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Meyijungla Imsong

Nagaland University

H. P. Chaturvedi

Nagaland University

D. Purushotama Rao

purushotamadatti@gmail.com

Nagaland University

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Genetic Dissection and Multi-Trait Selection in French Bean (*Phaseolus vulgaris* L.) Genotypes Using MGIDI and Multivariate Approaches

Meyijungla Imsong¹, H. P. Chaturvedi¹ and D. Purushotama Rao^{1*} and

Department of Genetics and Plant Breeding, School of Agricultural Sciences, Nagaland University, Medziphema Campus-797 106, Nagaland, India.

✉ *purushotamadatti@gmail.com (ORCID: 0000-0002-5092-5429)

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Abstract

Productivity enhancement of French beans faces numerous challenges owing to the complexity of interactions between yield traits and the limitations of conventional univariate selection methods. The current selection index, like the Smith-Hazel index, suffers from multicollinearity and subjective weighting of market traits. Therefore, there is a need for a robust index capable of simultaneously selecting for multiple desirable traits to identify promising genotypes. To address this, a current field investigation was conducted during Rabi 2024–25 using 22 French bean primitive cultivars in a randomized block design. Eleven agronomic traits were assessed, and the Multi-Trait Genotype Ideotype Distance Index (MGIDI), a metric quantifying closeness of genotypes to an ideotype trait combination, was used to identify candidate lines. Significant genotypic variation ($p < 0.01$) was observed for all traits except pods per cluster. The seed yield per plot (1.3 m^2) ranges from 71.0 g to 217.5 g, and the top-performing genotypes were Deep red kholar, Luli, Kholar light brown, and Kholar medium brown. High GCV, PCV, heritability, and genetic advance were observed in relation to plant height, seed index, and seed yield, indicating strong additive genetic effects. Seed yield per plot was positively and significantly associated with all traits except days to 50% flowering. Path analysis showed that seed index, pod length, and secondary branches have a high positive direct effect on seed yield. PCA explained 88.54% of total variation, with PC1 (51.18%) dominated by key yield traits, clearly separating high-performing genotypes (Deep red kholar, Luli). MGIDI identified Deep red kholar, TSG1, and Kholar Yellow large as closest to the ideotype with >80% selection success and maximum predicted gain for seed yield (32.35%). Overall, MGIDI proved superior in identifying balanced genotypes by overcoming multicollinearity and integrating multi-trait information. These findings provide a robust framework for ideotype-based breeding and accelerate the development of high-yielding, stable French bean cultivars.

Key words: Correlation, Genetic variability, PCA, Simulation Selection Index and Smith–Hazel Index

Introduction

French bean (*Phaseolus vulgaris* L.) is a major legume crop worldwide. It is an herbaceous dicotyledonous plant in the family Fabaceae [1]. The total global production of this bean has grown consistently over the last two decades. In 2023, it recorded around 30 million metric tonnes [2]. Brazil produces 3 to 4 million tonnes per year, and India produces 2 to 3 million tonnes per year. Their yields range from 800 to 1200 kg per hectare [3]. Nutritionally, French beans are a great source of protein (20-25%) and carbohydrates, with minimal fat [4].

Plant breeding programs aim to combine desirable traits into a single genotype to improve agronomic performance [5]. Efficient selection methods are needed to save time and resources. For bean breeders, grain yield is a primary goal. Achieving this depends on related traits, so univariate selection is not ideal for fully balanced bean phenotypes [6]. Instead, breeders use multi-trait selection to create cultivars that improve main traits such grain yield, while also excelling in secondary commercial traits.

When selecting a multi-trait combination phenotype, several biological limitations exist. The main obstacle is the negative correlation between yield traits and the yield compensation principle [7]. These trade-offs among agronomic traits make it difficult to improve yield by selecting a single trait, underscoring the need for multi-trait selection approaches [8]. Statistical approaches assess genetic variability and partition phenotypic variance into additive and non-additive components within the breeding population at the initial level [9]. Correlation and path analysis help in understanding trait associations and trade-offs. The Smith-Hazel (SH) Index is the most commonly used by plant breeders to identify promising lines [10]. Using phenotypic and genotypic variance-covariance matrices, this index optimises selection weights to maximise the correlation between the index and aggregate genetic merit [11]. When supplemented with simulation based selection indices, breeders can computationally model expected genetic gains across scenarios, enabling precise identification of promising lines.

The classical Smith-Hazel (SH) Index has long been the standard for multi-trait selection for a long time, but it has two serious drawbacks. First, it requires arbitrary economic weights, which are hard to define for non-market traits like plant height. Second, it faces multicollinearity issues [12]. The SH index needs to invert a phenotypic covariance matrix, but highly correlated traits, common in French bean yield components can make the matrix poorly conditioned and bias genetic gain estimates [13]. The Multi-Trait Genotype Ideotype Distance Index (MGIDI) helps address these problems MGIDI selects genotypes closest to the ideal by simultaneously considering all phenotypic traits. It uses a multi-step method with trait rescaling (on a 0–100 scale) and factor analysis [12]. This reduces the number of variables and groups highly correlated traits into independent factors, so no matrix inversion is needed. In

this study, we used several selection index models to identify promising French bean genotypes in the foothills of the Nagaland.

Materials and methods

The study was carried out during the Rabi season of 2024-25 in an irrigated cultivation environment at the Department of Genetics and Plant Breeding, experimental farm at the School of Agricultural Sciences, Nagaland University, Medziphema. The experimental farm is located in the foothills of Medziphema, a subdivision of Dimapur, Nagaland. It has an altitude of 310 meters above mean sea level, with coordinates of 25° 45' 43" North and 93° 53' 04" East. The experimental material comprised 22 local French bean varieties. The names of the genotypes and the collection sites are shown in Table 1. The plant materials used in this study were cultivated French bean (*Phaseolus vulgaris* L.) landraces collected with permission from farmers and local custodians. Collection and experimental use of the plant materials complied with institutional and national guidelines governing plant genetic resources. The experiments were carried out following a randomized block design with two replications. Each replication had 22 plots, and each plot size is 1.35 m². The spacing for each variety was maintained at 45 cm x 15 cm for row-to-row and plant-to-plant. Each variety was grown under standard agronomic practices commonly used in common bean cultivation, along with plant protection measures.

Data were recorded for 11 agronomic traits; for each trait, 5 random samples from each genotype and replication were selected to obtain the required information. These traits were chosen according to the descriptions and guidelines specified by the PPV&FRA, 2001 DUS guidelines. The yield-related traits include plant height (cm) (PH), number of primary branches (NPB), number of secondary branches (NSB), number of pods per cluster (NPPC), number of pods per plant (NPPP), pod length (cm) (PL), number of seeds per pod (NSPP), seed index (g) SI, and seed yield per plot (g) (SYPP). The phenological traits, such as days to 50% flowering and days to maturity, were recorded per plot.

