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Genetic Diversity and Agro-Morphological Characterization of Fenugreek (Trigonella foenum-graecum L.) Germplasm

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Genetic Diversity and Agro-Morphological Characterization of Fenugreek (*Trigonella foenum-graecum* L.) Germplasm

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Abstract:

The present investigation was conducted at the Experimental Farm, Muraul, Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar, during the Rabi seasons of 2022–23 and 2023–24, with the objective of assessing genetic diversity in 36 genotypes of fenugreek (*Trigonella foenum-graecum* L.). Considerable variability was observed, as reflected in the high phenotypic and genotypic coefficients of variation (PCV and GCV), particularly for seed yield per plant (34.46% and 34.17%) and plant height. Heritability values ranged from 73.26% for harvest index to 98.37% for seed yield per plant, accompanied by high genetic advance, suggesting strong genetic control over these characters. Mahalanobis D^2 statistics grouped the genotypes into six distinct clusters, while Principal Component Analysis (PCA) further confirmed wide genetic divergence. Path coefficient analysis indicated very low residual effects at both phenotypic (–0.0184) and genotypic (0.0379) levels, highlighting the reliability of the key traits in explaining variation. Moreover, the MGIDI index identified RM-206, RM-185, RM-128, RM-209 and RM-1 as promising genotypes due to their desirable trait combinations. It was concluded that the study provides a valuable foundation for developing high-yielding cultivars, thereby contributing to genetic improvement and sustainable crop production.

Keywords: Fenugreek, MGIDI, Genetic diversity, Mahalanobis, PCA and D^2 Analysis

Introduction

Fenugreek (*Trigonella foenum-graecum* L.) is an annual herbaceous plant that is a member of the Leguminosae family with a chromosome number of 2n =16. Due to its numerous industrial, culinary, and medicinal uses, it is considered a crop of worldwide importance [1,2,3]. Fenugreek, which is native to the Mediterranean area, is a rich source of bioactive components such alkaloids, flavonoids, and saponins [4,5,6]. These compounds are primarily responsible for its well-documented antidiabetic, antioxidant and antimicrobial properties [7,8,9,10]. India is the world's leading producer of fenugreek, with an estimated cultivation area of about

147,000 hectares and an annual output of nearly 227,000 metric tons [11]. Rajasthan (41%), Gujarat (20%), and Madhya Pradesh (11%) account for the majority of the crop [12]. Fenugreek is suited for a variety of agroecological settings since it thrives in well-drained loamy soils with a pH range of 6.0–7.5 and can be grown at elevations ranging from sea level to 2600 m [13]. India has become a significant exporter, supplying markets in the United States, the United Arab Emirates, and other European nations, thanks to rising worldwide demand [14].

The predominance of low-yielding native cultivars, which are distinguished by low biomass and low seed output, limits fenugreek cultivation in the middle Gangetic plains, especially Bihar [2]. In India, lowland areas have been the focus of the majority of research activities. For example, research conducted in Rajasthan revealed that plant height and seed yield had substantial heritability, indicating that they might be used as selection criteria in semi-arid environments [15]. Similarly, studies conducted in Madhya Pradesh found genotypes that were ideal for plains agriculture because to their better pod and seed weights [16]. The middle Gangetic plains remain underexplored, with scarce information on the genetic diversity and adaptability of fenugreek under these conditions [2]. This knowledge gap highlights the necessity of exploring the breeding potential of fenugreek in this region to enhance productivity and adaptability. To address this, the present investigation was undertaken to evaluate thirty-six fenugreek genotypes sourced from the middle Gangetic plains of Bihar, India. The region is characterized by a semi-arid, subtropical climate with moderate rainfall and lies at 24.41°N latitude, 84.60°E longitude and an elevation of 52.8 meters above sea level. The primary aim of the study was to identify key agronomic traits that could contribute to the development of climate-resilient, high-yielding fenugreek cultivars suited to subtropical environments.

The study employs advanced multivariate statistical approaches to improve the precision of genetic diversity assessment. Mahalanobis D^2 statistics were used to quantify genetic divergence, facilitating reliable clustering of genotypes. Tocher's method was applied

for grouping based on trait similarity, offering greater accuracy compared to conventional hierarchical approaches [17]. Additionally, Principal Component Analysis (PCA) was carried out to reduce data dimensionality and identify the traits contributing most to variability. The study also utilized the Multi-Trait Genotype-Ideotype Distance Index (MGIDI), which ranks genotypes based on their proximity to an ideal ideotype, thereby providing a more holistic evaluation than single-trait methods such as ANOVA [18]. This research provides an in-depth evaluation of genetic diversity in fenugreek under semi-arid, subtropical conditions and highlights superior genotypes with potential for targeted breeding. Through the application of advanced statistical tools, the study supports the development of high-yielding and climate-resilient cultivars adapted to subtropical agro-ecosystems. In addition, conserving genetically diverse germplasm will enhance future breeding programs and contribute to sustained productivity and long-term sustainability in fenugreek cultivation.

2. Material and Methods

2.1. Germplasm Collection and Experimental Design

The field experiment was conducted at the Experimental Farm, Muraul, Tirhut College of Agriculture (TCA), Dholi, Muzaffarpur, Bihar, during the Rabi seasons of 2022–23 and 2023–24. The site falls within agro-climatic zone I, characterized by a semi-arid, subtropical climate with moderate rainfall. Geographically, it is located at 24.41°N latitude, 84.60°E longitude, at an elevation of 52.8 meters above mean sea level. The experimental soil had a pH of 7.78, with 0.48% organic carbon and available nutrient contents of 274.00 kg ha^{-1} nitrogen, 19.78 kg ha^{-1} phosphorus and 136.00 kg ha^{-1} potassium. A set of 36 fenugreek (*Trigonella foenum-graecum* L.) genotypes (*Figure 1*), including one check variety (Rajendra Kanti), were evaluated in a Randomized Block Design (RBD) with three replications. Manual sowing was done on October 15th in both years, maintaining a spacing of 30 cm between rows and 10 cm between plants. Plot dimensions were 3.0 m × 1.0 m, accommodating about 100 plants per

genotype, with 75 cm spacing between plots and 1 m between replications, as per recommendations for fenugreek. Six further irrigations were given during the crop's growth phase, starting as soon as the seeds were sown. The fertiliser schedule called for 40 kg of potassium (MOP), 80 kg of phosphorus (DAP), and 60 kg of nitrogen (urea). After the first and second harvests, the remaining nitrogen was top-dressed in two equal splits. Half of the nitrogen was applied during planting, together with the full dosages of potassium and phosphorus. To ensure vigorous crop development and maximum production potential, manual weeding and other advised agronomic techniques were used.

2.2. Data collection

Data on morphological and yield-related traits were recorded from ten randomly selected mature plants per plot at relevant growth stages during both years of experimentation. Observations commenced with the onset of reproductive development and continued until physiological maturity. Plant height (cm) was measured at maturity from the soil surface to the apex of the main stem using a meter scale. Branching was assessed by counting the number of primary branches arising from the main stem and the secondary branches emerging from them. All observations were taken at maturity and averaged across plants for each genotype. Flowering behavior was evaluated by recording days to flower initiation (from sowing to the appearance of the first flower) and days to 50% flowering, defined as the time required for half the plants in a plot to reach the flowering stage. Days to maturity were also noted, representing the duration from sowing to physiological maturity. Reproductive traits included number of pods per plant and number of seeds per pod, recorded after pod development. Mature pods from sampled plants were harvested, counted and threshed to determine average pod and seed counts. Seed yield per plant (g) was calculated by weighing cleaned seeds from sampled plants, while test weight (g) was estimated by weighing 1000 seeds from each plot to assess seed size and density. Biological yield per plant (g), representing total above-ground biomass (excluding

roots), was measured by harvesting, drying and weighing plants at maturity. Harvest index (HI, %) was calculated as: HI = (Seed yield per plant / Biological yield per plant) × 100. Plot yield (g/3 m²) was obtained by weighing clean, dried seeds harvested from each 3 m² plot and seed yield per hectare (q/ha) was extrapolated from plot yields using standard conversion factors. The abbreviations used were: PH – Plant Height (cm), PB – Primary Branches, SB – Secondary Branches, FI – Days to Flower Initiation, 50%F – Days to 50% Flowering, DM – Days to Maturity, NPP – Number of Pods per Plant, NSP – Number of Seeds per Pod, SYP – Seed Yield per Plant (g), BI – Biological Yield per Plant (g), HI – Harvest Index (%), TW – Test Weight (g/1000 seeds), YP – Seed Yield per Plot (g/3 m²) and YH – Seed Yield per Hectare (q/ha).

2.3. Assessment of Morphological Variation

To quantify important genetic factors and aid in grouping, morphological heterogeneity among fenugreek genotypes was examined. While phenotypic and environmental variances, as well as covariance components reflecting trait interrelationships and environmental influence, were calculated according to [19]. genotypic variance, which represents the portion of phenotypic variation explained by genetic factors, was derived using the method of [20]. The extent of relative variation was assessed through phenotypic and genotypic coefficients of variation (PCV and GCV) using the formulae of [21]. Broad-sense heritability (h^2b), which measures the proportion of genetic contribution to trait expression, was estimated according to [22]. Expected genetic advance (GA), indicating the potential improvement under selection, was calculated following [23]. Genetic divergence among genotypes was quantified using Mahalanobis' D^2 statistics, which incorporates correlations among traits and genotypes were grouped through Tocher's clustering method that minimizes within-cluster variability [17]. Direct and indirect contributions of yield-related traits were assessed via path coefficient analysis using the approach of [24]. Additionally, the Multi-Trait Genotype–Ideotype Distance

Index (MGIDI) was employed to rank genotypes based on their proximity to an ideal ideotype, offering a comprehensive evaluation of multi-trait performance [18].

2.4. Statistical Evaluation of Agronomic Characteristics

The pooled data from the 2022–23 and 2023–24 cropping seasons were analyzed using a range of statistical techniques to assess genetic variability and genotype performance. Analyses included ANOVA, path coefficient analysis (with residual effects indicating unexplained variation), phenotypic and genotypic correlation studies, as well as variance and covariance analysis. Principal component analysis (PCA) was employed to identify major sources of variation among traits. Genetic parameters such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2b), genetic advance (GA) and genetic divergence were estimated, with Mahalanobis' D^2 statistics used to quantify inter-genotypic distances. Genotypic clustering was carried out using Tocher's method and the Multi-Trait Genotype–Ideotype Distance Index (MGIDI) was computed in R (version 4.6.1). Together, these approaches provided an integrated understanding of trait associations, variability and the identification of superior genotypes for breeding.

