate the variability of agromorphological traits of 16 common bean genotypes collected from Priobias steppe; (ii) analyze the genetic relationships among genotypes based on Euclidean distances combined with UPGMA clustering to determine similarity and dissimilarity levels; and (iii) apply multivariate analysis methods, including Principal Component Analysis (PCA) and GGE biplot, to classify and select superior genotypes.

Materials and Methods

Plant material

A collection of sixteen domestic common bean genotypes from the Priobias steppe, originating from the Federal Scientific Center of Legumes and Groat Crops (FSCLGC), the Krasnoyarsk Scientific Center of the Siberian Branch (KSCS), and All-Russian selection and genetic institutions (ARGI), were evaluated for both agronomic traits and performance as well as genetic diversity. The plant material adopted in this study is listed in Table 1.

Experimental design

The field experiments were carried out during the growing seasons 2023 and 2024 at the experimental farm of the Novosibirsk State Agrarian University, located in Siberia, Russia, (38°10' N, 15° 45' E, 232 m a.s.l.). 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 & Parkina, 2019](#)). The varieties were grown from May to August over two seasons in 2023 and 2024. The experiment was conducted using a randomized block design with three replications. The experimental field was 80 m in length and 3 m in width. Each plot included four rows 3 m long with 0.7 m distance between rows and 22 plants m⁻²; the two central rows constituted the assay area.

Morphological description

Phenological and morphological traits were measured and recorded according to the list of *Phaseolus vulgaris* descriptors published in 1982 by International Biodiversity Plant Genetic Resources ([IBPGR, 1982](#)). Days to flowering (DF) was recorded as the number of days from planting to 50% of the plants exhibit flowering per plot. Days to physiological maturity (PM) was recorded when 50% of plants in the plot lose green color of pod. Plant height (PH) obtained by measurement from ground level until the extreme plant. Number of nodes per stem (NS) and number of pods per plant (NP) obtained by the count of nodes per stem and the count of pods per plant with a random sample of the ten evaluated plants per plot. The number of seeds per pod (NSP) was obtained by counting the seeds in pods from a random sample of ten pods per plot. Seed length (SL) and seed width (SW) obtained with a ruler graduated, measuring with a random sample of ten seeds of the ten evaluated

plants per plot. Hundred seed weight (HSW) obtained by weighing of four samples of 100 seeds of each plot, with moisture content of 10%. Seed yield (SY) obtained by the ratio between the total weight of seeds in each plots and plant number, converted to hectares.

Table 1. Origin and pheno-morphological traits of the common bean genotypes

No	Name	Origin	Seed coat colour percentage
1	<i>Redvar</i>	FSCLGC	90% Cream 10% Red
2	<i>Sinenikov</i>	FSCLGC	100% White
3	<i>Varchin</i>	FSCLGC	90% Cream 10% Red
4	<i>Stringless</i>	FSCLGC	100% Light brown
5	<i>Canario</i>	FSCLGC	100% Light beige
6	<i>Oran</i>	FSCLGC	100% White
7	<i>Ruby</i>	FSCLGC	100% Pink
8	<i>Nerusa</i>	FSCLGC	100% White
9	<i>Bichanka</i>	KSCS	90 Cream 10% Black
10	<i>Mukbranula</i>	ARGI	100% Dark brown
11	<i>Golden</i>	ARGI	100% Light purple
12	<i>Bomba</i>	ARGI	50% Cream 50% Black
13	<i>Katia</i>	ARGI	90% Purple 10% Cream
14	<i>Vernoorl</i>	ARGI	100% Dark beige
15	<i>Brunot</i>	ARGI	90% Purple 10% Cream
16	<i>Larspot</i>	ARGI	50% White 50% Red

Note: *FSCLGC* Federal Scientific Center of Legumes and Groat Crops, *KSCS* Krasnoyarsk Scientific Center of the Siberian, *ARGI* All-Russian selection and genetic institutions