Variance analysis for all traits, correlation, and path coefficient analysis using replicated data were performed using the GREAPS software. The phenotypic and genotypic coefficients of variation were estimated using the method of [14]. Heritability was calculated using the method of [15], and expected genetic advancement under selection was calculated using the method of [16]. The genotypic and phenotypic correlation coefficients were calculated using the method of [17], and the partitioning of genotypic correlation coefficients into their direct and indirect effects was done using the method of [18]. Principal component analysis (PCA) was used to determine the contribution of each trait to the overall phenotypic variation. The relationship between the genotypes was also explored by performing PCA on

the standardised trait data using the *prcomp* function of the stats package. Principal component biplots were also generated using the *fviz_pca_biplot* function from the factoextra package [19].

The multi-trait genotype-ideotype distance index (MGIDI) was used to select superior genotypes based on their performance for multiple traits. The analysis was done using the metan R package (version 1.18.0) developed by Olivoto and Lúcio (2020) and R software (version 4.3.1). The MGIDI method consisted of the following steps: i) All traits were rescaled to a common range from 0 to 100 for the purpose of standardisation and comparison between the traits. ii) Ideotype was defined by the assignment of the desired target values for the traits. This represents the optimal combination of trait expressions for a genotype. iii) The distance between each genotype and the defined ideotype was calculated using factor scores derived from multivariate analysis. The MGIDI for the i th genotype was estimated as [20]:

$$MGIDI_i = \left[\sum_{j=1}^f (\gamma_{ij} - \gamma_j)^2 \right]^{0.5}$$

where γ_{ij} represents the score of the i th genotype in the j th factor, γ_j denotes the ideotype score for the j th factor, and f is the number of retained factors.

iv) The contribution of each factor to the MGIDI index was computed to assess the strengths and weaknesses of genotypes as:

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^f \sqrt{D_{ij}^2}}$$

where D_{ij} is the distance between the i th genotype and the ideotype for the j th factor. Lower contribution values indicate that the traits within a factor are closer to the ideotype, whereas higher values suggest traits that require improvement. This methodology facilitates simultaneous selection based on multiple traits and enables the identification of genotypes with overall superior performance and desirable trait combinations. Calculation of Smith Hazel index and simulation selection index was done through the use of the ‘metan’ package in R environment [20].

Results and discussion

Analysis of variation

The evaluation of genetic variation is the primary objective for the identification of divergent lines for hybridization to develop new cultivars in the common bean market-segmented lines. The genetic variation of seed yield and yield-related traits among twenty-two lines was illustrated in **Table 2**. The ANOVA shows the mean sum of the genotypes was a high degree of significance ($p < 0.01$ & $p < 0.05$) for all traits under study except the number of pods per cluster. These results indicate a high amount of genetic variation existing among the evaluated lines. These findings agree with those of [21, 3, 22] for seed yield and related traits in common bean.

Mean performance of common bean genotypes

The mean performance and trait expression range demonstrate phenotypic variation among genotypes. All traits under study show a broad range of mean performance, as illustrated in **Table 1**. Among them, the phonological traits, such as days to 50% flowering, ranged from 48.00 to 54.00, with a mean of 50.44, while days to maturity ranged from 80.00 to 94.00, with an average of 86.79. This phonological variation among genotypes reflects the same pattern of maturity duration, making them suitable for specific adoption in this region. These results align with [23, 24].

Compared with phonological traits, morphological traits showed greater variation. Plant height ranged from 34.14 cm to 162.04 cm, with a mean of 97.02 cm, suggesting a wide variation in growth habit among genotypes. While the number of primary branches ranges from 2.70 to 4.30, with an average of 3.36, the number of secondary branches ranges from 3.70 to 5.50 for men, with an average of 4.51, indicating differences in canopy architecture among the genotypes. These results align with [25].

On the other hand, yield component characteristics also showed significant variation. Seed yield per plot ranged from 71.00 to 217.50 g, with a mean of 120.06 g (**Fig 1**). The 100-seed weight ranged from 26.00 to 47.00 g, with an average of 35.71 g. The number of pods per cluster ranges from 1.70 to 2.30 pods with an average of 1.94, while pods per plant were within the ranges of 6.10 to 8.20 pods with an average of 7.05; likewise, pod length varied between 9.25 and 13.25 cm with an average of 11.08 cm and seeds per pod between 4.50 and 6.40 with an average of 5.28. Overall, the observed variation across traits suggests sufficient diversity for effective selection and breeding. Based on mean performance, Deep red kholar (217.5g), Luli (181.0g), Kholar light brown (158.5g), and Kholar Yellow large (153.5g) showed a high mean seed yield; hence, these lines are rare as candidate genotypes.

Estimation of genetic parameters

Estimates of genetic parameters for 22 common bean genotypes across 11 agronomic traits are presented in **Table 3**. The PCV and GCV values are considered low, moderate, or high if they are less than 10%,

between 10% and 20%, or greater than 20%, respectively, [14]. On the other hand, if the heritability value is less than 30, between 30 and 60, or greater than 60, it can be termed as low, moderate, and high, respectively [26]. The GAM values are classified as low (<10%), moderate (10%-20%), or high (>20%) [16].

Findings from the analysis of genetic parameters reveal information on the nature of genetic variation and phenotypic differences observed to be heritable. In the current study, variables such as plant height and seed yield per plot showed high GCV and PCV, indicating the presence of positive genetic variation. The number of primary and secondary branches and the seed index showed moderate GCV and PCV, suggesting relatively low environmental effects. These findings align with [27, 28] in common bean. In this study, all traits showed high heritability, except phonological traits and the number of pods per cluster, which showed low to moderate heritability. Such highly heritable characters indicate that their expression depends on genetic components and are thus very suitable for selection. These findings depend on [27] for seed yield and related traits in common bean.

Moreover, high-to-moderate GAM values were observed for all morphological and yield traits, except for the number of pods per cluster. Traits such as the number of primary and secondary branches, plant height, seed index, and seed yield per plot show high heritability and high GAM, suggesting that additive gene action plays a vital role in influencing these traits and that they can be used directly for selection in bean improvement. Recent studies [29, 30] highlight that selecting traits with both high heritability and GAM is effective. Traits such as number of pods per plant, pod length, and number of seeds per pod showed high heritability and moderate GAM, suggesting that these traits are governed by both additive and non-additive gene actions, yet selection is reliable. However, phonological traits and the number of pods per cluster have low heritability and low GAM. This indicates that these traits are strongly influenced by the environment. The findings agree with previous observations made [31].