3. Results and discussion

3.1. Determination of Variability Parameters via ANOVA

Analysis of variance, mean performance and genetic parameters were assessed for fourteen distinct traits. Among these, the maximum coefficient of variation (CV) was observed for PH at 12.986%, followed by BI at 11.684%, SYP at 10.767%, PB at 10.583% and SB at 10.545%. The lowest CV was observed for DM which accounted only for 3.286% (Table 2). Significant variation was recorded in both PCV and GCV values exhibits a substantial degree of genetic diversity within the evaluated germplasm (Table 1 and Figure 2). The maximum PCV and GCV were observed for SYP with values of 34.456% and 34.174%, respectively. However, the minimum PCV and GCV values were observed for DM at 3.770% and 3.523%,

50% F at 4.518% and 4.256%, FI at 6.448% and 6.236 and NSP at 7.488% and 6.943%, respectively. Other traits exhibited moderate levels of both PCV and GCV such as SB at 25.001% and 24.628%, BI at 23.596% and 22.394%, PH at 23.145% and 22.529%, PB at 20.873 and 20.421%, NPP at 20.116% and 19.692%, YP at 19.702% and 19.433%, YH at 19.562% and 19.288%, HI at 16.145% and 13.819% and TW at 14.926% and 14.714%, respectively. The consistently higher magnitude of PCV over the corresponding GCV for these traits suggest the influence of environmental factors play a notable role in phenotypic expression along with genetic factors [25, 15]. This divergence can be ascribed to non-additive gene action. Supporting these findings, earlier studies on fenugreek also reported similar patterns of variability. [26, 1, 27] documented significant differences in PCV and GCV across fenugreek genotypes. Additionally, [28] also reported elevated PCV values in fenugreek, reflecting considerable phenotypic variability.

These findings highlight the significance of GCV as a key indicator for evaluating the inherent genetic potential of traits, consistent with the observations of [2]. High PCV values highlight considerable natural variation and signal opportunities for selecting superior genotypes adapted to diverse environments. However, traits with low GCV suggest a more stable genetic basis providing a foundation for long-term genetic improvement approaches [29]. The broad-sense heritability (h^2b) values ranged from 98.372% for SYP to 73.268% for HI indicating a high degree of genetic control for these traits. According to [30] heritability estimates below 30% are considered low, those between 30% and 60% are moderate and values exceeding 60% are regarded as high. The high heritability observed across traits suggests the feasibility for effective selection and genetic improvement. GA, estimated at a 5% selection intensity, varied from 181.496% for YP to 2.074 for PB. [31] reported that, at a 5% selection intensity, genetic advance (GA) is classified as low if below 10%, moderate if between 10% and 20% and high if it exceeds 20%. The results revealed high heritability estimates for all

traits studied which suggest that a significant proportion of the observed phenotypic variation is governed by genetic factors. Furthermore, YP and PH exhibited high GA values at 5% selection intensity, suggesting high potential for genetic improvement through selection. The concurrent presence of high h^2b and substantial GA underscores that these traits are likely regulated by additive gene action and exhibit considerable stability across different environments. This stability implies reduced environmental influence, thereby enhancing the reliability of genotype selection based on phenotypic performance. Nonetheless, selecting genotypes based on these traits is anticipated to be effective for identifying superior lines [32].

3.2. Assessment of Genetic Diversity

The genetic divergence between thirty-six fenugreek genotypes was assessed in this study using Mahalanobis D^2 statistics. A thorough evaluation of genetic diversity is made possible by this multivariate statistical method, which results in the grouping of genotypes into six different groups according to their physical traits. The research provided a foundation for choosing prospective parental lines for next breeding initiatives by revealing the degree of genetic difference across the genotypes [23, 33]. As shown in *Table 2*, the D^2 analysis revealed significant genetic diversity among the six groups.

Cluster I, comprising six genotypes showed the highest divergence with Cluster VI (938.95) followed by Clusters V (312.42), II (256.52), IV (279.28) and III (183.33). Similarly, Cluster II, which consisted of 14 genotypes exhibits the greatest genetic distance from Cluster III (535.02) while Cluster III, including six genotypes recorded its maximum divergence with Cluster IV (593.63). Cluster IV, including seven genotypes, recorded its maximum divergence with Cluster III (593.63). Cluster V, with two genotypes showed notable divergence from Cluster III (584.86). Notably, Cluster VI comprised only a single genotype. The smallest inter-cluster distances were observed between Clusters II and IV (106.55) and Clusters II and V (182.20), suggesting a closer genetic relationship between these groups (Figure 3a). Intra-

cluster distance was zero for Cluster VI due to its single-genotype composition, whereas Clusters I, II, III, IV and V exhibited intra-cluster distances of 57.10, 75.60, 82.51, 49.38 and 48.94, respectively, reflecting moderate variability within these groups. These findings underscore the presence of substantial genetic diversity, which can be effectively exploited in fenugreek improvement programs. These findings are consistent with the observations of [34]. The substantial difference between inter- and intra-cluster distances further confirms a high degree of genetic diversity. The genotypes belonging to highly divergent clusters are ideal candidates for hybridization which aims at maximum heterosis. These genotypes were collected from the middle Gangetic plains region of Bihar India and they were grouped into different clusters indicating that geographic origin alone did not determine their genetic relatedness. This divergence may be attributed to genetic drift, spontaneous mutations, or local selection pressures rather than geography alone. The data suggest considerable genetic variation exists within the natural populations of fenugreek in this region. Trait-wise contribution to cluster formation was assessed (*Table 3, Fig. 3b*). Among the traits, PH and PB were the most influential, contributing 141% and 118% respectively. SB contributed 80% also plays a major role in the clustering. Traits such as FI had modest contributions (72%) while 50%F, DM, NPP, NSP, SYP and BI contributed minimally (62%, 50%, 37%, 21%, 18% and 14%. HI, TW, YP and YH which shows negligible influence on cluster formation. These results are consistent with those studied by [35,36].

3.3 Cluster Analysis Using Tocher's Method and PCA

The Tocher clustering method (*Figure 4*) classified the 36 fenugreek genotypes into six distinct clusters, demonstrating the substantial genetic diversity present among them. Cluster I, with six genotypes *i.e.*, RM-1, RM-12, RM-206, RM-210, RM-215, RM-220 and Cluster II with 14 genotypes i.e., RM-10, RM-188, RM-191, RM-194, RM-195, RM-198, RM-199, RM-201, RM-203, RM-205, RM-211, RM-216, RM-28 and RM-44 suggested a relatively narrow

genetic base. Cluster III included RM-13, RM-18, RM-185, RM-196, RM-212 and RM-219, while Cluster IV comprised of RM-14, RM-15, RM-16, RM-187, RM-202, RM-217, RM-70. Cluster V was represented by two genotypes *i.e.*, RM-128 and Rajendra Kanti. Cluster VI consisted of solely genotype RM-209 indicating its distinct genetic makeup. The reliability of the Tocher method is supported by findings of [37,38]. Principal Component Analysis (PCA) (*Table 4 and Figure 5*) further supported the clustering pattern. The three principal components (PC_1, PC_2 and PC_3) captured the majority of total variation which reveals the extent of genotypic dispersion. Genotypes i.e., RM-209, RM-217 and RM-196 exhibits extreme PCA scores which indicates unique morphological traits. Genotypes forming Clusters III, IV and VI (*e.g.*, RM-209, RM-217 and RM-196) aligned well with the Mahalanobis D^2 clustering, reinforcing the consistency of the grouping. Similar corroboration between PCA and clustering methods were observed by [39,40,41]. Trait means across clusters (*Table 3*) revealed cluster specific performance. Cluster I and Cluster II exhibits moderate mean values for all the studied characters indicates a balanced performance across traits. Cluster III showed superior values for most of the characters *i.e.*, PH (114.77), PB (6.59), SB (9.89), SYP (5.65), BI (21.99), HI (25.84), TW (14.38), YP (570.95) and YH (19.03) and least for the NSP (15.61). Cluster IV had the significant earliest for 50%F (80.67) and DM (121.48) and lowest for NPP (30.85). Cluster V recorded highest values for NPP (49.13) and NSP (16.88) and earliest for FI (41.83). Cluster VI displays the significantly lowest mean performance for PH (58.86), SB (4.44), SYP (1.49), BI (10.40), HI (14.34), TW (8.56), YP (227.50) and YH (7.58) and delaying for FI (55.50), 50%F (80.67) and DM (146.17). PCA results indicated that PC_1 was largely influenced by 50%F, DM, FI, NPP and NSP particularly defining Cluster II, IV, V and VI whereas PC_2, comprising PH, PB, SB, BI, SYP, FW, HI, YH and YP explains the variation observed in Clusters I and III (*Figure 6*).

3.4. Interrelationship Analysis of Agronomic Characters

The phenotypic (P) and genotypic (G) correlation matrices (*Table 5; Figure 7a and 7b*) highlight significant relationships among fourteen growth and yield-related traits in *Trigonella foenum-graecum* L. PH demonstrated a strong positive correlation with YP at both phenotypic (0.778^{**}) and genotypic (0.879^{**}) levels implying that the taller plants are associated with greater seed yield. PB exhibited a positive correlation with YP both phenotypically (0.683^{**}) and genotypically (0.815^{**}) indicating a potential contribution to yield. Similarly, SB showed a positive correlation with YP both phenotypically (0.753^{**}) and genotypically (0.841^{**}) underlining their role in yield enhancement. FI revealed a negative but significant phenotypic and genotypic correlation (0.457^{**}) and (-0.495^{**}) with YP, indicating that higher values of FI which may be associated with reduced yield potential. Similarly, 50%F showed a statistically significant negative correlation with YP at the phenotypic (-0.395^{**}) and genotypic (-0.449^{**}) levels suggesting that earlier flowering may contribute to higher yield potential. DM was also revealed a significant negative correlation with YP at the phenotypic (-0.345^{**}) and genotypic (-0.393^{**}) levels suggesting that earlier flowering may contribute to higher yield potential. NPP exhibited non-significant negative correlations with YP at both phenotypic (-0.104) and genotypic (-0.103) levels which indicates a weak and negligible association. NSP showed a weak and non-significant positive correlation with YP at both phenotypic (0.072) and genotypic (0.062) levels, suggesting a minimal contribution to yield expression. NSP showed a weak and non-significant positive correlation with YP at both phenotypic (0.072) and genotypic (0.062) levels, suggesting a minimal contribution to yield expression. SYP showed a strong and significant positive correlation with YP at both phenotypic (0.817^{**}) and genotypic (0.886^{**}) levels, indicating its substantial contribution to yield enhancement. BI exhibited a strong and significant positive correlation with YP at both phenotypic (0.718^{**}) and genotypic (0.808^{**}) levels, emphasizing the critical role of biomass pro duction traits in YP enhancement. HI exhibited significant positive correlation with YP at both phenotypic (0.633^{**}) and genotypic

(0.705**) levels, suggesting its crucial role in enhancing overall yield. TW exhibited significant positive correlation with YP at both phenotypic (0.615**) and genotypic (0.667**) levels, indicating its positive influence on yield performance. YH exhibited significant positive correlation with YP at both phenotypic (0.979**) and genotypic (0.951**) levels, reflecting a strong association and direct contribution to overall yield. These results are in consistent with findings by [42] who noted highly significant positive genotypic correlations of PB, SB, SYP and HI in *T. foenum-graecum* L. Similarly, [16] observed significant positive correlations of SYP with NPP. Their study also revealed strong associations of agronomic traits such as PH and BI with YH. These results emphasize the need to target key traits such as plant height, branching, pod characteristics and biomass accumulation in breeding programs to improve seed yield in fenugreek.

