Print ISSN : 0972-8813
e-ISSN : 2582-2780

[Vol. 24(1) January-April 2026]

Pantnagar Journal of Research

(Formerly International Journal of Basic and Applied Agricultural Research ISSN : 2349-8765)

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https://doi.org/10.67063/pjr.vol.24.issue.01.06

Genetic divergence and yield trait impact in French bean (*Phaseolus vulgaris* L.)

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ABSTRACT: The present investigation was undertaken to study Genetic Divergence and Yield Trait Impact in French Bean (*Phaseolus vulgaris* L.). The experiment was conducted at the Vegetable Research and Demonstration Block, Department of Vegetable Science, College of Horticulture, VCSG Uttarakhand University of Horticulture and Forestry, Bharsar, Pauri Garhwal (Uttarakhand). A total of 24 genotypes were evaluated in a randomized block design with three replications. Genotypic correlation coefficients were estimated to determine associations among yield and its component traits, while path coefficient analysis was employed to partition correlations into direct and indirect effects on seed yield per plant. Genetic divergence among genotypes was grouped the genotypes into four distinct clusters, indicating substantial genetic variability. The maximum inter-cluster distance was observed between Cluster I ($D^2 = 2.920$) and Cluster III ($D^2 = 5.571$), reflecting the highest level of genetic divergence. Seed weight, number of primary branches per plant, and seed yield per plot exhibited strong positive direct effects on seed yield per plant and this shows their importance as selection criteria. The identified genetically divergent clusters and key yield-influencing traits can be effectively utilized in future French bean breeding programmes for yield improvement.

Keywords: Components, Correlation analysis, Genetic divergence, French bean, Path coefficient analysis, Yield

French bean (*Phaseolus vulgaris* L.) is one of the most important grain and vegetable legumes cultivated across temperate, subtropical, and tropical regions of the world. It is valued for its tender green pods and dry seeds, which are rich sources of protein, dietary fibre, vitamins, and essential minerals, thereby contributing significantly to nutritional security and farm income (Singh, 2001; Beebe *et al.,* 2013).

Despite its economic importance, the productivity of French bean remains relatively low, largely due to a narrow genetic base and the complex inheritance of yield and its component traits. Seed yield is a polygenic trait governed by several interrelated morphological and physiological characters, whose expression is strongly influenced by environmental conditions (Rana *et al*., 2015). Consequently, direct selection for yield alone is often ineffective, necessitating an understanding of the relationships among yield-contributing traits.

Correlation analysis provides information on the degree and direction of association among characters but does not reveal their true cause effect relationships (Falconer and Mackay, 1996). Path coefficient analysis, originally proposed by Wright (1921) and later refined by Dewey and Lu (1959), addresses this limitation by partitioning correlation coefficients into direct and indirect effects, thereby identifying traits that exert a real and substantial influence on yield. The usefulness of correlation and path analysis in defining effective selection criteria for yield improvement in French bean and related legumes has been well documented (Dutta *et al*., 2018; Santos *et al*., 2017).

Genetic divergence analysis using Mahalanobis D^2 statistics further complements these approaches by assessing genetic diversity and classifying genotypes into distinct clusters to identification of genetically divergent parents is essential for exploiting heterosis and generating broad variability in segregating

populations (Singh, 2001). However, information integrating genetic divergence, character association, and path coefficient analysis in French bean under the mid-hill agro-climatic conditions of Uttarakhand is limited. The unique environmental conditions of this region, characterized by moderate temperatures and variable rainfall, may significantly influence trait expression and interrelationships, making region-specific evaluation essential. Therefore, the present study was undertaken to analyze genetic divergence, correlation, and direct and indirect effects of yield-related traits in French bean genotypes under mid-hill conditions of Uttarakhand, with the objective of identifying key selection traits and genetically diverse parents for future breeding programmes.