Correlation studies

The correlation coefficients at both genotypic and phenotypic levels for eleven agronomic traits are presented in **Table 4**. Seed yield per plot demonstrated a positive and significant association with all morphological, yield-related, and phenological traits, except for days to 50% flowering at both genotypic and phenotypic levels. The number of pods per cluster showed a positive but non-significant association at the phenotypic level. The strong correlations observed at both levels indicate that these trait relationships are primarily governed by genetic factors rather than environmental influences. This suggests that improving these traits is likely to enhance seed yield. A high magnitude and significant positive correlation were observed between pod length and seed yield, indicating that genotypes with

longer pods tend to yield more. These findings are consistent with [32], who reported a strong association between pod length and seed yield in common bean. Additionally, a significant positive association was found between seed yield and days to maturity, suggesting that genotypes with a longer vegetative growth phase may possess greater yield potential. Similar results were reported [27] in common bean. The positive associations between seed yield and morphological traits (NPB, NSB, and PH) as well as yield-related traits (NPPP, NSPP, and SI) further suggest that efficient reproductive capacity is crucial for maximising seed yield [27]. Plant height showed a positive, significant association with the number of primary and secondary branches, days to maturity, and number of pods per plant at both the genotypic and phenotypic levels. This indicates that taller plants are associated with higher biological yield and greater yield potential, likely due to increased light interception and greater accumulation of biological yield. These results are consistent with previous reports suggesting that tall genotypes may contribute indirectly to yield performance [34]. Overall, these correlation studies identify plant height, number of pods per plant, pod length, and number of seeds per pod as key traits for improving seed yield.

Path analysis

Path analysis at the genotypic level for 22 common bean genotypes across 11 traits is presented in **Table 5**. Number of secondary branches, plant height, number of pods per cluster, pod length, and seed index showed a significant positive direct effect and a positive correlation with seed yield, suggesting that selection for these trait clusters is rewarding and yields higher yields. Similar findings were reported by [3] in common bean. Days to maturity showed a positive correlation with seed yield but a negative direct effect; these results align with those of [29]. The number of primary branches exhibits a strong positive association with seed yield, while there is a negative direct effect due to multicollinearity with secondary branches, which was confirmed by a variance inflation factor (VIF) value exceeding ten (**Fig. 2**). Hence, in this scenario, principal component analysis is an effective way to reduce the multicollinearity. This analysis suggests that the seed index is an important trait for seed yield, as it shows a strong positive direct effect.

Principal Component Analysis

The principal component analysis (PCA) of 22 French bean genotypes, based on 11 quantitative characters, showed significant variation among genotypes, as shown in **Table 6**. Altogether, eleven principal components were derived from PCA, of which the first four PCs had eigenvalues greater than 1 and accounted for 88.545% of the total variance. Following the recommendation of [36], PCs with eigenvalues less than 1 were excluded because they carried less information than the original variables. A similar finding was reported by [34, 35] in common beans.

The first principal component explained 51.183% of the total variability; therefore, it was identified as the most important component. Characters such as the number of primary and secondary branches, the number of pods per plant, panicle length, and the number of seeds per pod exhibited significant positive loadings on PC1, indicating that these characters accounted for the greatest variability and were therefore considered important yield-related traits. As mentioned by [36], if a factor has a loading value of ± 0.3 or greater, its statistical significance can be established and the amount of variation it creates can be revealed. The percentage contribution of PC2 was 14.866%, which was strongly influenced by days to flowering, maturity, and plant height, indicating the importance of phenology. Principal component three (PC3) accounted for 12.437% of the variance, with seed index and seed yield per plot contributing most. The PC4 had a 10.06% contribution and was influenced by the number of pods per cluster. These findings align with [37, 38]

The PCA biplot effectively clusters common bean genotypes based on their performance across the eleven traits, as shown in **Fig. 3**. Traits with vectors forming small angles are positively related. This is illustrated by the clustering of seed yield per lot, number of pods per plant, number of primary and secondary branches and seed index traits, indicating that genotypes with high pod number and weight also have high seed yields. Genotypes Deep red kholar and Luli appear far to the right of the Dim1 (PC1) axis, suggesting they perform well for yield traits such as pod length, number of primary and secondary branches, number of seeds per pod, and number of pods per plant. Genotypes Kholar medium brown and Kholar Dark brown occupy high positions on the Dim2 (PC2) axis, meaning that their DF (Days to Flowering) is greater, hence likely late-maturing genotypes. Genotypes Rutsu and Kholar white small: They are found opposite the majority of the traits' vectors, suggesting they are low-yielding or early-maturing genotypes.

Identification of close ideotypes in common bean by MGIDI index

The MGIDI Indexing is a highly reliable, multidimensional index designed to identify a genotype that closely matches the "ideotype" (ideal genotype). In this investigation, among 22 genotypes, Deep red kholar, TSG1, and Kholar Yellow large were found to be closest to the ideotypes at 15% selection intensity. The ranking of the common bean genotypes was based on MGIDI scores, as indicated in **Fig. 4** (red dots: selected; white dots: non-selected) and in supplementary Table 2. It is a theoretical model representing the ideal combination of all evaluated traits. Unlike traditional selection indices, which may be biased by multicollinearity, the MGIDI index uses factor analysis to achieve balanced selection [39].

Factor Analysis and Predicted Selection Gain:

The factor analysis of twenty-two French bean genotypes tested for eleven agronomic traits has clearly shown that there was an inherent pattern of variability that can be classified into four factors (FA1 to FA4), which have eigenvalues greater than one and account for a significant amount of variance, and the explained cumulative variance is 88.52%; it is illustrated in Supplementary **Table 3**. It is clear from this finding that the dataset's dimensionality could be reduced by about 12% or more, with no significant loss of information, while preserving highly explanatory traits. Calculation of factor loadings, which indicate the degree of correlation between individual traits and the factors to which they belong, was performed via an orthogonal rotation [40]. Factor loading values ranged from -1 to +1 and indicate the strength and direction of the relations between the studied traits and factors [41]. Varimax rotation yielded the mean communality (h) equal to 0.88 and ranging from 0.72 for plant height to 0.96 for the number of primary branches (**supplementary Table 3**). Factor 1 correlates with morphological traits (NPB, NSB, PH, and NPP); factor 2 is associated with phenology (days to flowering and maturity); factor 3 is connected to yield-related traits (PL, SI, NSPP, and SYPP); and factor 4 is associated with NPPC. These findings are in complete agreement with [6] in sesame and [13] in sugarcane.

