



Genetic Variability and Trait-Based Selection in Common Bean (*Phaseolus vulgaris* L.) Germplasm Lines from the Kashmir, India

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Abstract

Common bean (*Phaseolus vulgaris* L.) is a vital legume crop with significant nutritional and economic value, yet its productivity is limited by genetic uniformity and environmental stresses. We evaluated 75 common bean germplasm lines from Kashmir, India, for eleven agro-morphological traits using an augmented block design. High phenotypic variability was observed for plant height (CV = 64.41%) and pods per plant (CV = 41.99%), while seeds per pod (CV = 14.72%) exhibited stability. ANOVA confirmed significant genetic differences ($p \leq 0.01$) for most traits, with high heritability for plant height ($h^2 = 76.16\%$), seed thickness ($h^2 = 75.06\%$), and seeds per pod ($h^2 = 83.58\%$), indicating strong genetic control. Multivariate analyses revealed important patterns in trait variability and genetic structure. Principal Component Analysis (PCA) showed that the first three components explained 90.08% of the total variation, driven primarily by plant height, pods per plant, and seed yield per plant. Clustering identified 16 distinct groups, with Alr-36, Kdr-45, and Alr-28 exhibiting the highest divergence and outperforming checks in yield-related traits (e.g., SYPP = 100.33 g/plant) via LSI analysis. These results highlight Kashmir's germplasm as a reservoir of genetic diversity for breeding programs targeting yield resilience and stress adaptation. Future work should integrate multi-environment trials and genomic tools to validate and accelerate the deployment of these superior genotypes.



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Abbreviations

| | | | |
|----------------|--------------------------------------|------|------------------------|
| ANOVA | Analysis of Variance) | PH | Plant Height) |
| CV | Coefficient of Variation) | PL | Pod Length) |
| DF | Days to 50% Flowering) | PPP | Pods per Plant |
| EV | Environmental Variance) | PV | Phenotypic Variance |
| GAM | Genetic Advance as % of Mean) | SB | Seed Breadth |
| GCV | Genotypic Coefficient of Variation) | SL | Seed Length |
| GV | Genotypic Variance) | SPP | Seeds per Pod |
| GWAS | Genome-Wide Association Study | S | Seed Thickness |
| h ² | Broad-Sense Heritability) | STW | Seed Test Weight |
| LSI | Least Significant Increase) | SYPH | Seed Yield per Hectare |
| PCA | Principal Component Analysis) | SYPP | Seed Yield Per Plant. |
| PCA | Phenotypic Coefficient of Variation) | | |

Introduction

Common bean (*Phaseolus vulgaris* L.) is the most widely produced grain legume globally, with an annual production of 18.9 million tons. It serves as a primary source of protein and micronutrients for over two-thirds of the world's population.^{1,2} As a staple food crop in many regions, particularly in Africa, Latin America, and Asia, common beans are critical for improving food security and addressing malnutrition.^{2,3} Rich in protein, iron, zinc, and bioactive compounds, common beans play an important role in combating nutrient deficiencies and preventing chronic diseases.^{4,5} Beyond their nutritional significance, common beans contribute to sustainable agriculture by fixing atmospheric nitrogen, improving soil fertility, and reducing reliance on synthetic fertilizers.⁶⁻⁸ However, climate change and shifting environmental conditions threaten the nutritional quality and productivity of common bean, with studies showing reduced iron content under drought stress.⁹ In Kashmir, erratic precipitation and anthracnose outbreaks reduce yields by up to 40%,¹⁰ exacerbating challenges like long cooking times and pest susceptibility in resource-constrained systems.^{11,12}

Climate projections suggest that by 2050, up to 50% of current bean cultivation zones may become unsuitable due to rising temperatures, erratic rainfall, and extreme weather events.^{9,13} Moreover, region-specific biotic stresses, including anthracnose (*Colletotrichum lindemuthianum*) and common bacterial blight (*Xanthomonas axonopodis*), disproportionately affect smallholder farmers with limited access to crop protection.¹⁴ In low-income regions, common bean yields often stagnate below 600 kg/ha, exacerbating food insecurity.¹⁵

Overcoming these challenges requires climate-resilient cultivars that balance yield potential with stress adaptation.

Modern breeding tools like genome-wide association studies (GWAS) and CRISPR/Cas9 have accelerated trait discovery in common bean. For instance, García-Fernández *et al.* identified QTNs for pod morphology and drought tolerance,¹⁶ while GWAS in *Medicago truncatula* revealed conserved genetic mechanisms for seed size.¹⁷ However, phenotypic screening of landraces remains critical to validate these findings in target environments, especially in underrepresented regions like the Himalayas. Landraces, with their broader genetic base and local adaptation, are invaluable for breeding programs aiming to enhance yield stability, nutritional quality, and resilience.^{18,19}

In India, common bean holds cultural and agronomic significance in Himalayan regions. Kashmir's germplasm, derived from both Mesoamerican and Andean gene pools,¹⁰ exhibits exceptional diversity in seed morphology (e.g., size, color), micronutrient content, and disease resistance.^{10,20} However, systematic evaluations using multivariate approaches are lacking, limiting the utilization of this diversity in breeding.