3.5. Path Coefficient Analysis of Yield Per Plots

Path coefficient analysis (*Table 6 and Figure 8a and 8b*) for YP in *Trigonella foenum-graecum* L. revealed the nature and magnitude of direct and indirect effects exerted by various agronomic traits. PH exhibits a positive direct effect at both phenotypic (0.0658) and genotypic (0.4867) levels along with significant positive correlations with yield per hectare (YP) at phenotypic (0.778**) and genotypic (0.879**) levels which suggests that taller plants yield more seeds. PB highlight a moderate direct effect at the phenotypic (0.0041) level and a negative direct effect at the genotypic (–0.6420) level. Despite the negative genotypic path coefficient, PB showed a significant and positive correlation with yield per hectare (YP) at both the phenotypic (0.683**) and genotypic (0.815**) levels. This highlights its substantial contribution to yield determination. SB demonstrated a negative direct effect phenotypically (–0.0314) but a positive direct effect genotypically (0.3112). In addition, SB showed a significant and strong positive correlation with YP at both phenotypic (0.753**) and genotypic (0.841**) levels. This suggests that, particularly at the genetic level, an increased number of secondary branches plays

a beneficial role in improving seed yield. FI, recorded positive direct effects phenotypically (0.0012) but a negative direct effect genotypically (-0.0159) and negative correlations with YP at both phenotypic (–0.457**) and genotypic (–0.495**) levels. 50%F recorded the negative direct effects phenotypically (-0.0235) and genotypically (-0.1204) and negative correlations with YP at both phenotypic (–0.395**) and genotypic (–0.449**) level. Similarly, DM recorded negative direct effects phenotypically (-0.0170) but a positive direct effect genotypically (0.1160) and negative correlations with YP at both phenotypic (–0.345**) and genotypic (–0.393**) level, indicating that delayed flowering and maturity have a detrimental impact on seed yield. Traits such as NPP and NSP exhibited subtle direct effects and non-significant correlations with YP, suggesting a limited influence on YP in fenugreek. SYP exhibited the positive direct effect on YP at both phenotypic (0.0992) and genotypic (1.1240) levels, accompanied by highly significant positive correlations with YP at both phenotypic (0.817**) and genotypic (0.886**) levels, highlighting their key roles in enhancing seed yield. Similarly, BI showed a substantial negative direct effect on YP at both phenotypic (-0.0671) and genotypic (-0.9147) levels, accompanied by highly significant positive correlations with YP at both phenotypic (0.718**) and genotypic (0.808**) suggesting its overall positive contribution through indirect effects. HI showed an adverse direct effect on YP at both phenotypic (-0.0152) and genotypic (-0.3458) levels which are accompanied by significant positive correlations with YP at both phenotypic (0.633**) and genotypic (0.705**) may possibly be due to strong indirect contributions via SYP and BI. TW also contributed negative direct effects phenotypically (-0.0102) but a positive direct effect genotypically (-0.1327), suggesting its indirect role in yield formation. YH being a composite trait, displayed direct effects on phenotypically (0.8940) and genotypically (0.8725) showed very strong positive correlations with YP at both phenotypic (0.979**) and genotypic (0.951**) levels, confirming its close association with actual yield performance. The persistent effect at phenotypic (r = 0.195) and genotypic (r = 0.214). The

analysis suggests that the studied traits contributed substantially to the overall variability in seed yield, with the remaining variation likely influenced by environmental factors. Comparable results were observed by [43] in *Vigna unguiculata* L., where pod yield per hectare was primarily affected by traits such as the number of nodes on the main stem, days to 50% flowering, days to 50% maturity and number of peduncles per plant at the genotypic level. Similarly, [42] reported that all agronomic traits had significant positive impacts on seed yield per plant in *Trigonella foenum-graecum* L., supporting findings by [44] for the same crop.

3.6. Genotypic Evaluation and Ranking Using MGIDI Analysis

The Multi-Trait Genotype–Ideotype Distance Index (MGIDI) was applied to the fenugreek genotypes using fourteen traits (*Tables 7, 8, Fig. 9a*), which were grouped into three functional categories to facilitate the selection of superior genotypes. In the first functional group (FA1) which included PH, PB, SB, SYP, BI, HI, TW, YP and YH, the selection gains ranged from 5.38% to 10.20%. The highest positive selection gain was observed for BI (10.20%) followed by SB (8.46%), PH (8.22%) and SYP (8.31%). All of them exhibits high heritability estimates ($h^2(bs) > 0.95$) indicating strong genetic control. However, traits like HI (–5.38%), YP (–1.52%) and YH (–0.95%) showed negative gains, reflecting potential trade-offs in selection under multi-trait optimization. The second functional group (FA_2), comprising days to FI, 50%F and DM, exhibits moderate selection gains. Positive gains were noted for all three traits, with FI (6.01%) recording the highest improvement, followed by 50%F (4.17%) and DM (2.88%) suggesting a modest but desirable shift toward earliness and phenological uniformity. All traits under FA_2 showed relatively high heritability ($h^2 \geq 0.87$). In the third functional group (FA_3) which included NPP and NSP, notable gains were observed. NPP recorded the highest gain of 22.20% while NSP improved by 3.25%. These traits are directly linked to yield and were associated with high heritability ($h^2 = 0.96$ for NPP and 0.85 for NSP), confirming their reliability for selection. The selection process resulted in substantial multi-

trait enhancement in genotypes RM-206, RM-185, RM-128, RM-209 and RM-1 which exhibited superior MGIDI values (*Figure 9b*). These results are consistent with earlier studies by [45,46,47,48], which highlighted the effectiveness of MGIDI in identifying genotypes with favorable multi-trait profiles. The MGIDI approach demonstrated its strength as a selection tool for integrating multiple traits, allowing the simultaneous enhancement of key yield, phenological and morphological characteristics. The high heritability values observed across traits indicate strong genetic stability, while the recorded gains validate the effectiveness of the selection approach. These outcomes are promising for advancing fenugreek breeding programs aimed at improving yield, early maturity and agronomic efficiency under diverse agro-climatic conditions.

4. Conclusion

Key agronomic characteristics, such as the number of primary and secondary branches, plant height, test weight, biological yield, harvest index, and yield per hectare, showed substantial positive associations with seed yield per plot in the fenugreek research. On the other hand, phenological characteristics including days to flower initiation, days to 50% flowering, and days to maturity showed a negative correlation, suggesting that higher yields are associated with earlier flowering and maturity. High broad-sense heritability coupled with substantial genetic advance for these traits suggests strong genetic control, making them promising targets for selection. The 36 fenugreek genotypes were effectively classified into distinct genetic clusters using the Tocher clustering method, reflecting clear patterns of genetic divergence. Principal Component Analysis further confirmed the presence of considerable genetic variability among the genotypes. Analyses based on Mahalanobis D^2 and Euclidean distances revealed significant intra- and inter-cluster differences. Multi-Trait Genotype–Ideotype Distance Index (MGIDI) analysis identified superior genotypes, such as RM-206, RM-185, RM-128, RM-209 and RM-1, with desirable multi-trait profiles, facilitating targeted breeding

strategies. these findings highlight the potential for developing climate-resilient fenugreek cultivars adapted to subtropical conditions. Conserving this diverse germplasm is essential to support sustainable breeding programs and ensure long-term productivity and adaptability in fenugreek cultivation.

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Lavkush Singh: Conceptualization, Formal analysis, Writing – original draft; Dhirendra Kumar Singh: review & editing Killi prasad and Suresh prasad Singh review & supervision.

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Data availability

All simulation data supporting the findings of this study are presented within the paper.

Declarations

Competing interests The authors declare no competing interests.

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Table 1. Analysis of variance (ANOVA), genetic parameters and mean performance of various traits of Fenugreek (*T. foenum-graecum* L.)

	Analysis of variance (ANOVA)				Estimation of genetic parameter							Mean performance					
Trait	MS Environment	MS Genotype	MS Environment x Genotype	MS Error	Phenotypic Var (σ^2p)	Genotypic Var (σ^2g)	GCV (%)	PCV (%)	h^2b (%)	GA @ 5%	GAM (%)	Mean	Minimum	Maximum	CV (%)	SE±(m)	CD ($p \leq 0.05$)
PH	117.174	2244.269**	0.999	124.218	394.581	373.878	22.529	23.145	94.753	38.773	45.177	85.83	58.86	119.89	12.986	4.550	12.720
PB	3.718**	6.469**	0.112	0.285	1.107	1.060	20.421	20.873	95.716	2.074	41.157	5.04	3.82	7.60	10.583	0.218	0.609
SB	0.502	17.95**	0.047	0.547	3.075	2.984	24.628	25.001	97.035	3.505	49.976	7.01	4.45	11.14	10.545	0.302	0.844
FI	35.042**	44.88**	0.585	3.066	7.894	7.383	6.236	6.448	93.526	5.413	12.424	43.57	39.50	55.50	4.019	0.715	1.999
50%F	124.519**	72.846**	0.985	9.134	13.499	11.977	4.256	4.518	88.722	6.715	8.258	81.32	76.00	94.83	3.717	1.234	3.449
DM	301.042**	113.919**	0.651	16.425	21.616	18.878	3.523	3.770	87.335	8.364	6.782	123.33	118.00	146.17	3.286	1.655	4.626
NPP	51.334*	263.842**	0.965	11.437	45.719	43.813	19.692	20.116	95.831	13.348	39.711	33.61	22.03	56.53	10.061	1.381	3.860
NSP	16.275**	7.91**	0.269	1.246	1.481	1.273	6.943	7.488	85.977	2.155	13.263	16.25	13.67	18.34	6.869	0.456	1.274
SYP	2.001**	9.318**	0.010	0.154	1.577	1.551	34.174	34.456	98.372	2.545	69.824	3.64	1.49	6.45	10.767	0.160	0.448
BI	66.334**	91.197**	9.055**	3.727	15.199	13.69	22.394	23.596	90.071	7.234	43.781	16.52	10.40	23.21	11.684	0.788	2.203
HI	489.065**	75.391**	20.154**	3.523	12.565	9.206	13.819	16.145	73.268	5.350	24.368	21.96	13.53	29.46	8.549	0.766	2.142
TW	3.383**	16.494**	0.037	0.477	2.822	2.743	14.714	14.926	97.183	3.363	29.881	11.26	8.56	15.53	6.136	0.282	0.788
YP	598.235	47879.527**	8.327	1332.35	8200.59	7978.530	19.433	19.702	97.292	181.496	39.486	459.65	227.50	614.67	7.941	14.902	41.659
YH	0.397	52.543**	0.061	1.503	8.997	8.747	19.288	19.562	97.216	6.007	39.177	15.33	7.58	20.49	7.995	0.500	1.399