The expected genetic gains and selection differentials (SD) for 11 agronomic traits across 22 genotypes are presented in **Table 7**. The MGIDI analysis demonstrated a strong and desirable response across all evaluated traits, indicating effective identification of superior genotypes. The overall success rate exceeded 80%, reflecting the precision of selection for targeted traits. The SD ranged from -0.270% (days to flowering) to 32.638% (seed yield per plot), with a mean of 13.146%, and all traits except days to flowering exhibited positive SD values. Correspondingly, the expected selection gains varied, ranging from -0.168% (days to flowering) to 32.356% (seed yield per plot), with a mean of 12.42%. Again, seed index proved to be a reliable trait for common bean yield improvement, as it showed a high degree of SD and high selection gains after plant height; these results are further confirmed by path analysis in this study.

The MGIDI strengths and weaknesses plot (**Fig. 5**) shows the relative contribution of each factor (FA1–FA4) to the selected genotypes (Deep red kholar, TSG1, and Kholar Yellow large), where factors closer to the centre indicate higher contribution (weakness) and those near the edge indicate lower contribution (strength), with the dashed line representing equal contribution [20]. TSG1 was characterized by a high contribution of FA2 as a sign of weakness in the traits of phenology, whereas strength was found in its yield-related traits (FA1, FA3, and FA4). Deep red kholar showed relatively higher contribution from FA3, suggesting limitations in seed-related traits but better performance in other factors. Kholar Yellow large had a high FA4 contribution, suggesting it is weak for traits related to the number of pods per

cluster. Overall, each genotype displayed distinct strengths and weaknesses, suggesting the potential for complementary selection and hybridization.

Comparison of Multi-Trait Selection Indices for the identification of promising common bean genotypes

Comparison of 22 French bean genotype selection processes across 11 agronomic traits using the Simulation Selection Index, Smith–Hazel Index, and MGIDI revealed differences in genotype selection and highlighted the importance of the underlying methodologies. The comparative data are illustrated in Table 8. There was also a significant degree of similarity between the Simulation Selection Index (Table 10) and the Smith–Hazel Index (Fig. 6).

Genotypes such as Deep red kholar, Kholar light brown, and Kholar medium brown were ranked among the top three promising lines in both the simulation index and the Smith-Hazel indices. The reason for this ranking lies in the use of the linear approach to indexation, since ranking depends on trait coefficients and variance-covariance properties. In both approaches, priority was given to important pod-related traits, such as NSB, NPPC, NPPP, and NSPP, indicating that the selection process relied primarily on the performance of specific traits. However, MGIDI yielded completely different results, selecting other genotypes, such as Deep red kholar, TSG1, and Kholar Yellow large, as among the best. The difference lies in the application of factor analysis, which enabled selecting genotypes based on their proximity to an ideal type.

The simulation selection index showed the largest positive weight for NSPP (9.36), then NSB (5.56), NPPP (5.45), and NPPC (4.02). On the other hand, some parameters like PL (−3.255) and NPB (−5.944) were assigned negative weights, while others, like SYPP (0.92), contributed a little positive weight (**Table 9**). From the assignment of the relatively smaller weight for yield parameters, one can observe that the process of genotype selection was based more on pod parameters than on seed yield itself. In contrast, path and factor analyses identified seed index (SI) and yield-related traits as more reliable selection criteria due to their higher heritability, accuracy, and genetic control. However, in the simulation index, the lower weight of these traits suggests their limited direct influence on genotype ranking.

Genotype Deep red kholar demonstrated superiority across all selection methods, indicating its consistency and performance. Genotypes such as Kholar Yellow large and TSG1, selected solely through the MGIDI method, demonstrate the effectiveness of selecting an ideotype, where the balance of traits is assured. Generally, although the simulated and Smith-Hazel selection methods are efficient for selecting specific traits, the MGIDI selection method has proved to be the best for multi-trait selection due to its

comprehensiveness. Thus, a combination of MGIDI and other indices can increase selection efficiency and select genotypes with good yield and quality performance.

Conclusion

This research showed that there is considerable genetic diversity among common bean varieties in yield and related characters. This shows great scope for selecting and improving common bean lines. The high heritability and genetic advance for characters such as plant height, branch number, seed index, and seed yield per plot indicate that dominance is absent and that genes act additively. Therefore, these characters can be used for direct selection. Correlation and path analysis indicated that pod length, number of secondary branches, plant height, and seed index contribute greatly towards seed yield. Principal Component Analysis also confirmed that yield-associated traits accounted for most of the variability, whereas MGIDI-assisted multiple trait selection enabled the efficient identification of superior genotypes with optimal performance. Among the genotypes evaluated, Deep red kholarwas was found to be the most promising across almost all selection methods, followed by Luli, Kholar light brown, Kholar medium brown, TSG1, and Kholar Yellow large, which are potential candidates for further breeding programs. As a result, it can be concluded that the combination of genetic information, multivariate techniques, and selection criteria was very useful in selecting high-yielding genotypes.

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Author Contributions: MJL conducted the field experiment, HPC guided the whole experiment, and DP did the data analysis and manuscript preparation. All authors approve the manuscript for publication.

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Data availability: The datasets generated and/or analysed during the current study are available from the corresponding author upon reasonable request. All data supporting the findings of this study are included within the article and its supplementary materials.

Declarations

Consent to Publish:

The authors declare that they consent to the publication of this manuscript.

Consent to Participate:

Not applicable.

Ethics Approval:

The study involved cultivated plant materials (*Phaseolus vulgaris* L.) collected from different locations in Nagaland, India. Permission for collection of plant materials and for conducting the field experiment was obtained from the respective farmers/landowners and local authorities where applicable. The field

experiment was conducted at the Experimental Farm, Department of Genetics and Plant Breeding, School of Agricultural Sciences, Nagaland University, Medziphema, Nagaland, India. All experimental research and field studies on plants were carried out in accordance with relevant institutional, national, and international guidelines and legislation for the conservation and use of plant genetic resources. The study complied with the guidelines of Nagaland University and the applicable regulations governing the collection and use of cultivated plant materials.

Clinical Trial Registration:

Not applicable. This study is not a clinical trial.