To address this gap, our study aims to

- Quantify genetic variability and heritability for 11 agro-morphological traits in 75 Kashmiri common bean lines;
- Decipher trait associations and genetic structure using PCA and hierarchical clustering;
- Identify superior genotypes via LSI analysis,

prioritizing lines exceeding yield and stress-tolerance thresholds;

- Provide actionable insights for breeding programs targeting temperate agro-ecologies.

By integrating multivariate statistics with phenotypic screening, this study unlocks the potential of Kashmir's germplasm. The findings will directly inform breeding strategies, with stress-resistant clusters to develop climate-smart varieties. Such efforts are essential to safeguard food security in climate-vulnerable temperate regions.

Materials and Methods

Study Area and Plant Material

The study was conducted at the Dryland Agricultural Research Station (DARS), SKUAST-K, located in Budgam, Jammu and Kashmir. The site is situated at 74.83°E longitude, 34.08°N latitude, and 1587 meters above sea level. Seventy-five common bean germplasm accessions, sourced from diverse regions of Kashmir, were selected for evaluation. The germplasm was sourced from diverse agro-ecological zones of Kashmir, ensuring representation of variation in seed morphology, growth habit, and stress adaptation. Detailed passport information, including site of collection and codes of individual germplasm lines, has been previously published in the DUS characterization study of these lines.²¹ The same germplasm lines were used in the present study to evaluate genetic variability and trait associations under augmented block design.

Experimental Design

The experiment was laid out in an augmented block design with four blocks, each containing 19 test entries and five standard checks. This design allowed for an effective comparison of a large number of unreplicated test entries against replicated checks to control environmental variation. Each entry was planted in a single row of 1.5 meters length, with a spacing of 40 cm between rows and 15 cm between plants. This setup minimized inter-plant competition and allowed uniform growth. Standard agronomic practices were followed throughout the cropping period.

Data Collection

Eleven agro-morphological traits were recorded, encompassing phenological, morphological, and yield-related parameters.

- **Phenological Trait:** Days to 50% flowering (DF) (recorded on a plot basis).
- **Morphological Traits:** Plant height (PH), pod length (PL), seeds per pod (SPP), seed length (SL), seed breadth (SB), and seed thickness (ST).
- **Yield-Related Traits:** Pods per plant (PPP), seed yield per plant (SYPP), seed test weight (STW), and seed yield per hectare (SYPH).

For all traits except flowering, measurements were taken from five randomly selected competitive plants per plot at maturity to ensure accuracy and minimize bias. Flowering data were collected on a plot basis when approximately 50% of the plants exhibited open flowers.

Statistical Analysis

All statistical analyses were performed using R software (version 4.1.2) and SPSS (version 25.0). The following procedures were employed.

- **Descriptive Statistics:** Means, standard deviations, and coefficients of variation (CV) were computed to summarize trait distributions.
- **Analysis of Variance (ANOVA):** Conducted to detect significant differences among germplasm lines for each trait ($p \leq 0.05$, $p \leq 0.01$).
- **Genetic Parameters:** Genotypic (GCV) and phenotypic (PCV) coefficients of variation, broad-sense heritability (H^2), and genetic advance as a percentage of the mean (GAM) were calculated following standard formulas.
- **Principal Component Analysis (PCA):** Conducted to identify traits contributing most to overall variation. Components with eigenvalues greater than 1 (Kaiser's criterion) were retained for interpretation.
- **Hierarchical Clustering:** Performed using Ward's method with Euclidean distance to group genotypes based on trait similarity. The optimal number of clusters was determined using the NbClust package in R.
- **Least Significant Increase (LSI) Analysis:** Applied to identify genotypes exceeding the performance of the best checks.
- The **LSI threshold** was calculated at a 5% significance level ($p \leq 0.05$), and genotypes surpassing this threshold were considered superior for the respective trait.

- **Correlation Analysis:** Pearson correlation coefficients were computed to examine trait associations and potential for co-selection.

Data visualization was conducted using the ggplot2, pals, and factoextra packages in R, and final outputs were compiled using the writexl package for reporting. All analyses adhered to established statistical protocols to ensure reproducibility and reliability of results.

Results

Phenotypic Variation and Trait Distribution

Substantial genetic variability was observed among the 75 common bean germplasm lines evaluated for

11 agro-morphological traits (Table 1). Plant height (PH) exhibited the highest phenotypic variability (CV = 64.41%), followed by pods per plant (PPP; CV = 41.99%), suggesting these traits hold strong potential for selection. Yield-related traits such as seed yield per plant (SYPP) and seed thickness (ST) showed moderate variability (CV = 35.99% and 35.90%, respectively), while traits like seeds per pod (SPP) and seed test weight (STW) demonstrated lower variability (CV = 14.72% and 22.53%). Days to 50% flowering (DF) showed moderate variability (CV = 39.22%), indicating potential for breeding programs to optimize flowering time for different agro-ecological zones