Statistical analysis

Analysis of variance (ANOVA) was performed using Microsoft Excel 2013, while Least Significant Difference (LSD) test at a significance level of $p < 0.05$ was carried out using IRRISTAT software version 5.0 (IRRI). The genetic distances among 16 common bean genotypes were estimated using the Euclidean distance, and hierarchical cluster analysis was performed using NTSYS software version 2.1. Principal Component Analysis (PCA) was used to classify 16 common bean genotypes based on agro-morphological traits ([Hotelling, 1933](#)). This analysis was performed using GGE biplot software version 4.1 ([Yan, Kang, Ma, Woods, & Cornelius, 2007](#)). Genotypic (r_g) and phenotypic correlation coefficient (r_p) were computed using procedure recommended by [Miller, Kang, and Tai \(1983\)](#).

Results

Variation of investigation traits

Evaluation of growth characteristics in common bean genotypes showed an average growth duration of 86 days, with *Ruby*, *Brunot*, *Bichanka*, *Bomba*, *Canario*, *Mukbranula*, *Golden*, *Katia*, *Vernoorl*, *Stringless* maturing earlier (81-85 days) and *Redvar*, *Varchin* later (97-98 days). In the present study, all genotypes exhibited a bush growth habit, resulting in relatively low plant heights, ranging from 42.34 to 59.76 cm (CV = 2.77%). The genotypes *Sinenikov*, *Bichanka*, and *Bomba* showed significantly greater plant height than the remaining genotypes.

As shown in Table 2, the average number of pods per plant among the genotypes was 18.24 (CV = 2.64%). The genotypes *Sinenikov* and *Nerusa* exhibited a significantly higher number of pods

per plant, ranging from 39.71 to 43.27. The hundred-seed weight of the genotypes ranged from 21.15 to 87.13 g, with most genotypes exhibiting hundred seed weight greater than 40 grams (62.5%). Our genotypes can be grouped into small (13 %; < 25 g 100 grains⁻¹), medium (25%; 25–40 g 100 grains⁻¹) and large seeds (69 %; > 40 g 100 grains⁻¹).

Yield is a critical parameter for evaluating the performance of the common bean genotypes. The average seed yield per plant was 17.83 g, with the genotypes *Redvar*, *Varchin*, *Larspot*, *Nerusa*, *Golden*, *Mukbranula*, *Canario Brunot*, and *Ruby* exhibiting significantly higher seed yields per plant compared to the other genotypes.