MATERIALS AND METHODS

The present investigation was carried out during the kharif season of 2018-2019 at the Vegetable Research and Demonstration Block, Department of Vegetable Science, College of Horticulture, VCSG Uttarakhand University of Horticulture and Forestry, Bharsar, Pauri Garhwal, Uttarakhand. The experimental site represents the mid-hill agroclimatic conditions of Uttarakhand, characterized by moderate temperature and variable rainfall, and is well suited for French bean cultivation.

A total of 24 French bean genotypes, comprising released varieties and germplasm accessions, were evaluated during the cropping season. The experiment was laid out in a Randomized Block Design (RBD) with three replications. The plots of size 3m × 1m and each genotype was grown in individual plots at the spacing 100cm × 50cm. Observations were recorded on growth, phenological, yield, and quality-related traits. The characters studied included days to germination, days to first flowering, days to 50% flowering, days to first harvest, pod maturity duration, plant height (cm), number of primary branches per plant, number of pods per plant, pod length (cm), pod diameter (cm), number of seeds per pod, average pod weight (g), 100-seed weight (g), seed yield per plant (g), seed yield per plot (kg), and protein content (%). Observations were recorded from five randomly selected plants in each plot, and the mean values were used for statistical analysis. Protein content of dry seeds was determined by estimating the nitrogen content as per the modified Kejldhal's method (Jackson, 1965) and multiplying it with the factor 6.25 (Dubetz and Wells, 1968) and expressed on percent basis for each genotype.

Genotypic correlation coefficients were computed to assess the association among different traits following the procedure outlined by Al-Jibouri *et al.* (1958). Path coefficient analysis was performed according to the method suggested by Wright (1921) and elaborated by Dewey and Lu (1959) to partition correlation coefficients into direct and indirect effects on seed yield per plant. Genetic divergence among genotypes was estimated using Mahalanobis D^2 statistics (Mahalanobis, 1936), and clustering of genotypes was carried out using Tocher's method to determine the pattern of genetic diversity. All statistical analyses were performed using SPSS and R software.

RESULTS AND DISSCUSSION

The genetic divergence analysis based on Mahalanobis D^2 statistics grouped the 24 French bean genotypes into four distinct clusters (Table 1), indicating the presence of substantial genetic variability among the evaluated germplasm. Cluster IV accommodated the maximum number of genotypes (8), followed by Cluster III (7) and Cluster II (5), while Cluster I contained the minimum number of genotypes (4). The distribution of genotypes across clusters irrespective of their geographic origin suggests that genetic constitution rather than geographical collection influenced cluster formation, a trend widely reported in French bean diversity studies (Verma *et al*., 2014).

The average intra-cluster distances were lower than the corresponding inter-cluster distances, reflecting greater homogeneity within clusters and pronounced divergence among clusters. Cluster III exhibited the lowest intra-cluster distance (2.598), indicating close genetic similarity among its genotypes, whereas Cluster I recorded the highest intra-cluster distance

(2.920), suggesting comparatively greater variability within that cluster. Similar patterns of intra-cluster variation have been reported in D^2-based diversity analyses of common bean germplasm (Kumar, 2024).

Analysis of inter-cluster distances revealed varying degrees of genetic divergence among clusters. The maximum inter-cluster distance was observed between Cluster I and Cluster III (5.571), followed by Cluster I and Cluster IV (4.970) and Cluster I and Cluster II (4.853), indicating that genotypes belonging to these clusters are genetically most divergent. In contrast, the minimum inter-cluster distance occurred between Cluster II and Cluster III (3.758), reflecting closer genetic affinity between these groups. High inter-cluster distances are particularly important for breeding programmes, as crosses between genetically divergent parents are more likely to generate higher heterosis and wider variability in segregating populations (Chhetri *et al*., 2025).

Overall, the clustering pattern and magnitude of D^2 values confirm the existence of wide genetic divergence among the studied French bean genotypes, highlighting the availability of a broad genetic base that can be effectively exploited for selection and hybridization aimed at yield improvement (Verma *et al.,* 2014).