Table 1: Descriptive Statistics for 11 selected traits of common bean germplasm accessions

| Trait | Mean | Std. Deviation | Min | Max | CV (%) |
|--------------------------------------|-------|----------------|-------|--------|--------|
| Plant Height (PH) (cm) | 43.49 | 28.01 | 11.75 | 182.05 | 64.41 |
| Pod Length (PL) (cm) | 9.89 | 2.85 | 3.96 | 21.66 | 28.82 |
| Pods per Plant (PPP) | 19.36 | 8.13 | 2.36 | 46.55 | 41.99 |
| Seeds per Pod (SPP) | 6.18 | 0.91 | 4.08 | 8.88 | 14.72 |
| Seed Length (SL) (mm) | 12.04 | 3.12 | 4.3 | 21.42 | 25.91 |
| Seed Breadth (SB) (mm) | 6.04 | 1.66 | 3.41 | 9.5 | 27.48 |
| Seed Thickness (ST) (mm) | 4.15 | 1.49 | 1.1 | 7.35 | 35.9 |
| Seed Test Weight (STW) (g) | 39.14 | 8.82 | 14.81 | 56.05 | 22.53 |
| Seed Yield per Plant (SYPP) (g) | 45.7 | 16.45 | 11.16 | 100.33 | 35.99 |
| Seed Yield per Hectare (SYPH) (q/ha) | 9.13 | 3.29 | 2.24 | 20.06 | 36.04 |
| Days to 50% Flowering (DF) | 60.96 | 23.91 | 28.0 | 122.0 | 39.22 |

Table 2: Analysis of Variance for Different Traits in Common Bean Accessions; NS P > 0.05; * P <= 0.05; ** P <= 0.01

| Source | Df | Mean Sq | | | | | | | | | | |
|-----------------------|----|-----------|---------|---------|---------|---------|--------|---------|----------|----------|--------|----------|
| | | (PH) | (PL) | (PP) | (SPP) | (SL) | (SB) | (ST) | (STW) | (SYPP) | (SYPH) | (DF) |
| Treatment (Germplasm) | 79 | 663.57** | 6.6** | 42.03** | 0.67** | 4.29** | 1.65** | 7.30** | 45.99** | 172.11** | 6.96** | 365.99** |
| Treatment: Check | 4 | 395.0* | 10.33** | 8.65* | 0.36** | 2.5NS | 0.25NS | 5.2* | 22.5** | 90* | 2.25NS | 250** |
| Treatment: Test | 74 | 670* | 6.5* | 44** | 0.75** | 3.8** | 1.6** | 12.0* | 44.5** | 170** | 7.1* | 360** |
| Test vs Check | 1 | 1327.14** | 8.48** | 67.24** | 12.62** | 42.92** | 7.32** | 18.24** | 101.12** | 290.58** | 7.89** | 600** |
| Block | 4 | 6.98NS | 0.5NS | 3.14NS | 0.29NS | 1.37NS | 1.85NS | 1.12NS | 5NS | 13.27NS | 12.5NS | 1.78NS |
| Residuals | 16 | 158.38 | 1.86 | 16.27 | 0.11 | 1.36 | 0.64 | 1.82 | 20.61 | 73.4 | 2.85 | 223.54 |

ANOVA and Trait Significance

ANOVA revealed highly significant differences ($p \leq 0.01$) among accessions for most traits (Table 2), confirming the presence of substantial genetic variability. The significant Test vs. Check contrasts for nearly all traits, except pod length (PL) and seed breadth (SB), indicate the potential of certain lines to outperform existing checks. The non-significant block effects affirm the reliability of the field design and minimize confounding spatial variability.

Genetic Parameters and Selection Potential

High genotypic variance (GV) and heritability (h^2) estimates were observed for key traits (Table 3). PH

(GV = 505.19; $h^2 = 76.16\%$) and ST (GV=5.48; $h^2 = 75.06\%$) demonstrated the highest genetic advance as a percentage of mean (GAM = 92.93% and 100.67%), indicating strong additive genetic effects and high selection efficiency. Traits like PPP ($h^2 = 61.30\%$, GAM = 42.29%) and SYPP ($h^2 = 57.36\%$, GAM = 33.92%) exhibited moderate heritability, suggesting the need for multi-environment trials to confirm their stability. The narrow GCV–PCV differences for traits like SPP, SL, and ST (Fig. 1) indicate that these traits are largely under genetic control, whereas wider gaps for SYPP and STW reflect stronger environmental influences.