Table 2. Morphologic and agronomic traits of common bean genotypes

Genotypes	DF	PM	PH	NS	NP	NSP	SL	SW	SYP	HSW
<i>Ruby</i>	40.31 ^a	81.16 ^a	51.16 ^{a-d}	3.26 ^{a-c}	12.24 ^a	4.13 ^a	15.62 ^a	8.01 ^a	20.11 ^{abc}	50.56 ^{abc}
<i>Brunot</i>	41.62 ^{ab}	85.31 ^a	46.14 ^{ab}	3.38 ^{a-c}	10.51 ^a	4.56 ^a	14.70 ^a	9.30 ^a	17.43 ^{abc}	48.97 ^{abc}
<i>Bichanka</i>	39.81 ^a	82.43 ^a	59.27 ^{a-f}	2.8 ^{a-d}	14.11 ^a	5.21 ^{ab}	15.10 ^a	8.07 ^a	13.72 ^{ab}	48.43 ^{abc}
<i>Bomba</i>	38.76 ^a	82.14 ^a	58.93 ^{a-f}	3.77 ^{a-g}	20.76 ^{ab}	5.17 ^{ab}	15.43 ^a	6.60 ^a	15.66 ^{ab}	34.52 ^{ab}
<i>Canario</i>	41.84 ^{ab}	82.64 ^a	51.64 ^{a-d}	2.41 ^{abc}	14.28 ^a	4.75 ^{ab}	15.40 ^a	7.81 ^a	20.61 ^{abc}	39.66 ^{ab}
<i>Oran</i>	41.63 ^{ab}	86.67 ^{ab}	48.38 ^{abc}	3.24 ^{a-c}	29.17 ^{abc}	4.23 ^a	11.12 ^a	6.93 ^a	13.63 ^{ab}	26.50 ^a
<i>Mukbranula</i>	40.76 ^a	83.42 ^a	57.42 ^{a-e}	2.62 ^{a-d}	18.24 ^{ab}	6.04 ^{abc}	15.60 ^a	7.40 ^a	19.67 ^{abc}	46.74 ^{ab}
<i>Golden</i>	40.58 ^a	84.74 ^a	48.57 ^{abc}	3.96 ^{a-h}	17.56 ^{ab}	4.24 ^a	11.10 ^a	7.85 ^a	20.43 ^{abc}	43.74 ^{ab}
<i>Nerusa</i>	43.13 ^{ab}	89.81 ^{ab}	48.61 ^{abc}	5.31 ^{a-i}	39.71 ^{a-d}	5.26 ^{ab}	8.51 ^a	5.90 ^a	20.50 ^{abc}	21.15 ^a
<i>Katia</i>	40.51 ^a	82.34 ^a	42.34 ^a	2.58 ^{abc}	10.08 ^a	4.51 ^a	18.40 ^a	7.82 ^a	15.51 ^{ab}	44.12 ^{ab}
<i>Vernoorl</i>	42.67 ^{ab}	83.48 ^a	48.51 ^{abc}	2.17 ^{ab}	10.26 ^a	4.53 ^a	16.93 ^a	7.41 ^a	16.13 ^{ab}	46.63 ^{ab}
<i>Stringless</i>	42.31 ^{ab}	83.57 ^a	45.49 ^{ab}	1.45 ^a	7.18 ^a	5.07 ^{ab}	17.08 ^a	7.43 ^a	7.96 ^a	37.44 ^{ab}
<i>Redvar</i>	43.57 ^{ab}	98.11 ^{a-d}	52.13 ^{a-d}	3.98 ^{a-h}	11.34 ^a	4.76 ^{ab}	14.61 ^a	8.87 ^a	26.64 ^a	65.96 ^{a-d}
<i>Sinenikov</i>	44.91 ^{abc}	92.33 ^{abc}	59.76 ^{a-f}	4.06 ^{a-h}	43.27 ^{a-d}	6.03 ^{abc}	8.50 ^a	6.24 ^a	16.70 ^a	22.86 ^a
<i>Varchin</i>	45.38 ^{abc}	97.16 ^{a-d}	56.31 ^{a-e}	3.77 ^{a-g}	18.51 ^{ab}	6.08 ^{abc}	14.91 ^a	9.11 ^a	21.80 ^a	68.16 ^{a-d}
<i>Larspot</i>	43.18 ^b	91.24 ^{abc}	58.17 ^{a-e}	3.58 ^{a-f}	14.57 ^a	4.13 ^a	14.60 ^a	9.03 ^a	18.70 ^a	87.13 ^{a-c}
LSD _{0.05}	2.53	4.22	2.33	0.15	7.63	0.51	16.12	5.65	3.65	12.59
CV%	4.87	7.46	8.77	3.51	14.64	4.17	5.35	3.88	7.26	11.36

Note: *DF* day to flowering, *PM* day to physiological maturity, *PH* plant height (cm), *NS* number of nodes per stem, *NP* number of pods per plant, *NSP* number of seeds per pod, *SL* seed length (mm), *SW* seed width (mm), *SYP* seed yield per plant (g), *HSW* hundred seed weight (g). Means followed by a different letter(s) within a column differ significantly ($P < 0.05$) according to Duncan's LSD.