PH - Plant Height (cm), PB - Primary Branches, SB - Secondary Branches, FI - Days to Flower Initiation, 50%F - Days to 50% Flowering, DM - Days to Maturity, NPP - Number of Pods per Plant, NSP - Number of Seeds per Pod, SYP - Seed Yield per Plant (g), BI - Biological Yield per Plant (g), HI - Harvest Index (%), TW - Test Weight (g/1000 seeds), YP - Seed Yield per Plot (g/3 m^2) and YH - Seed Yield per Hectare (q/ha). DF – Degrees of freedom; * – Significant at ($p \leq 0.05$) level; ** – Significant at 1% level. σ^2p – Phenotypic variance; σ^2g – Genotypic variance; PCV – Phenotypic coefficient of variation; GCV – Genotypic coefficient of variation; h^2b – Heritability (broad sense); GA – Genetic advance; CV – Coefficient of variation; SE (±) – Standard error; CD – Critical difference.

Table 2. Clusters of thirty-six fenugreek (*T. foenum-graecum* L.) genotypes based on genetic diversity.

Cluster	Genotypes	Total Genotype
1	RM-1, RM-12, RM-206, RM-210, RM-215, RM-220	6
2	RM-10, RM-188, RM-191, RM-194, RM-195, RM-198, RM-199, RM-201, RM-203, RM-205, RM-211, RM-216, RM-28, RM-44	14
3	RM-13, RM-18, RM-185, RM-196, RM-212, RM-219	6
4	RM-14, RM-15, RM-16, RM-187, RM-202, RM-217, RM-70	7
5	RM-128, Rajendra Kanti	2
6	RM-209	1

Table 3. Cluster mean and Contribution percentages of traits in Fenugreek (*T. foenum-graecum* L.).

Trait	PH	PB	SB	FI	50%F	DM	NPP	NSP	SYP	BI	HI	TW	YP	YH
Cluster-I	109.01	6.05	8.44	43.08	81.11	123.39	33.29	16.39	4.76	20.94	22.91	11.06	548.03	18.25
Cluster-II	72.20	4.43	5.97	43.77	81.05	122.57	33.64	16.32	3.15	13.81	23.24	10.64	420.91	14.03
Cluster-III	114.77	6.59	9.89	42.97	80.78	123.36	32.06	15.61	5.65	21.99	25.84	14.38	570.95	19.03
Cluster-IV	75.29	4.41	5.99	42.88	80.67	121.48	30.85	16.43	2.52	14.37	17.66	10.28	413.36	13.78
Cluster-V	75.22	4.23	6.26	41.83	80.92	123.42	49.13	16.88	2.84	16.46	17.30	11.60	409.83	13.94
Cluster-VI	58.86	4.26	4.44	55.50	94.83	146.17	32.80	15.90	1.49	10.40	14.34	8.56	227.50	7.58
Times ranked 1st	22.38	18.73	12.70	11.43	9.84	7.94	5.87	3.33	2.86	2.22	1.27	0.79	0.63	0.00
Contribution %	141.00	118.00	80.00	72.00	62.00	50.00	37.00	21.00	18.00	14.00	8.00	5.00	4.00	0.00

PH - Plant Height (cm), PB - Primary Branches, SB - Secondary Branches, FI - Days to Flower Initiation, 50%F - Days to 50% Flowering, DM - Days to Maturity, NPP - Number of Pods per Plant, NSP - Number of Seeds per Pod, SYP - Seed Yield per Plant (g), BI - Biological Yield per Plant (g), HI - Harvest Index (%), TW - Test Weight (g/1000 seeds), YP - Seed Yield per Plot (g/3 m^2) and YH - Seed Yield per Hectare (q/ha).

Table 4. Principal Component Analysis

PC	Eigenvalues	Variance (%)	Cumulative Variance (%)
PC1	7.54	53.80	53.80
PC2	2.42	17.30	71.10
PC3	1.27	9.06	80.20
PC4	0.75	5.34	85.50
PC5	0.65	4.68	90.20
PC6	0.50	3.58	93.80
PC7	0.32	2.27	96.00
PC8	0.23	1.64	97.70
PC9	0.14	0.98	98.70
PC10	0.11	0.76	99.40
PC11	0.05	0.36	99.80
PC12	0.03	0.20	100.00
PC13	0.00	0.02	100.00
PC14	0.00	0.00	100.00

Table 5. Phenotypic (P) and Genotypic (G) correlation matrix of growth and yield traits of *T. foenum graecum* L. Genotypes.

Trait		PH	PB	SB	FI	50%F	DM	NPP	NSP	SYP	BI	HI	TW	YH	YP
PH	P	1	0.763**	0.849**	-0.213*	-0.124	-0.074	-0.084	-0.16	0.867**	0.855**	0.483**	0.636**	0.778**	0.778**
	G	1	0.944**	0.961**	-0.261**	-0.148	-0.115	-0.101	-0.220*	0.938**	0.958**	0.529**	0.716**	0.881**	0.879**
PB	P		1	0.818**	-0.148	-0.148	0.011	0.042	-0.105	0.819**	0.757**	0.524**	0.581**	0.693**	0.683**
	G		1	0.959**	-0.175	-0.190*	0.058	0.009	-0.186	0.937**	0.890**	0.615**	0.675**	0.809**	0.815**
SB	P			1	-0.181	-0.170	-0.078	0.055	-0.102	0.878**	0.823**	0.557**	0.719**	0.766**	0.753**
	G			1	-0.215*	-0.228*	-0.119	0.057	-0.132	0.952**	0.935**	0.599**	0.794**	0.838**	0.841**
FI	P				1	0.749**	0.698**	0.054	-0.077	-0.234*	-0.220*	-0.235*	-0.254**	-0.456**	-0.457**
	G				1	0.799**	0.723**	0.047	-0.088	-0.258**	-0.236*	-0.280**	-0.288**	-0.500**	-0.495**
50%F	P					1	0.668**	0.020	-0.147	-0.201*	-0.154	-0.281**	-0.103	-0.386**	-0.395**
	G					1	0.611**	0.047	-0.153	-0.238*	-0.178	-0.368**	-0.139	-0.456**	-0.449**
DM	P						1	0.082	-0.198*	-0.097	-0.097	-0.175	-0.150	-0.337**	-0.345**
	G						1	0.098	-0.215*	-0.129	-0.097	-0.277**	-0.194*	-0.401**	-0.393**
NPP	P							1	0.263**	-0.016	0.005	-0.026	-0.025	-0.084	-0.104
	G							1	0.297**	-0.012	0.030	-0.047	-0.012	-0.086	-0.103
NSP	P								1	-0.123	-0.110	-0.058	-0.134	0.069	0.072
	G								1	-0.146	-0.124	-0.063	-0.188	0.077	0.062
SYP	P									1	0.905**	0.711**	0.703**	0.824**	0.817**
	G									1	0.923**	0.744**	0.764**	0.883**	0.886**
BI	P										1	0.364**	0.633**	0.728**	0.718**
	G										1	0.445**	0.702**	0.809**	0.808**
HI	P											1	0.457**	0.635**	0.633**
	G											1	0.518**	0.700**	0.705**
TW	P												1	0.621**	0.615**
	G												1	0.671**	0.667**
YH	P													1	0.979**
	G													1	0.951**

PH - Plant Height (cm), PB - Primary Branches, SB - Secondary Branches, FI - Days to Flower Initiation, 50%F - Days to 50% Flowering, DM - Days to Maturity, NPP - Number of Pods per Plant, NSP - Number of Seeds per Pod, SYP - Seed Yield per Plant (g), BI - Biological Yield per Plant (g), HI - Harvest Index (%), TW - Test Weight (g/1000 seeds), YP - Seed Yield per Plot (g/3 m^2) and YH - Seed Yield per Hectare (q/ha). * – Significant at ($p \leq 0.05$) level; ** – Significant at ($p \leq 0.01$) level.

Table 6. Phenotypic (P) and Genotypic (G) path-coefficient analysis for seed yield per plot showing direct (bold) and indirect effects of different characteristics in *T. foenum graecum* L.