Table 3: Genetic Variability Analysis of Common Bean Germplasm Traits

| Trait | Mean | GV | EV | PV | GCV (%) | PCV (%) | Heritability (h^2) | Heritability Category | GA | GAM (%) |
|-------|-------|--------|--------|--------|---------|---------|------------------------|-----------------------|-------|---------|
| PH | 43.49 | 505.19 | 158.38 | 663.57 | 51.6 | 59.1 | 76.16 | High | 40.41 | 92.93 |
| PL | 9.89 | 4.74 | 1.86 | 6.60 | 21.9 | 26.0 | 71.82 | High | 3.80 | 38.43 |
| PP | 19.36 | 25.76 | 16.27 | 42.03 | 26.2 | 33.5 | 61.30 | Medium | 8.19 | 42.29 |
| SPP | 6.18 | 0.56 | 0.11 | 0.67 | 12.1 | 13.4 | 83.58 | High | 1.41 | 22.80 |
| SL | 12.04 | 2.93 | 1.36 | 4.29 | 14.1 | 17.2 | 68.27 | Medium | 2.91 | 24.19 |
| SB | 6.04 | 1.01 | 0.64 | 1.65 | 16.6 | 21.2 | 61.21 | Medium | 1.62 | 26.82 |
| ST | 4.15 | 5.48 | 1.82 | 7.30 | 17.9 | 20.6 | 75.06 | High | 4.18 | 100.67 |
| STW | 39.14 | 25.38 | 20.61 | 45.99 | 13.0 | 16.4 | 55.18 | Medium | 7.71 | 19.70 |
| SYPP | 45.70 | 98.71 | 73.40 | 172.11 | 21.7 | 28.3 | 57.36 | Medium | 15.50 | 33.92 |
| SYPH | 9.13 | 4.11 | 2.85 | 6.96 | 17.6 | 24.2 | 59.04 | Medium | 3.21 | 35.14 |
| DF | 60.96 | 142.45 | 223.54 | 365.99 | 19.6 | 24.8 | 38.93 | Low | 15.34 | 25.17 |

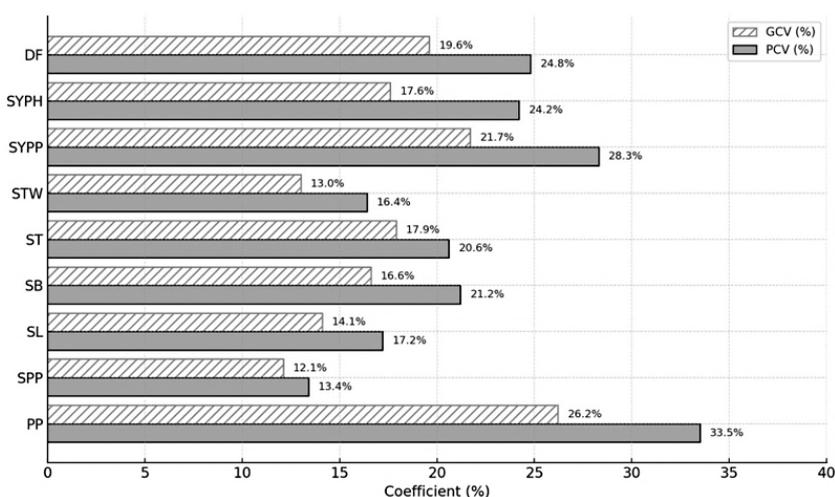


Fig. 1: Genotypic vs Phenotypic Coefficients of Variation (GCV vs PCV) for 11 agro-morphological traits in 75 common bean germplasm accessions.

The graph illustrates the genetic and phenotypic coefficients of variation for each trait. Narrow differences between GCV and PCV (e.g., for SPP, SL, ST) indicate stronger genetic control, while wider differences (e.g., SYPP, STW, DF) reflect greater environmental influence. These variations guide trait prioritization in selection and breeding strategies.

Principal Component and Cluster Analysis

Principal component analysis (PCA) revealed that the first three principal components accounted for 90.08% of the total variation, with PC1 (44.37%) primarily influenced by PH, PPP, and SYPP; PC2 (30.81%) by ST, STW, and SL; and PC3 (14.91%) by SB and DF (Table 4, Fig. 2). This indicates that breeding for yield potential should prioritize lines with high PH, PPP, and SYPP, while seed quality traits (size and shape) align with PC2. For example, Alr-36,

Kdr-45, and Alr-28 clustered with high values for yield traits and seed thickness, whereas genotypes like Ppr-12 and Kdr-4 aligned with seed size traits.

Hierarchical clustering grouped the 75 lines into 16 distinct clusters (Fig. 3). The greatest inter-cluster distance (77.36) was observed between Clusters 1 and 10 (Fig. 4), as shown in the heatmap of inter-cluster distances. Cluster 1 contained early-flowering, tall plants with high pod number, ideal for short-season environments. Cluster 10, in contrast, comprised late-flowering, large-seeded lines suitable for niche markets. Clusters 9, 13, and 14 showed the highest intra-cluster variability, offering opportunities for within-cluster selection. These insights guide hybridization strategies, such as crossing divergent clusters (e.g., Cluster 1 × Cluster 10) to maximize heterosis for yield and stress tolerance.