Genetic diversity based on morphological markers

A dendrogram constructed based on Euclidean distance using morpho-agronomic traits, including days to flowering (DF), days to physiological maturity (PM), plant height (PH), number of nodes per stem (NS), number of pods per plant (NP), seed length (SL), seed width (SW), hundred seed weight (HSW), and seed yield (SY), grouped the genotypes into four clusters at a similarity coefficient of 0.33 (Fig. 1).

Cluster I was composed of *Ruby*, *Brunot* and *Larspot*. These varieties had larger seed size but fewer seeds per pod and fewer pods per plant. The leaf, flower, pod, and seed colours of these genotypes were similar, but *Ruby* differed in the intensity of the leaf colour (Table 2). Cluster II was divided into sub-clusters IIA and IIB. Sub-cluster IIA was composed of *Bichanka* and *Bomba*. These varieties were associated with shorter growth periods, earlier flowering, greater plant height, longer pod and seed length, and similar seed coat color but with different color intensity. Sub-cluster IIB consisted of *Canario*, *Vernool*, *Stringless*, *Katia* and *Mukbranula*. This was the cluster with the largest genetic variation, with similarity coefficients ranging from 0.42 to 0.78, in which the *Vernool* and

Stringless were closely related genetically (0.78). These two varieties had many similar morphological traits, such as leaf, flower, and pod color; plant height; pod and seed size; as well as hundred seed weight (Table 2).

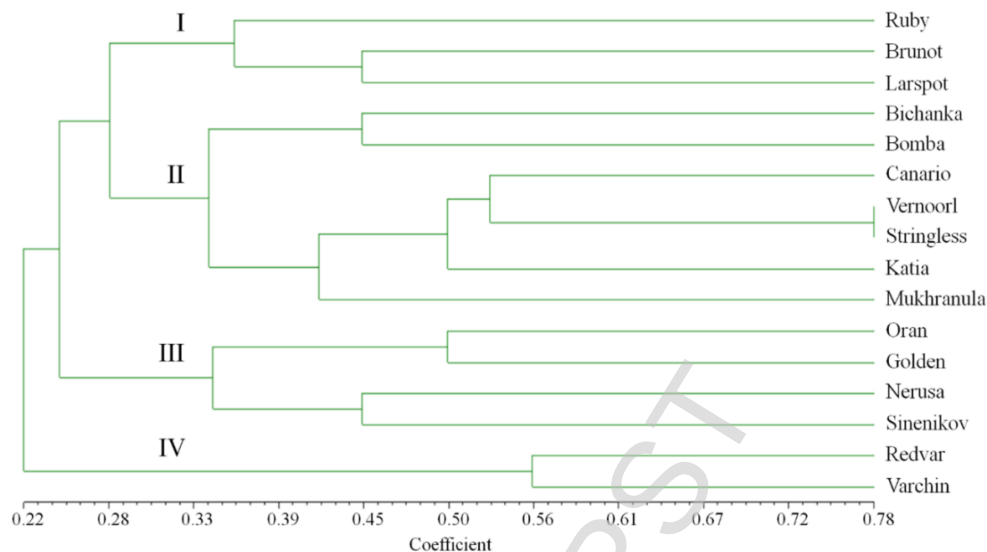


Figure 1. A Dendrogram of genetic relationships among 16 genotypes based on Euclidean distances and UPGMA cluster analysis

Cluster III consisted of *Oran*, *Golden*, *Nerusa* and *Sinenikov*. These genotypes were related to shorter pod and seed sizes, as well as lighter hundred seed weight (Table 2). Cluster IV included *Redvar* and *Varchin*. These varieties had larger pod and seed sizes, as well as greater hundred seed weight and higher seed yield (Table 2). This was the cluster with a relatively high similarity coefficient (0.56), while the similarity coefficient between this cluster and the other clusters was relatively low (0.22). Genotypes had a high level of genetic diversity, with genetic similarity coefficients ranging from 0.22 to 0.78.