Trait		PH	PB	SB	FI	50%F	DM	NPP	NSP	SYP	BI	HI	TW	YH	YP
PH	P	**0.0758**	0.0579	0.0644	-0.0162	-0.0094	-0.0056	-0.0064	-0.0121	0.0658	0.0648	0.0367	0.0482	0.0590	0.778**
	G	**0.5188**	0.4897	0.4985	-0.1356	-0.0765	-0.0598	-0.0526	-0.1139	0.4867	0.4972	0.2745	0.3715	0.4570	0.879**
PB	P	0.0031	**0.0041**	0.0033	-0.0006	-0.0006	0.0000	0.0002	-0.0004	0.0033	0.0031	0.0021	0.0024	0.0028	0.683**
	G	-0.6060	**-0.6420**	-0.6157	0.1125	0.1216	-0.0370	-0.0056	0.1191	-0.6016	-0.5715	-0.3948	-0.4332	-0.5191	0.815**
SB	P	-0.0267	-0.0257	**-0.0314**	0.0057	0.0054	0.0024	-0.0017	0.0032	-0.0276	-0.0259	-0.0175	-0.0226	-0.0241	0.753**
	G	0.2990	0.2984	**0.3112**	-0.0669	-0.0709	-0.0371	0.0178	-0.0411	0.2963	0.2912	0.1864	0.2472	0.2608	0.841**
FI	P	-0.0003	-0.0002	-0.0002	**0.0012**	0.0009	0.0008	0.0001	-0.0001	-0.0003	-0.0003	-0.0003	-0.0003	-0.0005	-0.457**
	G	0.0042	0.0028	0.0034	**-0.0159**	-0.0127	-0.0115	-0.0007	0.0014	0.0041	0.0038	0.0045	0.0046	0.0079	-0.495**
50%F	P	0.0029	0.0035	0.0040	-0.0176	**-0.0235**	-0.0157	-0.0005	0.0035	0.0047	0.0036	0.0066	0.0024	0.0091	-0.395**
	G	0.0178	0.0228	0.0274	-0.0963	**-0.1204**	-0.0736	-0.0057	0.0184	0.0287	0.0214	0.0443	0.0168	0.0548	-0.449**
DM	P	0.0013	-0.0002	0.0013	-0.0119	-0.0114	**-0.0170**	-0.0014	0.0034	0.0017	0.0017	0.0030	0.0026	0.0057	-0.345**
	G	-0.0134	0.0067	-0.0138	0.0839	0.0709	**0.1160**	0.0113	-0.0249	-0.0149	-0.0112	-0.0322	-0.0226	-0.0465	-0.393**
NPP	P	0.0020	-0.0010	-0.0013	-0.0013	-0.0005	-0.0019	**-0.0233**	-0.0061	0.0004	-0.0001	0.0006	0.0006	0.0020	-0.104
	G	-0.0020	0.0002	0.0012	0.0009	0.0009	0.0020	**0.0202**	0.0060	-0.0002	0.0006	-0.0010	-0.0002	-0.0017	-0.103
NSP	P	-0.0040	-0.0026	-0.0025	-0.0019	-0.0037	-0.0049	0.0065	**0.0249**	-0.0031	-0.0027	-0.0014	-0.0033	0.0017	0.072
	G	-0.0075	-0.0063	-0.0045	-0.0030	-0.0052	-0.0073	0.0101	**0.0341**	-0.0050	-0.0042	-0.0022	-0.0064	0.0026	0.062
SYP	P	0.0861	0.0812	0.0872	-0.0232	-0.0199	-0.0096	-0.0016	-0.0122	**0.0992**	0.0898	0.0706	0.0697	0.0818	0.817**
	G	1.0545	1.0532	1.0701	-0.2899	-0.2677	-0.1447	-0.0132	-0.1646	**1.1240**	1.0372	0.8367	0.8589	0.9931	0.886**
BI	P	-0.0573	-0.0508	-0.0552	0.0147	0.0103	0.0065	-0.0003	0.0074	-0.0607	**-0.0671**	-0.0244	-0.0425	-0.0488	0.718**
	G	-0.8766	-0.8142	-0.8557	0.2161	0.1629	0.0884	-0.0277	0.1137	-0.8440	**-0.9147**	-0.4069	-0.6425	-0.7399	0.808**
HI	P	-0.0073	-0.0079	-0.0085	0.0036	0.0043	0.0027	0.0004	0.0009	-0.0108	-0.0055	**-0.0152**	-0.0069	-0.0096	0.633**
	G	-0.1829	-0.2127	-0.2071	0.0969	0.1273	0.0958	0.0163	0.0219	-0.2574	-0.1538	**-0.3458**	-0.1793	-0.2419	0.705**
TW	P	0.0065	0.0059	0.0073	-0.0026	-0.0010	-0.0015	-0.0003	-0.0014	0.0071	0.0064	0.0046	**0.0102**	0.0063	0.615**
	G	-0.0950	-0.0895	-0.1054	0.0382	0.0185	0.0258	0.0016	0.0250	-0.1014	-0.0932	-0.0688	**-0.1327**	-0.0890	0.667**
YH	P	0.6960	0.6194	0.6846	-0.4072	-0.3454	-0.3012	-0.0754	0.0613	0.7367	0.6504	0.5678	0.5547	**0.8940**	0.979**
	G	0.7685	0.7055	0.7312	-0.4360	-0.3974	-0.3498	-0.0752	0.0675	0.7709	0.7058	0.6105	0.5852	**0.8725**	0.951**

PH - Plant Height (cm), PB - Primary Branches, SB - Secondary Branches, FI - Days to Flower Initiation, 50%F - Days to 50% Flowering, DM - Days to Maturity, NPP - Number of Pods per Plant, NSP - Number of Seeds per Pod, SYP - Seed Yield per Plant (g), BI - Biological Yield per Plant (g), HI - Harvest Index (%), TW - Test Weight (g/1000 seeds), YP - Seed Yield per Plot (g/3 m²) and YH - Seed Yield per Hectare (q/ha). * – Significant at 5% level; ** – Significant at 1% level. Residual Effect; phenotypic (r = 0.195) and genotypic (r = 0.214),

Table 7. Selection differentials and gains for key agronomic traits in *T. foenum graecum* L. genotypes.

VAR	Factor	Xo	Xs	SD	SDperc	h^2b	SG	SGperc	Sense	Goal
PH	FA1	85.80	93.20	7.42	8.65	0.95	7.05	8.22	increase	100
PB	FA1	5.04	5.31	0.27	5.37	0.96	0.26	5.13	increase	100
SB	FA1	7.02	7.63	0.62	8.76	0.97	0.59	8.46	increase	100
SYP	FA1	3.65	3.96	0.31	8.47	0.98	0.30	8.31	increase	100
BI	FA1	16.50	18.30	1.76	10.60	0.96	1.69	10.20	increase	100
HI	FA1	22.00	20.70	-1.22	-5.57	0.97	-1.18	-5.38	increase	0
TW	FA1	11.30	11.60	0.34	3.03	0.97	0.33	2.95	increase	100
YP	FA1	460.00	452.00	-7.25	-1.58	0.96	-6.99	-1.52	increase	0
YH	FA1	15.30	15.20	-0.15	-0.98	0.97	-0.15	-0.95	increase	0
FI	FA2	43.60	46.30	2.75	6.32	0.95	2.62	6.01	increase	100
50%F	FA2	81.30	85.20	3.85	4.74	0.88	3.39	4.17	increase	100
DM	FA2	123.00	127.00	4.07	3.30	0.87	3.55	2.88	increase	100
NPP	FA3	33.60	41.40	7.81	23.20	0.96	7.48	22.20	increase	100
NSP	FA3	16.30	16.90	0.62	3.83	0.85	0.53	3.25	increase	100

PH - Plant Height (cm), PB - Primary Branches, SB - Secondary Branches, FI - Days to Flower Initiation, 50%F - Days to 50% Flowering, DM - Days to Maturity, NPP - Number of Pods per Plant, NSP - Number of Seeds per Pod, SYP - Seed Yield per Plant (g), BI - Biological Yield per Plant (g), HI - Harvest Index (%), TW - Test Weight (g/1000 seeds), YP - Seed Yield per Plot (g/3 m²), YH - Seed Yield per Hectare (q/ha), VAR - Variable, Factor, Xo - initial value, Xs - final value, SD - standard deviation, SDperc - percentage change in SD, h^2b - heritability, SG - standardized gain, SGperc - percentage change in SG, Sense - direction of change and Goal - achievement indicator.

Table 8. Factor loadings for each variable (VAR) across three factors (FA1, FA2, FA3), along with Communality and Uniquenesses.

VAR	PH	PB	SB	FI	50%F	DM	NPP	NSP	SYP	BI	HI	TW	YP	YH
FA1	-0.95	-0.94	-0.96	0.19	0.15	0.04	-0.03	0.13	-0.98	-0.92	-0.65	-0.78	-0.86	-0.86
FA2	0.04	-0.03	0.03	-0.88	-0.86	-0.88	-0.16	0.25	0.09	0.02	0.28	0.10	0.41	0.41
FA3	0.13	0.02	-0.02	-0.02	0.05	0.03	-0.83	-0.77	0.04	0.00	0.04	0.09	-0.01	-0.03
Communality	0.91	0.89	0.93	0.81	0.77	0.77	0.71	0.67	0.96	0.85	0.50	0.62	0.91	0.91
Uniquenesses	0.09	0.11	0.07	0.19	0.23	0.23	0.29	0.33	0.04	0.15	0.50	0.38	0.09	0.09

PH - Plant Height (cm), PB - Primary Branches, SB - Secondary Branches, FI - Days to Flower Initiation, 50%F - Days to 50% Flowering, DM - Days to Maturity, NPP - Number of Pods per Plant, NSP - Number of Seeds per Pod, SYP - Seed Yield per Plant (g), BI - Biological Yield per Plant (g), HI - Harvest Index (%), TW - Test Weight (g/1000 seeds), YP - Seed Yield per Plot (g/3 m^2), YH - Seed Yield per Hectare (q/ha) and FA – functional group.

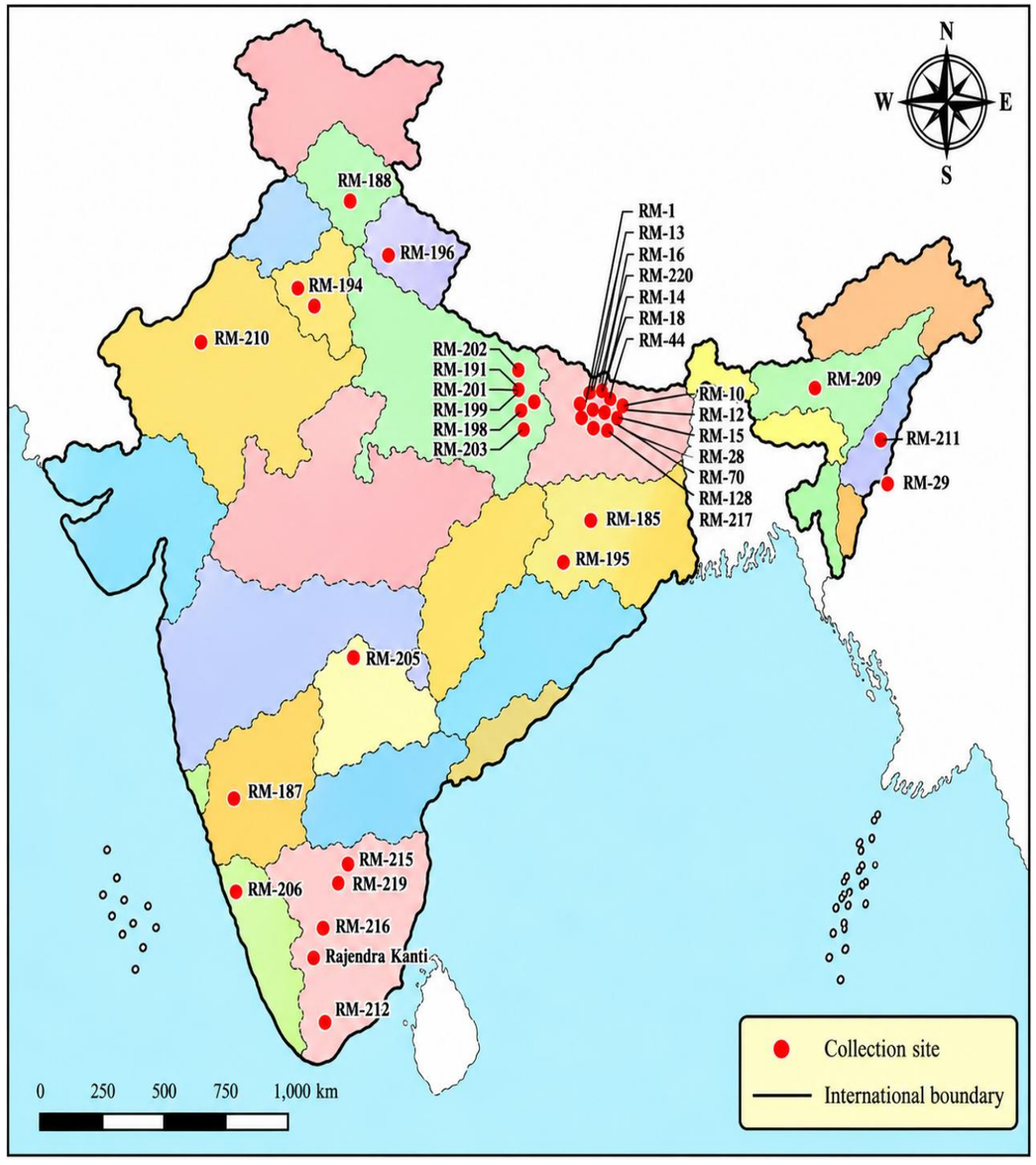


Figure 1. Collection sites and geographical coordinates of fenugreek (Trigonella foenum-graecum L.) genotypes collected from different regions of India.