Table 4: Principal Components (PCs) with eigenvalues >1 were retained for analysis. The first three PCs explained 90.08% of total variance, indicating their strong contribution to trait differentiation among genotypes.

| Principal Component | Eigenvalue | % Variance Explained | Cumulative Variance (%) |
|---------------------|------------|----------------------|-------------------------|
| PC1 | 739.80 | 44.37 | 44.37 |
| PC2 | 513.60 | 30.81 | 75.18 |
| PC3 | 248.51 | 14.91 | 90.08 |
| PC4 | 73.60 | 4.41 | 94.50 |
| PC5 | 59.74 | 3.58 | 98.08 |
| PC6 | 11.35 | 0.68 | 98.76 |
| PC7 | 8.48 | 0.51 | 99.27 |
| PC8 | 7.93 | 0.48 | 99.75 |
| PC9 | 1.97 | 0.12 | 99.86 |
| PC10 | 1.64 | 0.10 | 99.96 |
| PC11 | 0.63 | 0.04 | 100.00 |

Least Significant Increase (LSI) Analysis

The LSI analysis identified lines that exceeded best check thresholds (calculated at $p \leq 0.05$ significance) for various traits (Table 5). Notably, Alr-36, Kdr-45, and Alr-28 outperformed checks in key yield-related traits such as PPP and SYPP. Alr-36 exceeded the LSI thresholds in six traits, PPP, SPP, ST, SYPP, SYPH, and SB, establishing it as a high-performing and broadly superior genotype. Similarly, Kdr-45 demonstrated exceptional performance across five

traits, including ST, STW, and SYPP, indicating multi-trait superiority. The number of germplasm accessions exceeding LSI thresholds was highest for seed thickness (ST; 36 lines) and seed yield per plant (SYPP; 38 lines), underscoring considerable scope for selection. These findings empirically validate the genetic merit of these lines and reinforce their prioritization in breeding programs aimed at yield enhancement and stress adaptation.

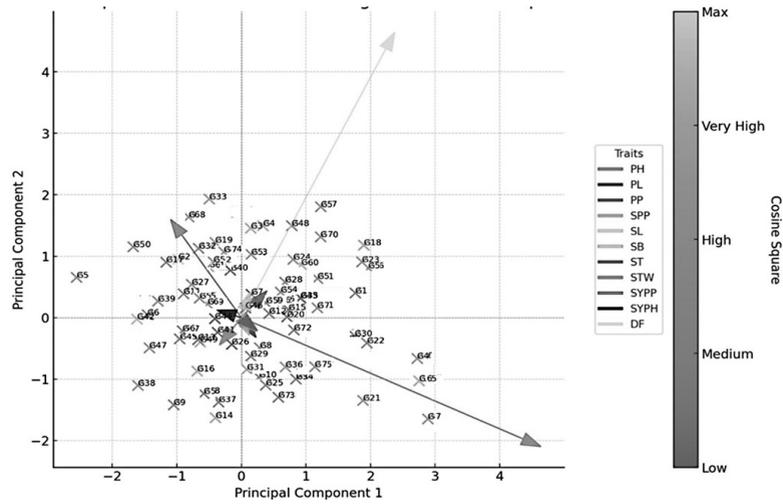


Fig. 2: Principal component analysis-Biplot

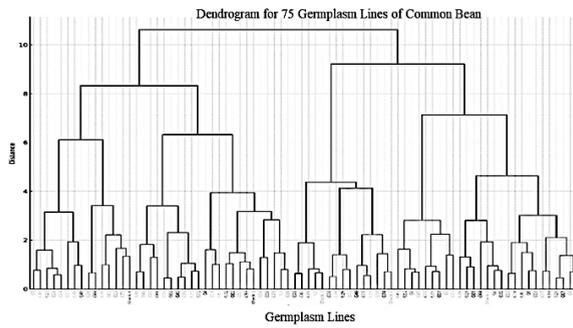


Fig. 3: Distribution Of Common Bean Germplasm Accessions Into Clusters Based on Hierarchical Clustering

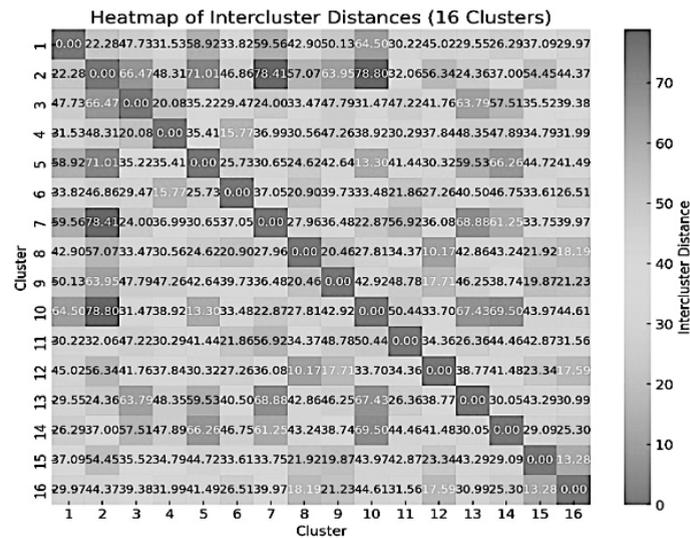


Fig. 4: Heatmap Showing Intercluster Distances Among 16 Clusters

Table 5: Germplasm lines exceeding best check thresholds based on Least Significant Increase (LSI) for key agro-morphological traits.