Principal Component Analysis (PCA) was performed using ten morpho-agronomic traits, including days to flowering (DF), days to physiological maturity (PM), plant height (PH), number of nodes per stem (NS), number of pods per plant (NP), seed length (SL), seed width (SW), hundred seed weight (HSW), and seed yield (SY). The first two principal components, derived from these traits, explained approximately 48% of the total variability (Fig. 2). Biplot clustered the common bean genotypes with similar morphological traits into three different groups. In the upper part of the first and second quadrants, the varieties *Varchin*, *Redvar*, and *Larspot* were grouped closer together. Among them, the *Larspot* variety was more distinct from all the varieties in the first quadrant. These varieties in this group had fewer pods per plant but larger pod and seed sizes, as well as heavier seeds and higher yield. In the lower parts of the second and third quadrants, the varieties *Sinenikov*, *Nerusa*, and *Oran* were dispersed far apart. These varieties had similar seed coat and flower colors, as well as shorter pod and seed sizes, more pods per plant, and lighter hundred seed weight. The remaining varieties were grouped in the fourth quadrant and the adjacent region. In the upper part, *Bichanka*, *Brunot*, and *Ruby* were closely related. In the lower part, *Canario*, *Katia*, *Vernool*, and *Stringless* were closely related; however, the varieties *Mukhranula*, *Golden*, and *Bomba* were more distantly related (Fig. 2).

The principal component analysis revealed that the first two principal components explained a substantial proportion of the total variation among the studied morpho-agronomic traits. PC1 was mainly associated with structural and yield-related traits such as number of pods per plant (NP), number of nodes per stem (NS), days to flowering (DF), and days to physiological maturity (PM), while showing negative associations with seed size traits, particularly seed length (SL), seed width (SW), and hundred seed weight (HSW). This component therefore reflects a trade-off between yield components and seed size. In contrast, PC2 was primarily influenced by seed-related traits, including

hundred seed weight (HSW) and seed width (SW), together with days to physiological maturity (PM) and seed yield (SY), indicating that this component represents variation in seed size and maturity (Table 3).

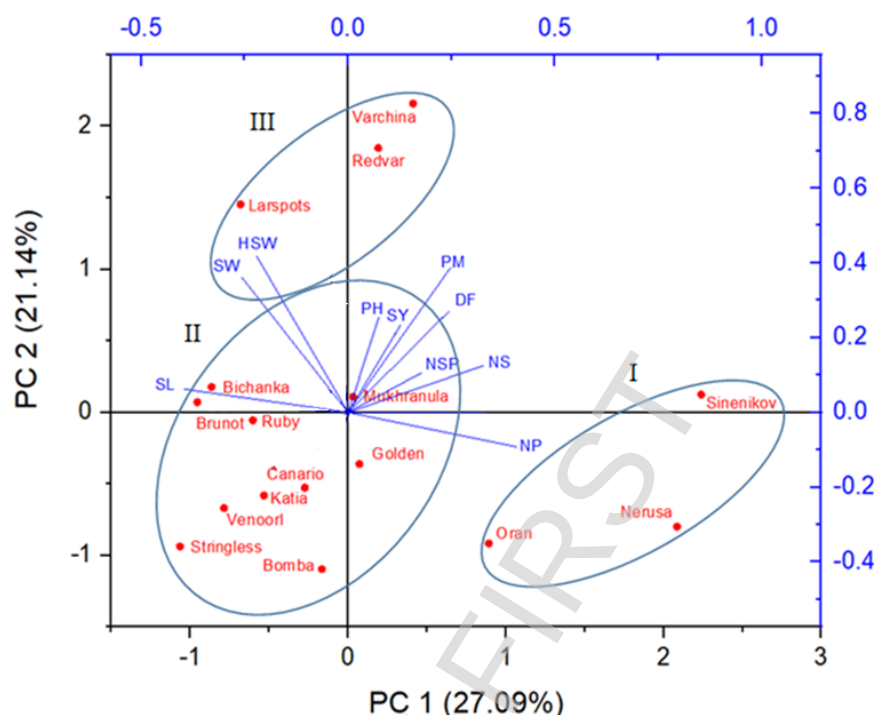


Figure 2. Biplot based on the first two principal components (PC) for morpho-agronomic traits