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Fig 1. Mean performance of 22 primitive common bean genotypes for seed yield

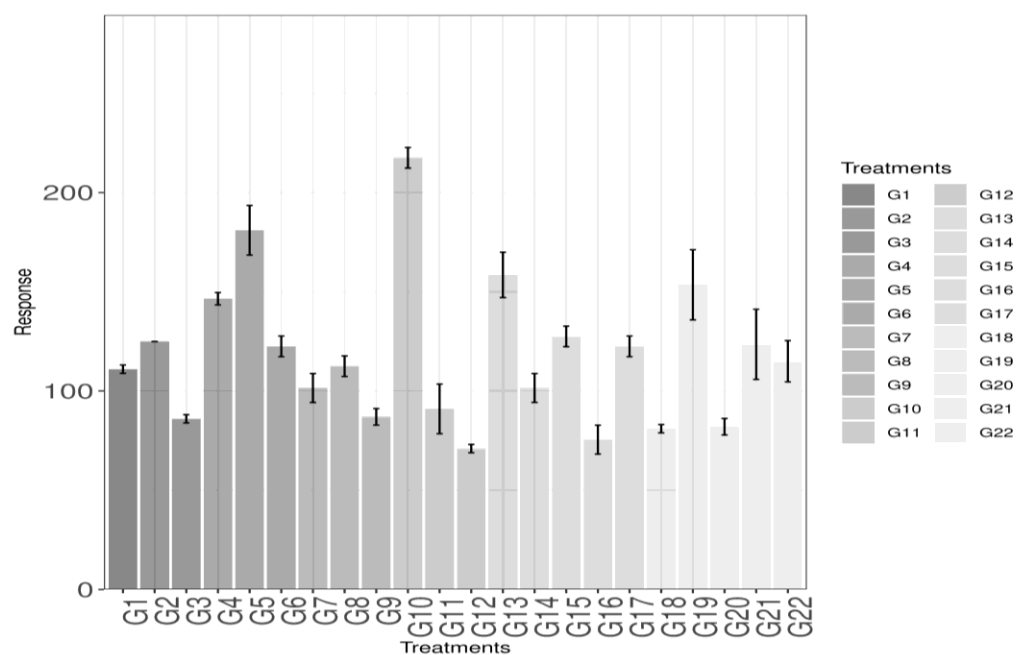


Fig 2. Variance inflation factor (VIF) eleven agronomic traits among 22common bean genotypes. Acronyms for traits are defined in Table 2.

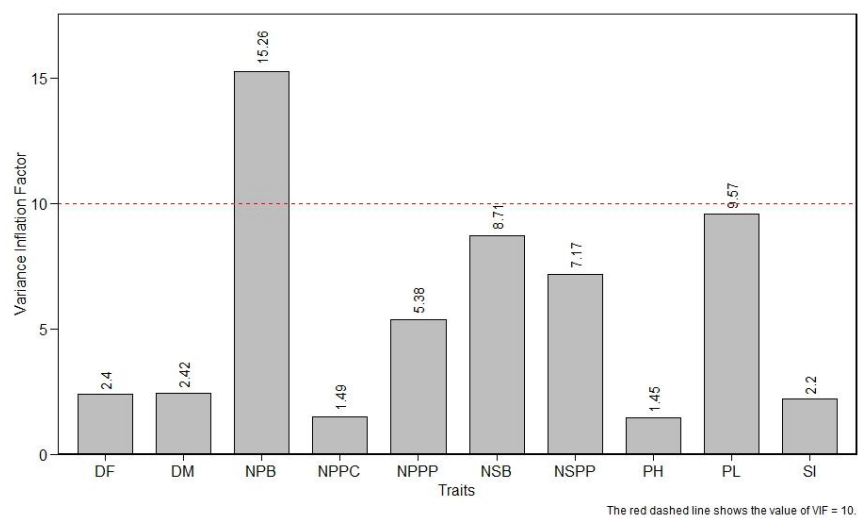


Fig 3. PCA Biplot illustrating trait loadings, genotype allocation pattern, and genotype-trait relationships.

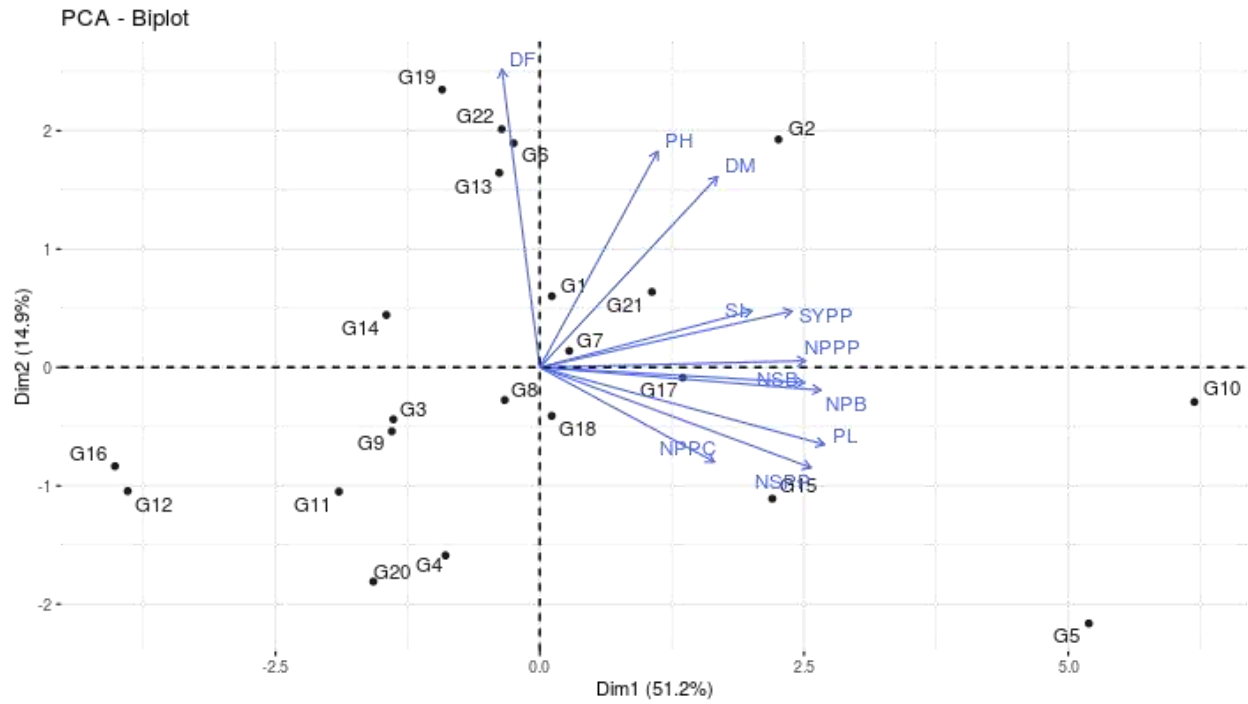


Fig. 4. French bean accessions rankings according to the MGIDI index. Red dots indicate selected accessions, black dots represent unselected ones, and the red circle denotes the cutoff defined by selection intensity.