| Traits | Best Check | Threshold (Best Check + LSI) | Germplasm Lines Better than Best Check | No. of Better G-Lines |
|--------|------------|------------------------------|--|-----------------------|
| PH | Check 2 | 56.94 | Ppr-12, Kdr-4, Alr-92, Alr-20, Alr-58 | 5 |
| PL | Check 1 | 45.48 | Kdr-45, Alr-6, Alr-63, Alr-12, Ppr-3, Alr-64, Kdr-4, Alr-28, Alr-19, Alr-105, Ppr-14, Alr-76, Alr-9, Alr-18, Alr-89, Alr-55, Alr-10, Alr-67, Alr-14, Alr-33 | 20 |
| PP | Check 3 | 38.19 | Alr-36, Ppr-9, Alr-63, Kdr-77, Alr-84, Alr-79, Alr-87, Alr-86, Ppr-7, Ppr-15, Alr-64, Kdr-4, Alr-19, Alr-2, Alr-105, Kdr-25, Ppr-14, Alr-62, Alr-51, Alr-18, Alr-56, Alr-3, Alr-89, Alr-25, Alr-77, Alr-55, Alr-10, Alr-90, Gurez local, Alr-58, Alr-67, Alr-22, Alr-192 | 33 |
| SPP | Check 2 | 48.39 | Alr-36, Alr-7, Kdr-45, Alr-326, Alr-6, Kdr-77, Ppr-11, Alr-12, Alr-111, Ppr-15, Alr-64, Kdr-4, Alr-19, Kdr-25, Ppr-14, Alr-3, Ppr-13, Gurez local, Alr-85, Alr-14 | 20 |
| SL | Check 5 | 49.01 | Kdr-77, Ppr-15, Alr-105, Alr-51, Alr-9, Alr-18, Ppr-6, Alr-77, Kdr-12, Ppr-13, Alr-58, Alr-67, Alr-22, Alr-40 | 14 |
| SB | Check 2 | 46.67 | Alr-36, Kdr-45, Ppr-12, Alr-6, Alr-4, Ppr-11, Ppr-3, Ppr-15, Alr-2, Alr-76, Alr-51, Alr-66, Alr-9, Alr-20, Alr-16, Alr-17, Alr-57, Alr-58, Alr-37, Alr-85, Alr-22, Alr-192 | 22 |
| ST | Check 2 | 38.78 | Alr-36, Kdr-45, Alr-326, Ppr-12, Alr-84, Alr-15, Alr-4, Alr-87, Alr-12, Ppr-7, Ppr-3, Kdr-46, Alr-91, Alr-64, Kdr-4, Alr-2, Alr-105, Ppr-10, Alr-62, Alr-51, Alr-88, Alr-20, Alr-56, Alr-3, Alr-89, Ang local, Ppr-6, Alr-10, Kdr-12, Alr-17, Alr-57, Alr-58, Alr-37, Alr-14, Alr-192, Alr-156 | 36 |
| STW | Check 1 | 41.37 | Kdr-45, Ppr-12, Alr-63, Kdr-36, Ppr-1, Ppr-11, Alr-92, Alr-19, Alr-88, Alr-56, Alr-89, Ang local, Alr-77, Alr-55, Alr-57, Alr-67, Alr-37 | 17 |
| SYPP | Check 4 | 29.16 | Alr-36, Alr-24, Alr-7, Kdr-45, Alr-326, Ppr-12, Alr-6, Ppr-4, Alr-84, Alr-15, Ppr-11, Alr-79, Ppr-15, Kdr-4, Alr-28, Alr-105, Kdr-25, Ppr-14, Alr-62, Alr-51, Alr-66, Alr-9, Alr-73, Alr-3, Ang local, Alr-25, Alr-55, Alr-10, Ppr-13, Alr-57, Alr-58, Alr-67, Alr-37, Alr-81, Alr-22, Alr-40, Alr-33, Alr-156 | 38 |
| SYPH | Check 1 | 48.72 | Alr-36, Alr-7, Ppr-12, Kdr-36, Ppr-1, Alr-86, Kdr-46, Ppr-15, Alr-105, Alr-18, Alr-88, Alr-56, Alr-89, Ppr-13, Alr-58, Alr-22, Alr-40, Alr-156 | 18 |
| DF | Check 1 | 48.88 | Alr-24, Alr-7, Ppr-9, Ppr-12, Ppr-4, Alr-63, Alr-4, Alr-86, Alr-19, Alr-62, Alr-18, Alr-16, Gurez local, Alr-58 | 14 |

Trait Correlations

Correlation analysis (Fig. 5) revealed key trait associations with implications for breeding. The

moderate positive correlation between SYPP and ST ($r = 0.27$) suggests that selecting for thicker seeds may indirectly enhance yield potential. However,

breeders must balance this with market preferences, as thicker seeds may alter cooking times and texture. The positive correlation between PPP and DF ($r = 0.20$) indicates that extended flowering duration can support higher pod development, useful in environments with longer growing seasons.

Conversely, the negative correlation between PH and DF ($r = -0.15$) suggests a trade-off: selecting for taller plants may inadvertently result in earlier flowering, a desirable trait for temperate, short-season regions.