Table 3. Eigenvectors for the first two principal components (PC), generated from morphological, phenological and agronomic traits

Trait	Coefficients of PC1	Coefficients of PC2
Days to physiological maturity	0.324	0.399
Days to flowering	0.286	0.289
Plant height	0.214	0.131
Number of nodes per stem	0.408	0.103
Number of pods per plant	0.466	-0.213
Number of seeds per pod	0.264	-0.012
Seed length	-0.447	0.124
Seed width	-0.229	0.490
Seed yield	0.189	0.385
Hundred seed weight	-0.160	0.529

Correlations among yield related traits

Crop improvement programs can be more effective through understanding the relationships between yield and its component traits. Correlation analysis was performed among the following yield-related traits: days to flowering (DF), days to physiological maturity (PM), plant height (PH), number of nodes per stem (NS), number of pods per plant (NP), number of seeds per pod (NSP), seed length (SL), seed width (SW), seed yield per plant (SYP), and hundred-seed weight (HSW).

As shown in Table 4, days to flowering was strongly correlated with days to maturity ($r_g = -0.23$ and $r_p = 0.72$). The number of nodes per stem was negatively correlated with PM ($r_g = -0.15$ and $r_p = -0.14$), but positively correlated with NP ($r_g = 0.52$ and $r_p = 0.65$).

The number of pods per plant showed a positive correlation with PH ($r_g = 0.5$ and $r_p = 0.42$) and hundred seed weight ($r_g = 0.71$ and $r_p = 0.63$). Correlation analysis showed that SYP was significantly positively correlated with DF ($r_g = 0.34$ and $r_p = 0.34$), NP ($r_g = 0.64$ and $r_p = 0.75$) and hundred seed weight ($r_g = 0.7$ and $r_p = 0.62$). Therefore, selecting genotypes with higher mean values for these traits may contribute to increased common bean yield.

Table 4. Correlation coefficients for quantitative traits

Character	DF	PM	PH	NS	NP	NSP	SYP	HSW
DF		-0.23	0.22	-0.51*	0.2	0.85*	0.34*	0.69*
PM	0.72*		-0.68*	-0.15	-0.54*	-0.19	-0.44*	-0.56*
PH	0.01	0.36*		0.27	0.50*	0.38*	0.17	0.42*
NS	0.26	-0.14	0.02		0.52*	-0.17	-0.02	-0.15
NP	0.53*	0.42*	0.42*	0.65*		0.17	0.64*	0.71*
NSP	0.62*	0.28	-0.26	-0.08	-0.26		0.07	0.51*
SYP	0.34*	0.39*	0.38*	0.24	0.75*	-0.41*		0.62*
HSW	0.65*	0.82*	0.35*	-0.04	0.63*	-0.05	0.70*	

Note: *DF* day to flowering, *PM* day to physiological maturity, *PH* plant height (cm), *NS* number of nodes per stem, *NP* number of pods per plant, *NSP* number of seeds per pod, *SYP* seed yield per plant (g), *HSW* hundred seed weight (g). Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for growth and yield components. * indicates significant differences at 5% level.