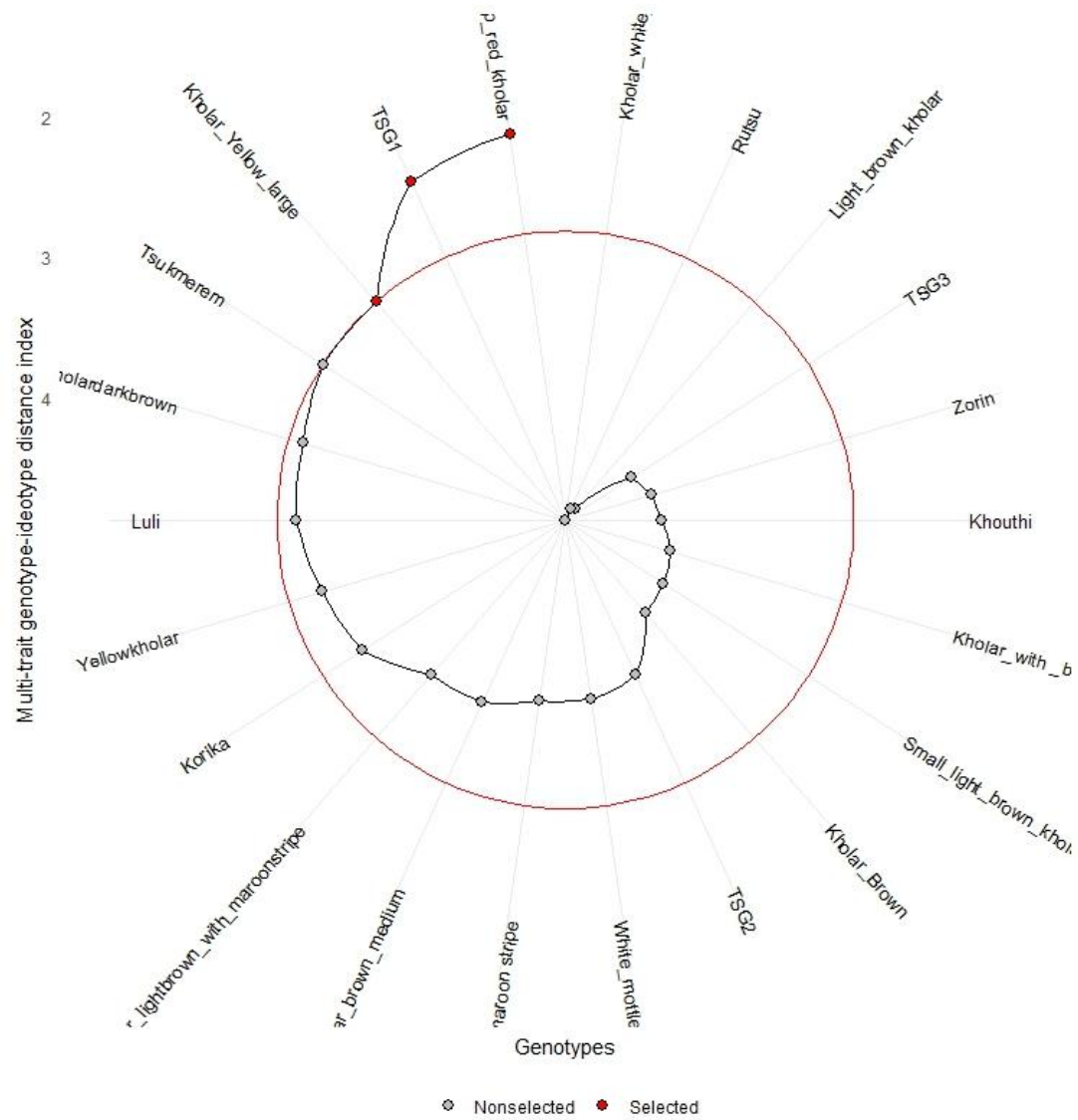


Fig 5. The strengths and weaknesses profile of selected genotypes under study.

Strengths and weaknesses view

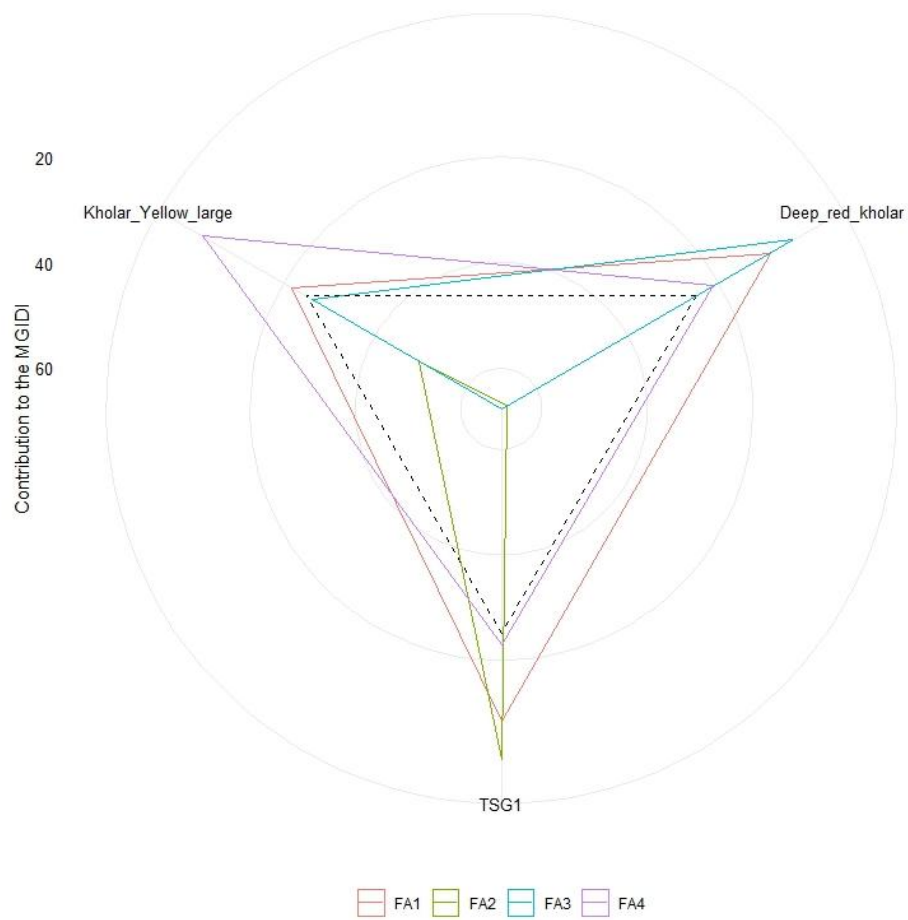


Fig. 6. French bean accessions rankings according to the Smith–Hazel Index.