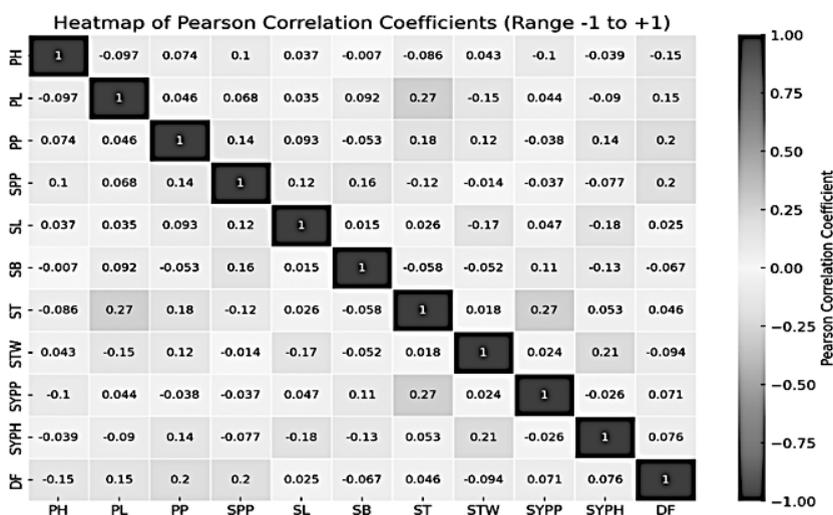


Fig. 5: Heatmap of Pearson Correlation Coefficients Among Common Bean Germplasm Traits

These findings highlight substantial genetic variability among common bean germplasm lines, with traits such as plant height, seed thickness, and pods per plant emerging as promising targets for selection due to their high heritability and genetic advance. PCA and clustering revealed clear trait associations and genetic divergence, while LSI analysis confirmed several genotypes outperforming standard checks. Together, the results provide actionable insights for selection and diversity-based improvement strategies.

Discussion

This study reveals substantial agro-morphological diversity among 75 common bean lines from Kashmir, offering critical insights for trait-targeted breeding and genetic enhancement. The wide phenotypic variation, significant heritability estimates, and robust multivariate analyses underscore the potential of this germplasm for developing high-yielding, climate-resilient cultivars.

Phenotypic Variation, Heritability, and Genetic Advance

The observed variability across traits, especially plant height (PH; CV = 64.41%) and pods per plant (PPP; CV = 41.99%), reflects the diverse genetic background of the Kashmir germplasm. Similar trends have been reported previously, highlighting PH as a phenotypically plastic trait responsive to both genetic background and environmental stimuli.^{20,22} High heritability estimates for PH (76.16%), ST (75.06%), and SPP (83.58%) indicate strong additive genetic control, suggesting these traits are stable across environments and can be prioritized for selection in early generations. These findings are in agreement with previous reports indicating moderate to high heritability for morphological and agronomic traits in common bean.^{16,23,24} Conversely, environmental stresses have been shown to reduce heritability estimates, as noted in studies previous studies,²⁵ emphasizing the genotype-by-environment interaction particularly for yield-associated traits.

Seed thickness (ST), in particular, exhibited the highest genetic advance as a percentage of mean (GAM = 100.67%), highlighting its utility as a selection target. Biologically, thicker seeds are often linked to improved seed coat integrity, higher protein reserves, and better resistance to mechanical damage during harvesting and storage.^{26,27} Similarly, PH influences light capture and canopy structure but must be balanced against the risk of lodging, especially under high-input conditions.^{28,29}

PPP and seed yield per plant (SYPP) showed moderate heritability (61.30% and 57.36%) but high GAM (42.29% and 33.92%), results similar to the previous studies,^{30,31} suggesting that despite some environmental influence, these traits offer considerable potential for gain under selection. Conversely, days to flowering (DF) had lower heritability (38.93%), reflecting strong genotype-by-environment interactions, a finding consistent with earlier studies.^{25,32,33} This highlights the need for multi-environment trials to ensure stable flowering behavior across diverse agro-climatic zones.

Multivariate Analysis and Genetic Structure

The PCA identified PH, PPP, and SYPP as primary contributors to genetic variation, aligning with findings from Asfaw *et al.*,³⁴ Kouam *et al.*,³⁵ and Girdel.³⁶ This confirms their importance as core yield determinants. Notably, genotypes such as Alr-36 and Kdr-45, which loaded heavily on PC1, exhibit a favorable combination of these traits, making them strong candidates for direct selection. PC2 (30.81% variance) captured seed size traits (ST, STW, SL), while PC3 (14.91%) included flowering time and seed breadth, underscoring the multi-dimensional nature of bean improvement.