Discussion

Variation in morpho-agronomic traits

The number of clusters in the dendrogram (Figure 1) and the biplot (Figure 2) differed despite both assessing morpho-agronomic variation. This discrepancy arises because the dendrogram was constructed based on Euclidean distance, whereas the biplot was generated using principal component analysis (Valencia & Nontuthuko, 2022). Except for the genotypes *Larspot*, *Golden*, *Bomba*, *Bichanka*, and *Mukbranula*, which exhibited group changes between the dendrogram and the biplot, all other genotypes consistently formed distinct clusters. In the current study, genotypes with similar origins and seed coat colors were grouped together, such as *Redvar* and *Vachin* in both the dendrogram (Cluster IV) and the biplot (Group III). Similarly, *Sinenikov*, *Nerusa*, and *Oran* were clustered in Cluster III of the dendrogram and Group I of the biplot (Figures 1 and 2). The association of *Larspot*, *Redvar*, and *Vachin* in Group III of the biplot indicates that common bean genotypes with similar seed coat colors, even if originating from different sources, can be grouped together (Figure 2). Comparable studies on common bean from South Africa, Poland, Bulgaria and Portugal showed accessions with the same seed coat colour but from different environments being clustered together (Boros, Wawer, & Borucka, 2014; Stoilova, Pereira, & Sousa, 2013; Valencia & Nontuthuko, 2022).

In both the dendrogram (Cluster III) and biplot (Group I), *Oran*, *Nerusa* and *Sinenikov* were perhaps grouped according to their similarity in area of origin and morpho-agronomic traits. The same clustering might also be due to their similarity in numerous pods which yielded smaller, lighter, and many seeds. These results are consistent with previous studies, in which genotypes with numerous pods, small seeds, and high seed numbers were clustered together (Bareke, 2019; Valencia & Nontuthuko, 2022). The furthest clustering of *Redvar* and *Varchin* in cluster IV from the remaining genotypes in the dendrogram indicated the highest degree of dissimilarity, which probably resulted from differences in seed coat colour, seed shape and possibly the different gene pools (Valencia & Nontuthuko, 2022). These variations can be attributed to large genetic differences between the two groups as a result of parental race differences; Andean origin and Mesoamerican origin based on seed weight (Gioia, Logozzo, Marzario, Zeuli, & Gepts, 2019). In previous studies, seed weight variation has been identified as one of the most important traits distinguishing the Mesoamerican and Andean gene pools (Singh et al., 1991). Therefore, most of our genotypes being classified as medium to large seeds, indicative of a Andean gene pool. In the current study, the large-seeded genotypes were

clustered together in the dendrogram (cluster I) and in the biplot (group IV), in agreement with the findings of some other reports ([Boros et al., 2014](#); [Burle et al., 2011](#); [Madakbas & Ergin, 2011](#)).

Genetic clustering plays an important role in plant breeding, especially in selecting parental lines for hybridization. Genotypes within the same cluster are genetically similar; thus, crossing them is unlikely to result in high heterosis. In contrast, genotypes from different clusters tend to have greater genetic divergence, increasing the likelihood of generating genetic variation and enhancing the chances of selecting superior hybrid varieties ([Canh et al., 2019](#)).

Correlation among yield related traits

In plant genetics and breeding studies, correlated traits are important because of genetic causes of correlations through pleiotropic action or developmental interactions of genes and changes can be brought in correlated traits either by natural or artificial selection ([Belay, Wassu, & Dagnachew, 2024](#); [Sharma, 1998](#)). Indirect improvement of a target trait may occur through the enhancement of another trait if they are positively correlated. The relationships among quantitative traits of common bean have been reported in previous studies ([Aisha et al., 2020](#); [Antonio et al., 2025](#); [Ballat & Araby, 2019](#); [Basavaraja et al., 2021](#); [Belay et al., 2024](#); [Chaibva, Musundire, Chivasa, & Lagat, 2024](#); [Fatema, Shompa, & Rahman, 2023](#); [Mojtaba, Danial, & Alireza, 2017](#); [Ngoc, Du, Hue, Le, & Liet, 2014](#)).

The research result showed that number of pods per plant showed a significant positive association with plant height ($r_g = 0.5$), number of nodes per stem ($r_g = 0.52$) and hundred-seed weight ($r_g = 0.71$). Days to flowering ($r_g = 0.34$), NPP ($r_g = 0.64$), number of pods per plant ($r_g = 0.51$) and hundred seed weight ($r_g = 0.62$) 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 agreement with previous research, in which [Sadeghi, Cheghamirza, and Dorri \(2011\)](#) 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.