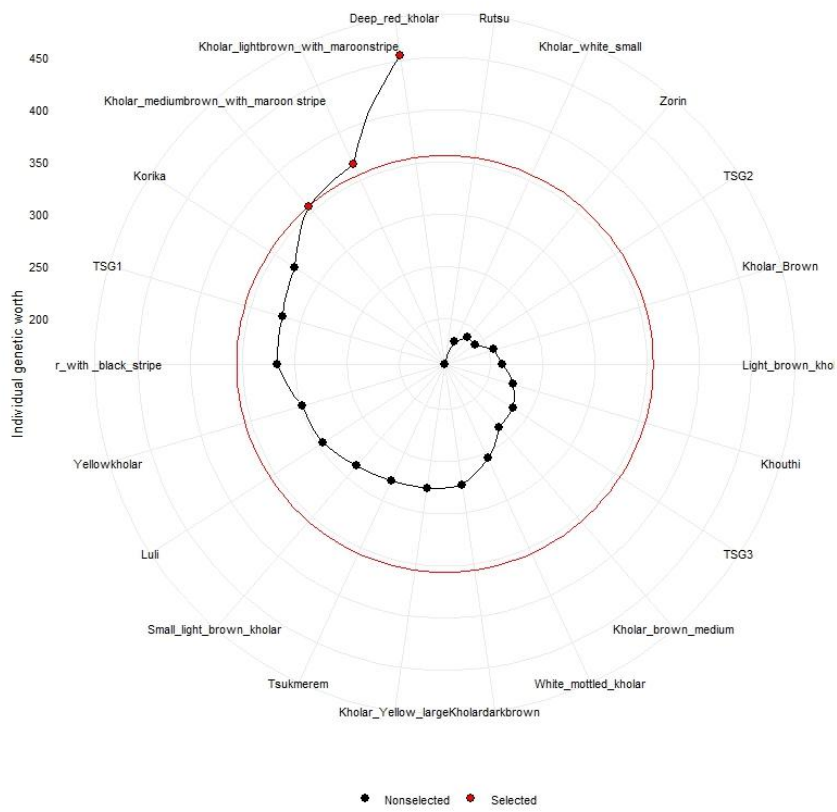


Table 1. Details of the experimental material

Genotypes	Name of genotypes	Plant type	Place of collection
G1	White mottled kholar	Pole type	Tuensang, Nagaland
G2	TSG1	Pole type	Tuensang, Nagaland
G3	TSG2	Pole type	Tuensang, Nagaland
G4	TSG3	Bush type	Tuensang, Nagaland
G5	Luli	Bush type	Yaongyimsen, Nagaland
G6	Tsukmerem	Pole type	Yaongyimsen, Nagaland
G7	Kholar with black stripe	Pole type	Tuensang, Nagaland
G8	Small light brown kholar	Pole type	Tuensang, Nagaland
G9	Light brown kholar	Pole type	Tuensang, Nagaland
G10	Deep red kholar	Pole type	Tuensang, Nagaland
G11	Khouthi	Pole type	Zunheboto, Nagaland
G12	Kholar white small	Pole type	Kohima, Nagaland
G13	Kholar light brown with maroon stripe	Pole type	Kiphire, Nagaland
G14	Kholar brown medium	Pole type	Kiphire, Nagaland
G15	Kholar Yellow large	Pole type	Medziphema, Nagaland
G16	Rutsu	Bush type	Kohima, Nagaland
G17	Korika	Pole type	Meghalaya
G18	Kholar Brown	Pole type	Mokokchung, Nagaland
G19	Kholar medium brown with maroon stripe	Pole type	Mokokchung, Nagaland
G20	Zorin	Pole type	Mizoram
G21	Yellow Kholar	Pole type	Cheesore, Nagaland
G22	Kholar Dark brown	Pole type	Kiphire, Nagaland

Table 2. ANOVA for eleven yield and yield contributing traits in 22 French bean genotypes

Character	Mean Squares			CD at 5 %	CV (%)
	Replication df(1)	Treatments df(21)	Error df(21)		
Seed yield per plot (g)	227.273	2649.390**	22.892	9.95	4.059
Days to 50% flowering	0.023	9.473*	3.594	3.943	3.763
No. of primary branches	0.015	0.481**	0.018	0.282	4.05
No. of secondary branches	0.481	0.599**	0.054	0.484	5.17
Days to maturity	4.455	51.797*	23.121	10.00	5.541
Plant height (cm)	0.03	2887.348**	1.194	2.273	1.128
No. of pods per cluster	0.033	0.052	0.033	0.376	9.343
No. of pods per plant	0.524	0.721**	0.074	0.566	3.869
Pod length (cm)	0.1	1.907**	0.079	0.584	2.538
No. of seeds per pod	0.154	0.445**	0.056	0.494	4.519
seed index (g)	0.091	67.437**	1.329	2.397	3.235

** = Significant at 1 % and * = Significant at 5 % level of significance

Table 3. Analysis of genetic parameters for eleven agronomic traits among 22 French bean genotypes

Trait	Genotypic variance	Phenotypic variance	Env. variance	PCV (%)	GCV (%)	heritability	Genetic advance(%) (i=5%)
Days to 50% flowering	2.94	6.53	3.59	5.07	3.40	0.45	4.70
No. of primary branches	0.231	0.25	0.02	14.93	14.38	0.93	28.54
No. of secondary branches	0.272	0.33	0.05	12.69	11.59	0.84	21.81
Days to maturity	14.338	37.46	23.12	7.05	4.36	0.38	5.56
Plant height (cm)	1443.08	1444.27	1.19	39.21	39.20	1.00	80.71
No. of pods per cluster	0.009	0.04	0.03	10.65	5.03	0.22	4.90
No. of pods per plant	0.324	0.40	0.07	8.96	8.08	0.81	15.02
Pod length (cm)	0.914	0.99	0.08	9.01	8.64	0.92	17.08
No. of seeds per pod	0.195	0.25	0.06	9.52	8.39	0.78	15.22
seed index (g)	33.054	34.38	1.33	16.45	16.13	0.96	32.59
Seed yield per plot (g)	1313.25	1336.14	22.89	31.01	30.75	0.98	62.79

Table 4: Genotypic and Phenotypic correlation of eleven agronomic traits among 22 common bean genotypes, Acronyms for traits are defined in Table 2.