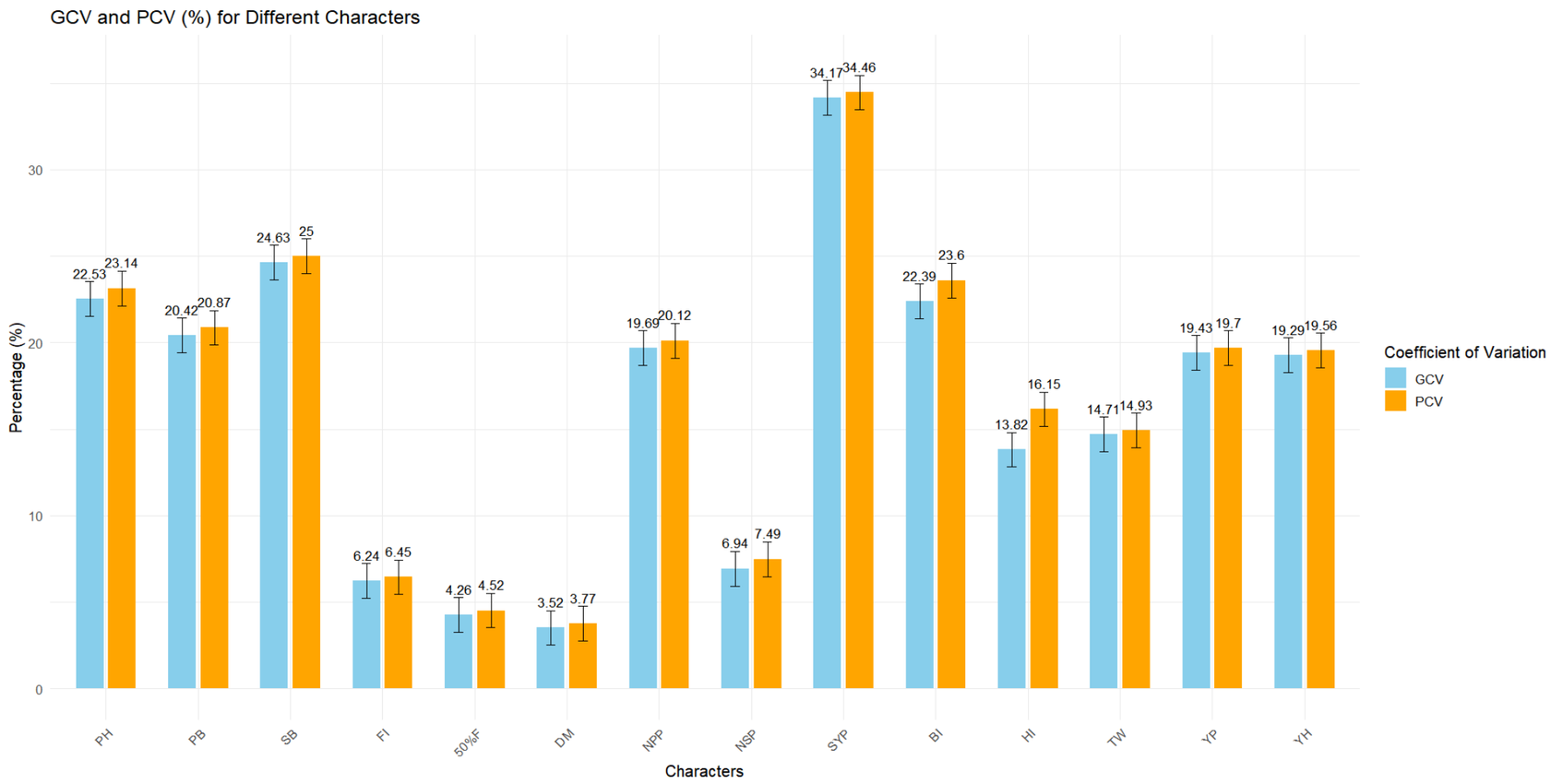
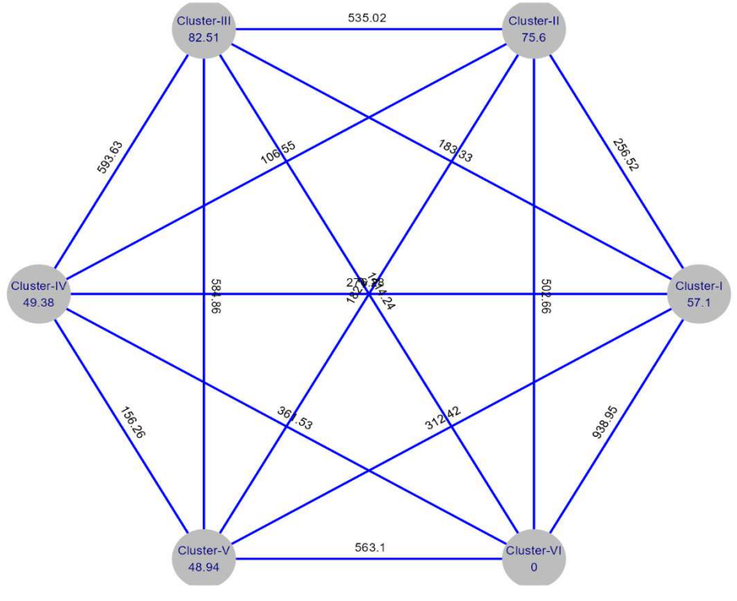


Figure 2. Phenotypic (PCV) vs Genotypic (GCV) Coefficient of Variation in Fenugreek Traits

a) Mahalanobis Euclidean distances



b) Contribution (%) of Traits to Divergence

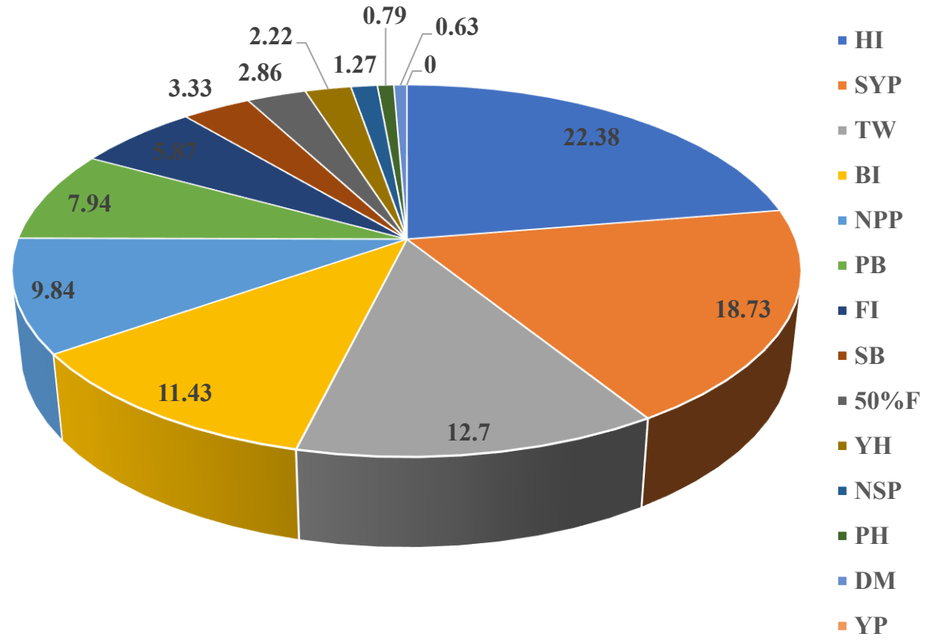


Figure 3. Genetic diversity analysis among fenugreek genotypes: (a) Mahalanobis Euclidean distances illustrating both intra- and inter-cluster relationships among the fenugreek genotypes; (b) Pie chart representing the relative contribution of various morphological and agronomic traits, PH - Plant Height (cm), PB - Primary Branches, SB - Secondary Branches, FI - Days to Flower Initiation, 50%F - Days to 50% Flowering, DM - Days to Maturity, NPP - Number of Pods per Plant, NSP - Number of Seeds per Pod, SYP - Seed Yield per Plant (g), BI - Biological Yield per Plant (g), HI - Harvest Index (%), TW - Test Weight (g/1000 seeds), YP - Seed Yield per Plot (g/3 m²) and YH - Seed Yield per Hectare (q/ha).