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 days to flowering ($r_p = 0.34$), days to maturity ($r_p = 0.39$), plant length ($r_p = 0.38$), number of pods per plant ($r_p = 0.75$) and hundred seed weight ($r_p = 0.7$). Number of pods per plant showed a significant positive association with days to flowering ($r_p = 0.53$), days to maturity ($r_p = 0.42$), plant length ($r_p = 0.42$), number of nodes per stem ($r_p = 0.65$) and hundred seed weight ($r_p = 0.63$).

Conclusions

This study assessed genetic variation and agromorphological traits in 16 common bean (*Phaseolus vulgaris* L.) genotypes from the Priobia steppe, Siberia, using cluster analysis, principal component analysis, and genetic parameter estimation. The results revealed significant genetic variation among genotypes, particularly in traits such as number of pods per plant, number of nodes per stem, hundred seed weight, and seed yield per plant. The genotypes *Ruby*, *Bomba*, *Mukhranula*, *Golden*, *Redvar*, *Varchin*, and *Larspot* showed high potential in terms of growth and yield performance. These accessions should be considered for future breeding programs. The findings may assist breeders and germplasm managers in improving the conservation, utilization, and development of bean genetic resources. Future studies should assess the adaptability of promising genotypes under different ecological conditions and incorporate molecular markers to deepen genetic insights.

Author contributions: N.T.N.: Data curation, Writing – original draft, Writing – review & editing; M.H.B.: Software, Visualization, Supervision, Validation; O.V.P.: Conceptualization, Data curation; O.E.Y.: Methodology, Formal analysis, Data curation.

Acknowledgements: 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 Vinh University, Vietnam National University of Forestry and Novosibirsk State Agrarian University for their encouragement and support.

Competing interests` statement: No competing interests were disclosed.

Funding statement: This research received no external funding.

Data availability statement: The data presented in this study are available from the corresponding author upon reasonable request.

Ethical issues statement: The authors confirm that no artificial intelligence (AI) tools were used in the writing, analysis, or preparation of this manuscript.

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Agro-morfološke osobine i genetska raznovrsnost genotipova pasulja (*Phaseolus vulgaris* L.) iz Priobске stepe, Sibir

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Sažetak: Pasulj (*Phaseolus vulgaris* L.) je važna mahunarka sa visokom hranljivom vrednošću i široko se gaji u različitim ekološkim zonama. Ova studija je imala za cilj da proceni genetsku raznolikost na osnovu morfoloških markera 16 prikupljenih sorti pasulja sakupljenih iz stepe Priobskije u Sibiru. Poljski eksperiment je sproveden korišćenjem randomizovanog blokovskog dizajna (RCBD) sa tri ponavljanja tokom vegetacionih sezona 2023. i 2024. godine na Nacionalnom agrarnom univerzitetu u Novosibirsku. Analiza varijanse je otkrila značajne razlike ($p < 0,05$) među genotipovima za većinu proučavanih osobina. Dendrogram zasnovan na koeficijentima genetske sličnosti u rasponu od 0,22 do 0,78 klasifikovao je genotipove u četiri različite genetske grupe, što ukazuje na visoku genetsku raznolikost među sakupljenim genotipovima pasulja. Korelacione analize su pokazale pozitivne povezanosti između prinosa semena i broja dana do cvetanja ($rg = 0,34$ i $rp = 0,34$), broja mahuna po biljci ($rg = 0,64$ i $rp = 0,75$), kao i mase sto zrna ($rg = 0,62$ i $rp = 0,70$), što sugerise da bi odabir genotipova sa višim srednjim vrednostima za ove osobine mogao povećati prinos pasulja. Nalazi pružaju naučnu osnovu za programe oplemenjivanja i doprinose očuvanju i efikasnom korišćenju genetskih resursa pasulja unutar sibirskog agroekosistema.

Ključne reči: pasulj, genetska raznolikost, germplazma, morfološki markeri, Sibir