Phenotypic Correlation	Trait	DF	NPB	NSB	DM	PH	NPPC	NPPP	PL	NSPP	SI	SYPP	Genotypic Correlation
	DF	1	-0.355*	-0.295*	0.21	0.269*	-0.334*	-0.272*	-0.253*	-0.361*	0.15	0.001	
	NPB	-0.169	1	0.125	0.638**	0.35*	0.746**	0.955**	0.718**	0.668**	0.425**	0.586**	
	NSB	-0.096	0.942**	1	0.576**	0.284*	0.832**	0.931**	0.681**	0.625**	0.404*	0.541**	
	DM	0.512**	0.406*	0.421**	1	0.468**	0.014	0.593**	0.525**	0.416**	0.391*	0.494**	
	PH	0.175	0.335*	0.258*	0.286*	1	-0.075	0.462**	0.171	0.101	0.215	0.408*	
	NPPC	-0.013	0.33*	0.228*	0.214	-0.043	1	0.856**	0.124	0.125	0.205	0.303*	
	NPPP	-0.052	0.883**	0.81**	0.367*	0.412**	0.28*	1	0.698**	0.694**	0.374*	0.538**	
	PL	-0.171	0.646**	0.579**	0.361*	0.167	0.426**	0.586**	1	0.236	0.682**	0.761**	
	NSPP	-0.211	0.58**	0.494**	0.283*	0.089	0.409**	0.479**	0.923**	1	0.735**	0.809**	
	SI	0.056	0.388*	0.354*	0.238*	0.212	0.077	0.305*	0.64**	0.607**	1	0.876**	
	SYPP	-0.003	0.55**	0.47**	0.286*	0.404*	0.175	0.464**	0.723**	0.694**	0.854**	1	

Table 5. Direct and indirect effects of yield components on seed yield at genotypic level in 22 common bean genotypes, Acronyms for traits are defined in Table 2.

	DF	NPB	NSB	DM	PH	NPPC	NPPP	PL	NSPP	SI	r _g
DF	-0.243	0.111	-0.129	-0.012	0.106	-0.037	0.066	-0.087	0.1	0.126	0.001
NPB	0.086	-0.313	0.44	-0.037	0.138	0.082	-0.231	0.247	-0.184	0.358	0.586
NSB	0.072	-0.315	0.437	-0.033	0.112	0.091	-0.226	0.235	-0.172	0.34	0.541
DM	-0.051	-0.2	0.252	-0.057	0.184	0.114	-0.144	0.181	-0.115	0.33	0.494
PH	-0.065	-0.109	0.124	-0.027	0.394	-0.008	-0.112	0.059	-0.028	0.181	0.408
NPPC	0.081	-0.233	0.364	-0.06	-0.03	0.109	-0.207	0.387	-0.281	0.173	0.303
NPPP	0.066	-0.299	0.407	-0.034	0.182	0.094	-0.242	0.241	-0.191	0.315	0.538
PL	0.061	-0.225	0.298	-0.03	0.067	0.123	-0.169	0.345	-0.284	0.575	0.761
NSPP	0.088	-0.209	0.273	-0.024	0.04	0.111	-0.168	0.354	-0.276	0.619	0.809

SI	-0.036	-0.133	0.176	-0.022	0.085	0.022	-0.091	0.235	-0.203	0.843	0.876
Residual effect square=0.1352											

Table 6. Principal component analysis for eleven agronomic traits among 22 French bean genotypes

variables	PC1	PC2	PC3	PC4
Days to 50% flowering	-0.051	0.66	-0.067	0.364
No. of primary branches	0.375	-0.051	0.305	-0.181
No. of secondary branches	0.354	-0.034	0.327	-0.155
Days to maturity	0.238	0.422	0.195	0.392
Plant height (cm)	0.158	0.478	0.116	-0.419
No. of pods per cluster	0.233	-0.209	0.2	0.608
No. of pods per plant	0.355	0.015	0.342	-0.179
Pod length (cm)	0.38	-0.171	-0.194	0.161
No. of seeds per pod	0.362	-0.222	-0.263	0.144
seed index (g)	0.284	0.126	-0.554	-0.077
Seed yield per plot (g)	0.337	0.125	-0.416	-0.165
Eigenvalue	5.63	1.635	1.368	1.107
percentage of variance	51.183	14.866	12.437	10.06
cumulative percentage of variance	51.183	66.049	78.486	88.545

Table7. Evaluation of selection differential and genetic gains for eleven agronomic traits among 22 French bean genotypes, Acronyms for traits are defined in Table 2.

VAR	Factor	Xo	Xs	SD	SDperc	h2	SG	SGperc	sense	goal
NPB	FA1	3.345	3.911	0.565	16.902	0.962	0.544	16.258	increase	100
NSB	FA1	4.505	5.107	0.602	13.368	0.909	0.548	12.157	increase	100
PH	FA1	96.921	123.246	26.324	27.161	1.000	26.314	27.149	increase	100
NPPP	FA1	7.036	7.662	0.625	8.887	0.897	0.561	7.974	increase	100
DF	FA2	50.386	50.250	-0.136	-0.271	0.621	-0.085	-0.168	increase	0
DM	FA2	86.773	89.298	2.525	2.910	0.554	1.398	1.611	increase	100
PL	FA3	11.061	12.345	1.283	11.602	0.959	1.230	11.123	increase	100
NSPP	FA3	5.259	5.760	0.501	9.533	0.873	0.438	8.323	increase	100
SI	FA3	35.636	42.528	6.892	19.339	0.980	6.756	18.958	increase	100
SYPP	FA3	117.864	156.331	38.468	32.638	0.991	38.135	32.356	increase	100
NPPC	FA4	1.936	1.985	0.049	2.532	0.376	0.018	0.953	increase	100
		variable	min	max	mean	sum	sense			
		SDperc	-0.271	32.638	13.146	144.601	increase			
		SGperc	-0.168	32.356	12.427	136.693	increase			

Table 8. Comparative selected genotypes across various selection indexes

Simulation Selection Index	Smith–Hazel Index	MGIDI	Common genotypes
G10, G13 and G19	G10, G13 and G19	G15, G10 and G2	G10

Table 9. Selection index coefficients for eleven agronomic traits among 22 French bean genotypes

Trait	Coefficients
Days to 50% flowering	0.240
No. of primary branches	-5.944
No. of secondary branches	5.679
Days to maturity	0.324
Plant height (cm)	1.048
No. of pods per cluster	4.028
No. of pods per plant	5.454
Pod length (cm)	-3.255
No. of seeds per pod	9.360
seed index (g)	1.452
Seed yield per plot (g)	0.920

Table 10. Selection Criterion or Index values of 22 French bean genotypes

Individuals	Index scores	Individuals	Index scores
Deep red kholar	554.316	Kholar Dark brown	366.946
Kholar light brown with maroon stripe	461.269	White mottled kholar	356.308
Kholar medium brown with maroon stripe	450.165	Kholar brown medium	333.353
TSG1	421.187	TSG3	327.82
Korika	411.624	Khouthi	326.844
Yellow Kholar	408.501	Light brown kholar	314.749
Kholar with black stripe	400.085	TSG2	312.853
Luli	393.383	Kholar Brown	294.147
Small light brown kholar	384.818	Zorin	291.882
Tsukmerem	372.782	Kholar white small	276.873
Kholar Yellow large	367.016	Rutsu	246.713

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