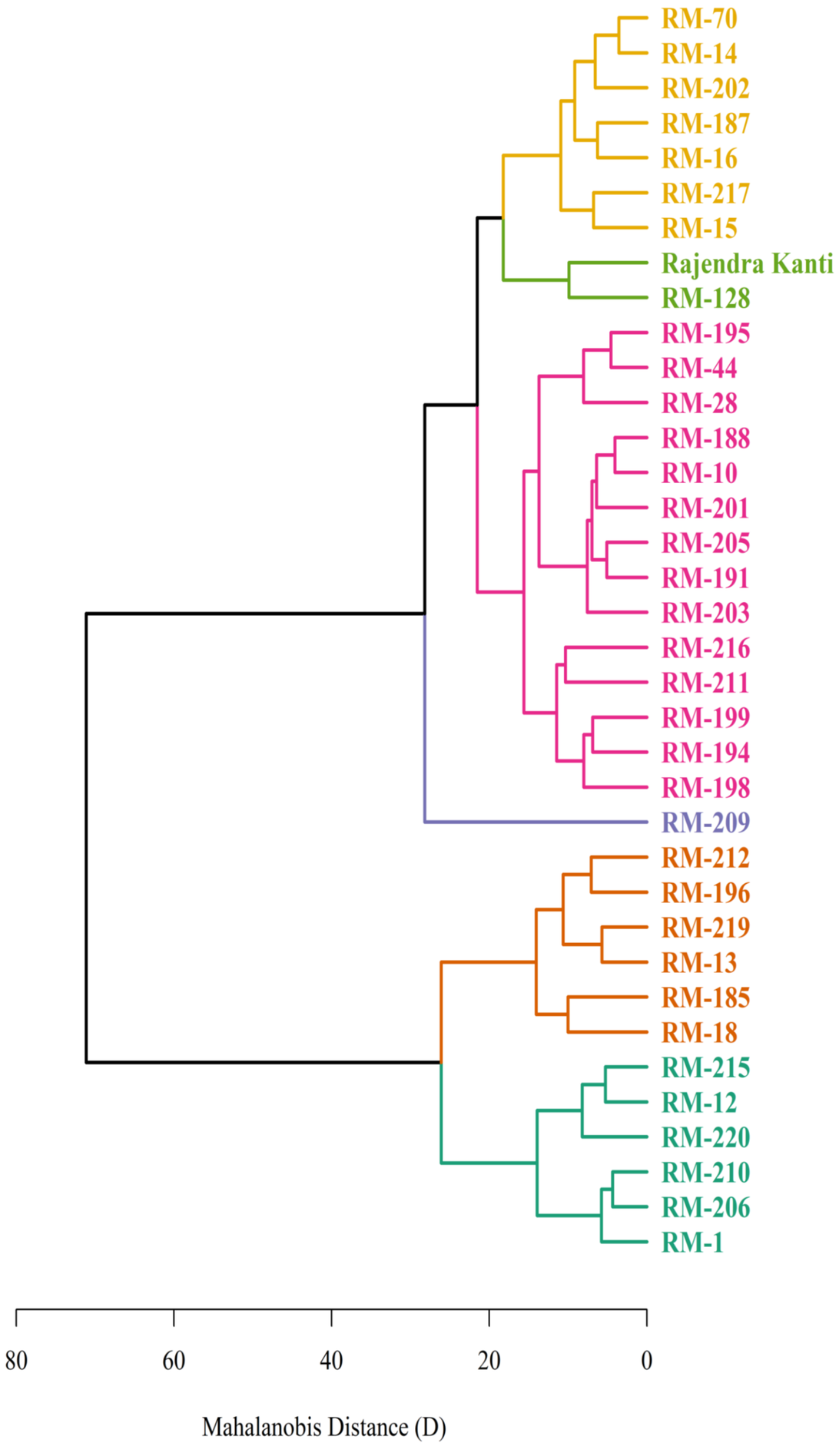


Figure 4: Clustering by Tocher method

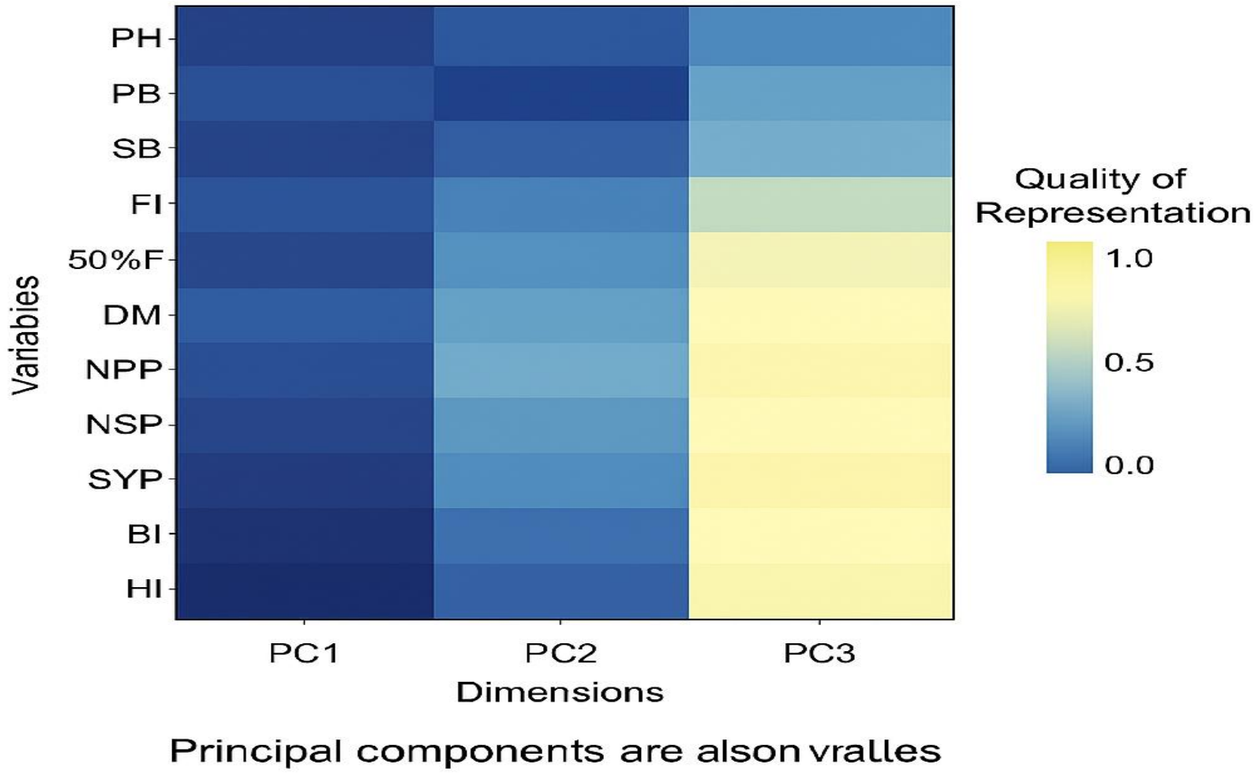


Figure 5. Quality of representation of different traits

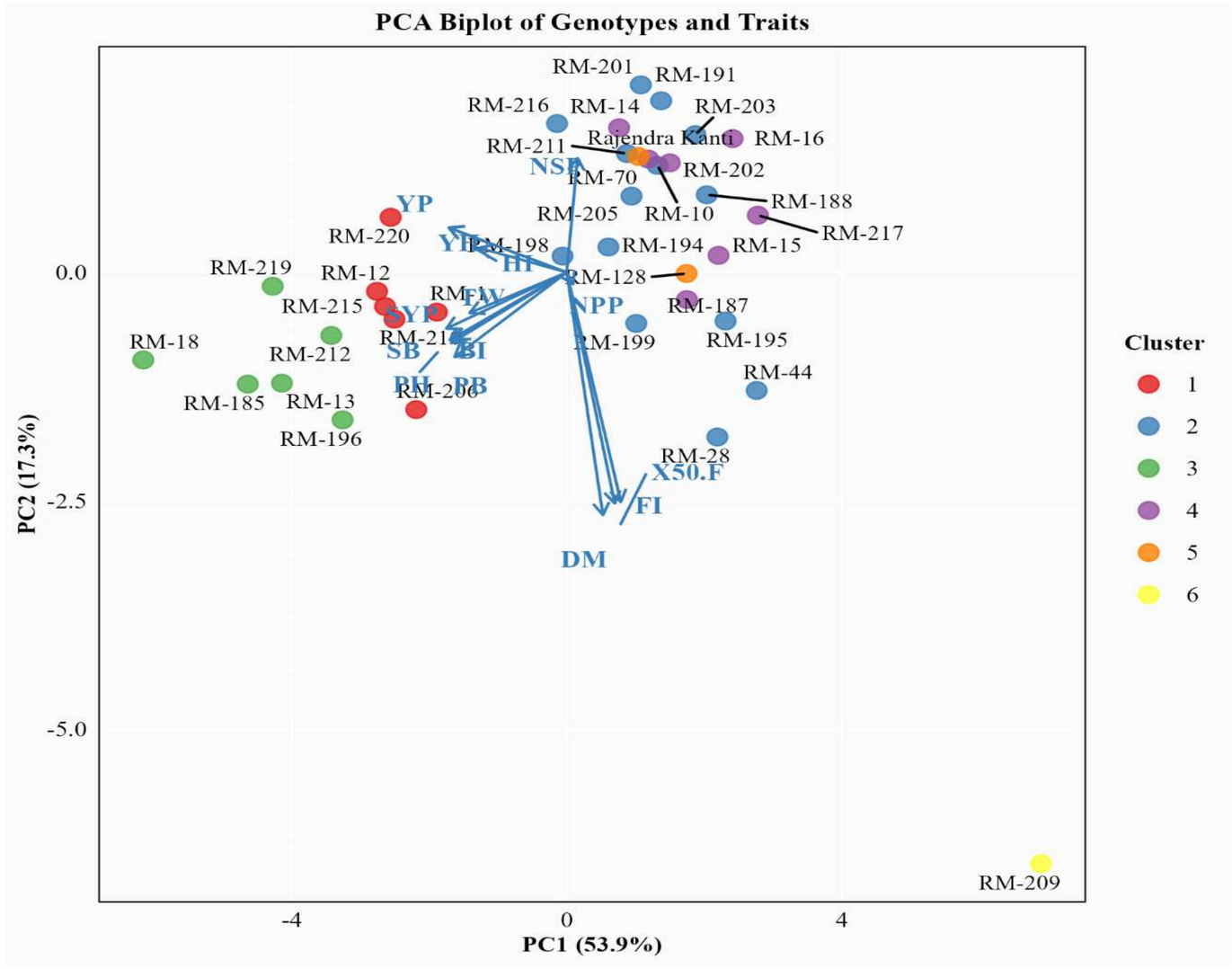


Figure 6. PCA Biplot of Genotypes and traits

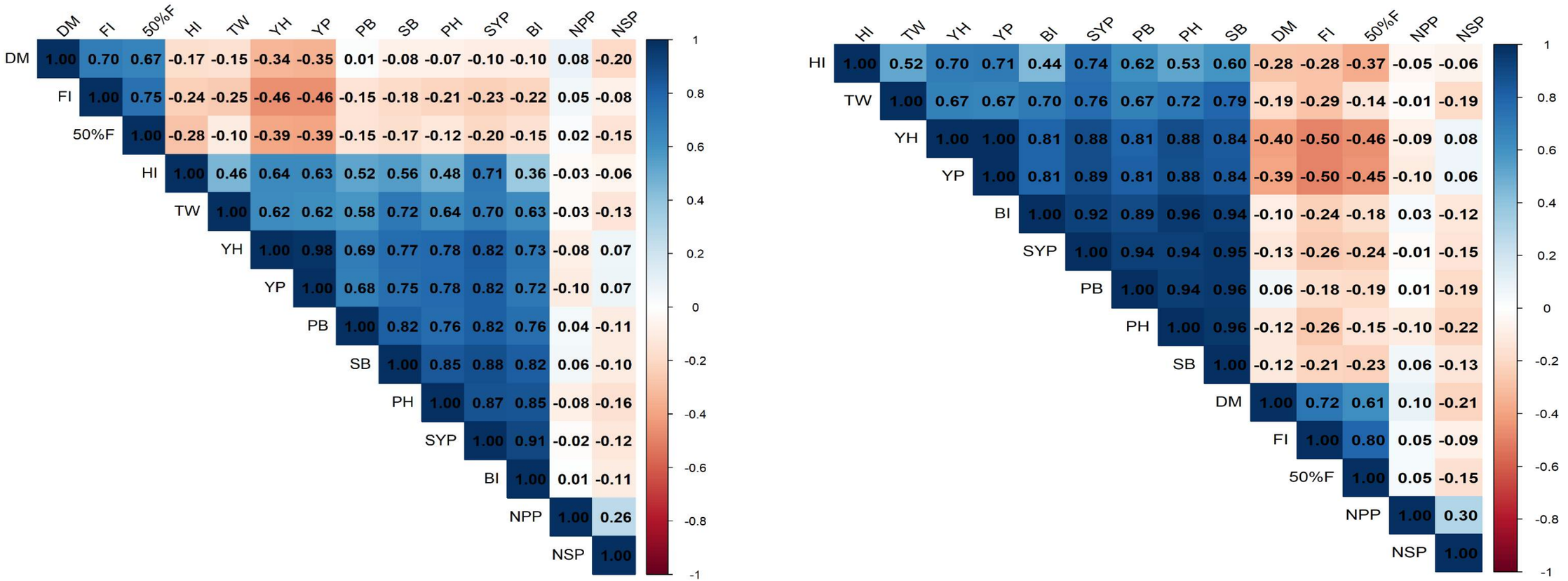


Figure 7. Phenotypic and Genotypic correlation analysis of morphological traits in fenugreek: (a) Heatmap showing phenotypic correlation coefficients among various traits. (b) Heatmap illustrating genotypic correlation coefficients for the same set of traits. PH - Plant Height (cm), PB - Primary Branches, SB - Secondary Branches, FI - Days to Flower Initiation, 50%F - Days to 50% Flowering, DM - Days to Maturity, NPP - Number of Pods per Plant, NSP - Number of Seeds per Pod, SYP - Seed Yield per Plant (g), BI - Biological Yield per Plant (g), HI - Harvest Index (%), TW - Test Weight (g/1000 seeds), YP - Seed Yield per Plot (g/3 m²) and YH - Seed Yield per Hectare (q/ha).

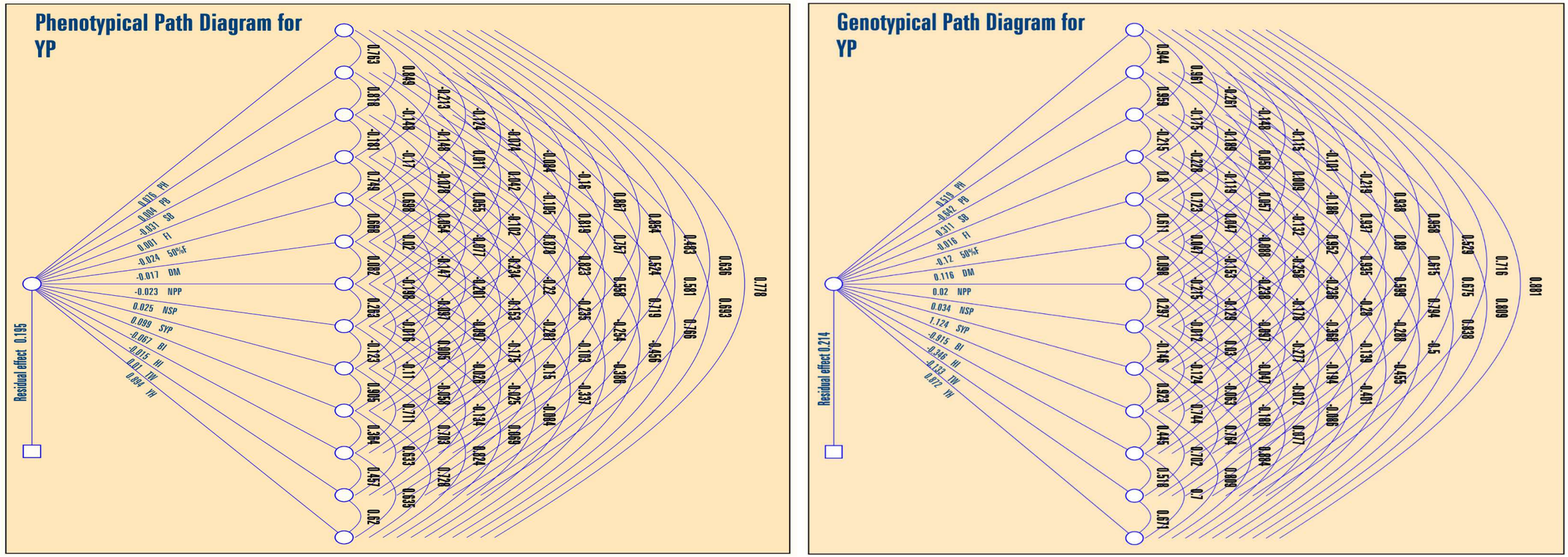