Hierarchical clustering provided additional insights into genetic structure by grouping accessions into 16 clusters. Cluster 1 contained early-flowering, tall, and high-podding genotypes, ideal for short-season environments, while Cluster 10 comprised late-flowering, large-seeded lines suited for niche markets. The largest inter-cluster distance (77.36) between Clusters 1 and 10 indicates these are the most genetically divergent and should be prioritized for hybridization to exploit heterosis,³⁵ as also demonstrated in chickpea and lentil.³⁷⁻³⁹ In particular, accessions at the extremes of clusters 1 and 10,

such as Alr-37, Alr-28, and Kdr-12, were found to be genetically distinct and high-performing, making them ideal candidates for hybridization efforts aimed at improving yield and resilience.^{40,41} Within-cluster variability, notably in Clusters 9, 13, and 14, presents opportunities for refining specific traits like seed size and disease resistance. This variation within clusters can be targeted to refine specific agronomic traits, such as disease resistance or seed size, leading to the development of more stable, high-performing genotypes.^{42,43}

Least Significant Increase (LSI) Analysis and Superior Genotypes

The LSI analysis applied a 5% significance threshold ($p \leq 0.05$) to define "superior genotypes" as those exceeding the best-performing check for each trait. This method, validated in earlier studies,^{44,45,38} ensures the statistically robust identification of elite lines. Alr-36 exceeded the thresholds for six traits, including PPP, SPP, ST, and SYPP, confirming its broad agronomic superiority. Kdr-45 excelled across five traits, including ST, STW, and SYPP, whereas Alr-28 showed strong yield traits. By integrating LSI-based results with multivariate analysis, genetic merit of superior genotypes like that of Alr-36, Kdr-45, and Alr-28 can be empirically validated to offer immediate value for breeding programs targeting multi-trait improvement in temperate regions like Kashmir.^{38,44,45}

Trait Associations and Breeding Implications

The correlation analysis provides practical guidance for breeders. The moderate positive correlation between SYPP and ST ($r = 0.27$) suggests that thicker seeds may contribute to higher yield, aligning with findings from Saba *et al.*⁴⁶ However, this relationship may vary across environments, thicker seeds may enhance yield in high-rainfall areas due to reduced seed shattering but may prolong cooking time, affecting market acceptability.⁴⁷ The positive correlation between PPP and DF ($r = 0.20$) indicates that longer flowering duration supports higher pod set, a relationship particularly relevant in environments with extended growing seasons.⁴⁸⁻⁵¹ In contrast, the negative correlation between PH and DF ($r = -0.15$) suggests a trade-off: selecting for taller plants may inadvertently lead to earlier flowering, which could be advantageous for short-season systems but may limit biomass accumulation

in longer seasons.⁵² These dynamics underscore the importance of co-selection strategies that balance trait interactions based on specific target environments.^{53,54} For example, breeders aiming for early-maturing, high-yielding varieties in temperate regions should prioritize lines with moderate PH, shorter DF, and high PPP, while those targeting high-value seed markets may focus on thicker seeds and uniform seed size. The integration of multi-trait selection indices and genomic prediction models could further optimize such breeding strategies, as discussed by Vieira *et al.*⁵⁵

Contextualizing Findings and Future Directions

This study demonstrates that Kashmir's common bean germplasm offers a rich resource for developing climate-resilient, high-yielding cultivars. However, the single-environment assessment limits the generalizability of the findings. Future research should validate these results across multiple agro-ecological zones and seasons to assess genotype-by-environment interactions.^{56,57} Additionally, incorporating molecular tools such as genome-wide association studies (GWAS) and marker-assisted selection (MAS) could accelerate the identification of stable, high-performing lines.^{58,59} Biologically, key traits like seed thickness may enhance protein content and seed viability,⁴⁶ while plant height influences competitive ability and photosynthetic efficiency,⁶⁰ traits that must be balanced for optimal performance. The practical application of trait correlations, cluster insights, and LSI-validated lines provides breeders with a roadmap for designing crossing programs tailored to specific environmental and market demands.^{34,59} By situating these findings within the broader context of legume improvement, this study lays the groundwork for future breeding efforts aimed at ensuring food and nutritional security in the face of climate change.

Conclusion

This study offers a comprehensive evaluation of 75 common bean germplasm lines from Kashmir, revealing substantial agro-morphological diversity that holds immense potential for breeding programs. The findings highlight the high variability across key traits like PH and PPP, with moderate to high heritability estimates for these traits, emphasizing their genetic control and suitability for direct selection in breeding programs. Furthermore, the high genetic

advance as a percentage of mean (GAM) for ST validates its potential as a target for selection. Multivariate analyses, including PCA and hierarchical clustering, revealed clear trait associations and significant genetic divergence within the germplasm. Notably, Alr-36, Kdr-45, and Alr-28 were identified as superior genotypes, consistently outperforming best checks across multiple key yield-related traits. This underscores their value for future breeding efforts aimed at improving yield and stress resilience in temperate regions like Kashmir. Moreover, the LSI analysis further confirmed the merit of these genotypes, offering empirical validation of their genetic superiority. The study also demonstrated the complex interactions among key traits, such as the positive correlation between SYPP and ST, which suggests that thicker seeds may contribute to higher yield potential, and the inverse relationship between PH and DF, indicating the potential for early-maturing genotypes in breeding programs. These findings provide a strong foundation for the development of targeted breeding strategies, particularly for improving the yield and adaptability of common bean in diverse agro-ecological regions. By integrating heritability estimates, genetic advance, and trait correlation data, the study offers actionable insights for improving the genetic quality of common bean germplasm for future agricultural productivity.

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Author Contributions

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