Mean Performance: The cluster mean analysis revealed substantial variation among the four clusters for all sixteen characters studied, confirming the presence of wide genetic diversity among the French bean genotypes (Fig. 2). Differences in cluster means indicate the relative contribution of component traits to genetic divergence and their potential influence on yield expression, as commonly reported in multivariate diversity studies of grain legumes (Mahalanobis, 1936; Singh, 2001).

Cluster I recorded the lowest mean values for days to germination, days to 50% germination, days to first flowering, and days to 50% flowering, indicating its association with earliness. This cluster also exhibited the highest mean values for number of primary branches per plant, seed weight, protein content, seed yield per plant, and seed yield per plot. The superior yield performance of Cluster I may be attributed to the combined effect of earliness and favourable expression of yield-contributing traits, which has been reported to enhance productivity in French bean and related legumes (Dewey and Lu, 1959; Dutta *et al.,* 2018).

Cluster II showed moderate mean performance for most characters and recorded higher values for plant height, pod length, and number of seeds per pod. However, seed yield per plant and per plot were lower compared to Cluster I, suggesting that individual component traits alone may not directly

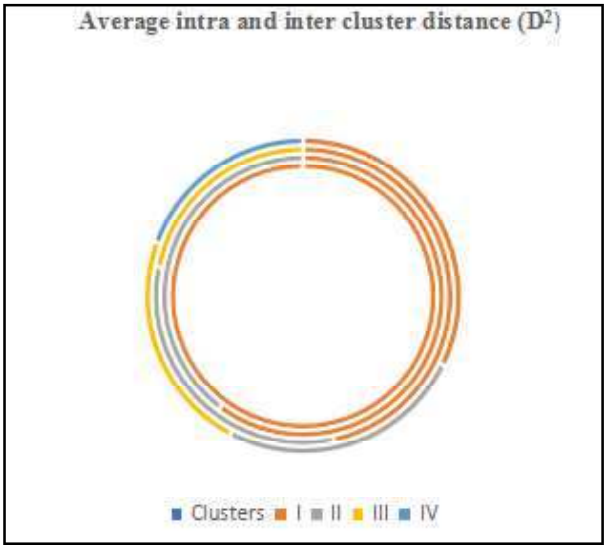

Fig. 1: Average intra and inter cluster distance (D^2)

Table 1: Clustering pattern of 24 genotypes of French bean on the basis of genetic divergence

Clusters	No. of genotypes	Genotype name
I	4	Lakshmi, LC-2, Harsil LC-1, LC-1
II	5	IC-049810, IC-199211, EC-755542, IC-199208, EC- 755484
III	7	EC-755510, Solan LC-1, Bean No.-2, IC-84337, EC- 755478, EC-755480, IC-84376
IV	8	755444, EC-755508EC-755509, EC- 755455, EC-755477

translate into higher yield unless supported by other complementary traits. Similar observations have been reported in earlier studies on French bean (Santos *et al.,* 2017).

Cluster III was characterized by relatively later flowering, as indicated by higher mean values for days to first flowering and days to 50% flowering. Although this cluster exhibited a shorter pod set to pod maturity duration, it recorded the lowest seed yield per plant and per plot. The lower yield observed in this cluster may be associated with less favourable combinations of yield-contributing traits rather than any single physiological limitation, and therefore warrants further investigation.

Cluster IV represented late-flowering genotypes and exhibited comparatively higher plant height and moderate average pod weight. Seed yield per plant and per plot were second highest after Cluster I, indicating that delayed phenology does not necessarily limit yield potential when supported by favourable yield attributes. Such genotypes may be useful in breeding programmes aimed at broadening the genetic base and improving yield stability (Singh, 2001; Beebe *et al*., 2013).

Overall, the marked differences in cluster means for yield and related traits suggest that genotypes from genetically divergent clusters, particularly Cluster I in combination with Cluster III or Cluster IV, could be exploited in hybridization programmes to generate wider variability and improved yield potential. However, a more definitive understanding of trait contributions to seed yield requires explicit integration of correlation and path coefficient analyses, including the magnitude of direct and indirect effects of individual traits. The absence of detailed discussion on these relationships represents a limitation of the present study and highlights the need for their comprehensive interpretation alongside cluster mean performance.