Figure 8. Phenotypic and Genotypic path analysis of morphological traits in fenugreek: (a) Heatmap showing phenotypic path coefficients among various traits. (b) Heatmap illustrating genotypic path coefficients for the same set of traits. PH - Plant Height (cm), PB - Primary Branches, SB - Secondary Branches, FI - Days to Flower Initiation, 50%F - Days to 50% Flowering, DM - Days to Maturity, NPP - Number of Pods per Plant, NSP - Number of Seeds per Pod, SYP - Seed Yield per Plant (g), BI - Biological Yield per Plant (g), HI - Harvest Index (%), TW - Test Weight (g/1000 seeds), YP - Seed Yield per Plot (g/3 m²) and YH - Seed Yield per Hectare (q/ha).

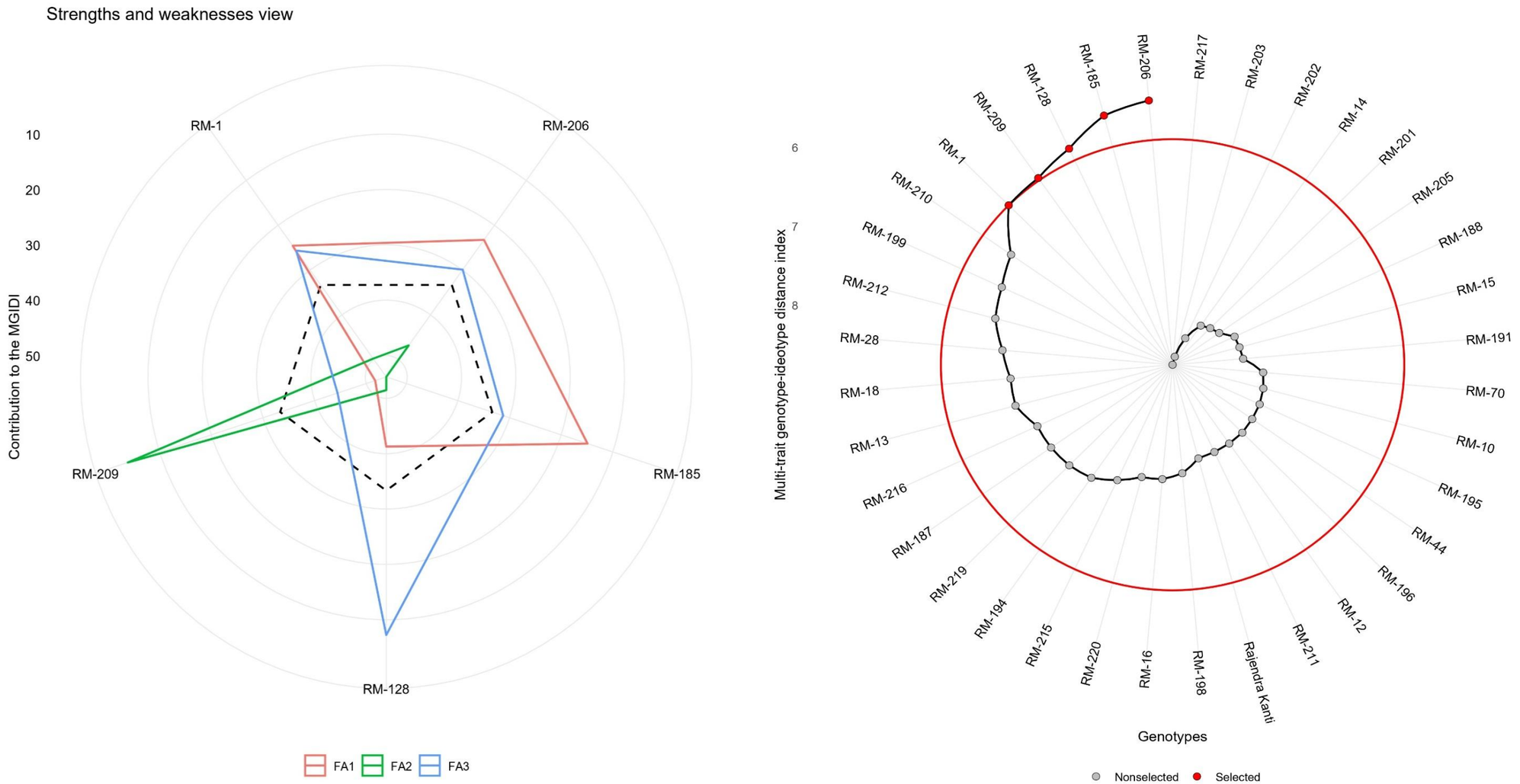


Figure 9. Contributions of genotypes: (a) Illustrates the contributions of selected fenugreek genotypes (RM-206, RM-185, RM-128, RM-209 and RM-1) across three factors (FA1, FA2 and FA3); (b) shows the MGIDI for all genotypes with the selected genotypes marked in red, indicating their higher desirability for multiple traits.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- 2yearfenugreekdata.xlsx