CONCLUSION

Based on cluster mean performance, Cluster I emerged as the most promising group, characterized by earliness, higher number of primary branches, greater seed weight, superior protein content, and maximum seed yield per plant and per plot. These traits—particularly seed weight, number of branches per plant, and earliness parameters should be given priority as key selection criteria for yield

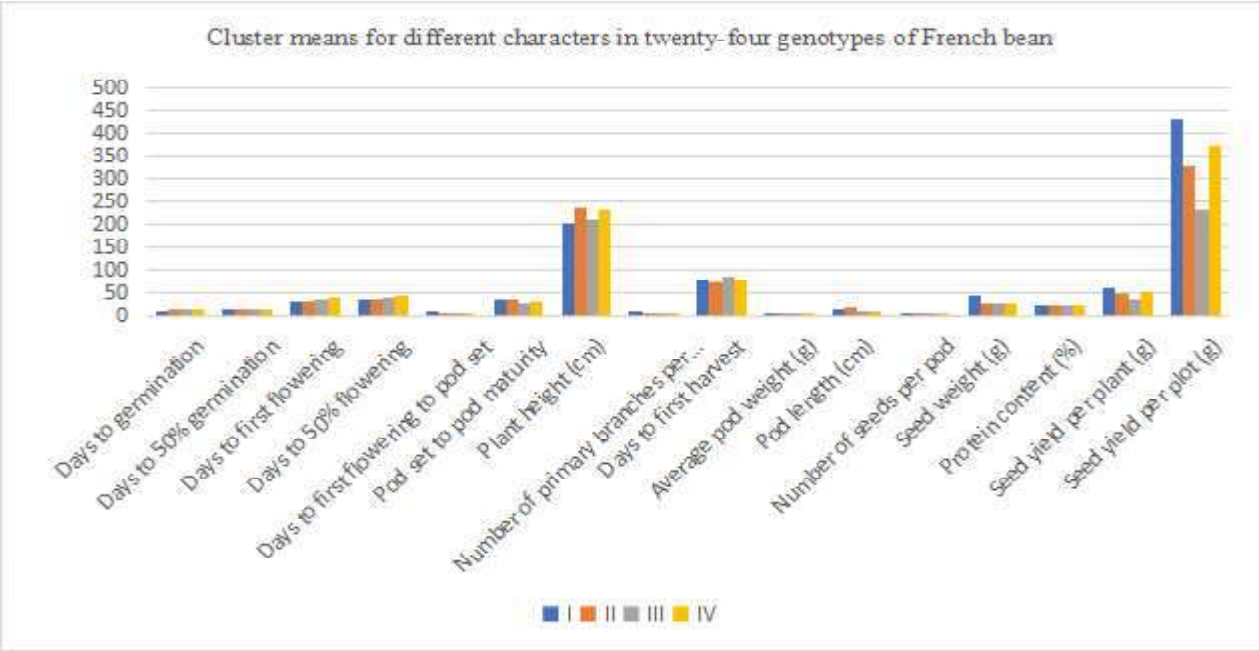

Fig. 2: Cluster means for different characters in twenty-four genotypes of French bean

improvement in French bean. Cluster IV, despite its relatively late flowering, also exhibited high yield potential and may serve as a valuable source of favorable yield attributes. Considering the magnitude of inter-cluster divergence and complementary trait expression, genotypes belonging to Cluster I in combination with those from Cluster III or Cluster IV are recommended for hybridization programmes. Such crosses are expected to generate greater heterosis and wider variability in segregating generations, facilitating the development of high-yielding and nutritionally superior French bean varieties. Overall, the findings provide clear trait-based selection guidelines and parent combinations that can be effectively utilized in future French bean breeding efforts.

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Received: December 27, 2025
Accepted: January 27, 2026