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ORIGINAL ARTICLE OPEN ACCESS

Identification of High-Performing Extra-Early Field Pea (*Pisum sativum* L.) Genotypes for Rice-Rice Cropping Systems Using MGIDI and Multivariate Analysis

Md. Golam Azam[1] | Md. Rafiqul Islam[2] | Mohammad Mamunur Rashid Sarker[3] | Md. Hasan Waliullah[4] | H. M. Khairul Bashar[5] | Md. Kamrul Islam[6] | Md. Bazlur Rahman[7] | Md Mashiur Rahman[8] | Umakanta Sarker[9]

[1]Pulses Research Centre, Bangladesh Agricultural Research Institute, Pabna, Bangladesh | [2]Agronomy Division, Regional Agricultural Research Station, Bangladesh Agricultural Research Institute, Pabna, Bangladesh | [3]On-Farm Research Division, Bangladesh Agricultural Research Institute, Gazipur, Bangladesh | [4]On-Farm Research Division, Bangladesh Agricultural Research Institute, Rajshahi, Bangladesh | [5]On-Farm Research Division, Bangladesh Agricultural Research Institute, Patuakhali, Bangladesh | [6]On-Farm Research Division, Bangladesh Agricultural Research Institute, Khulna, Bangladesh | [7]Bangladesh Agricultural Research Institute, Gazipur, Bangladesh | [8]Agricultural Engineering Division, Pulses Research Centre & Regional Agricultural Research Station, Bangladesh Agricultural Research Institute (BARI), Pabna, Bangladesh | [9]Department of Genetics and Plant Breeding, Faculty of Agriculture, Gazipur Agricultural University, Gazipur, Bangladesh

Correspondence: Md. Golam Azam (azamprcbari@gmail.com) | Md Mashiur Rahman (mashi.fpm84@gmail.com)

Received: 7 March 2026 | **Revised:** 17 April 2026 | **Accepted:** 28 April 2026

Keywords: field pea (*Pisum sativum* L.) | heritability | MGIDI index | multivariate analysis | rice-rice cropping system | variability

ABSTRACT

The development of rice–rice farming systems in South Asia necessitates extra-early maturing legumes that can fit into short planting windows without affecting yield productivity. This 2-year study evaluates 43 extra-early field pea (*Pisum sativum* L.) genotypes during two consecutive years at the Pulses Research Centre (PRC), Bangladesh Agricultural Research Institute (BARI), Bangladesh, to identify genetically diverse, early, and high-performing lines suitable for rice-fallow ecosystems. Seven phenological, growth, and yield-related variables were analyzed using multivariate analyses, variability and heritability estimations, cluster analysis, path analysis, and the multi-trait genotype–ideotype distance index (MGIDI). Significant variability was observed across all traits, with wide ranges for flowering (33–59 days), maturity (74–106 days), plant height (PH) (78–186 cm), pods per plant (PPP) (4.6–31.0), hundred seed weight (HSW) (4.9–28.8 g), yield per plant (YPP) (3.10–8.33 g), and seed yield productivity (SYPP) (950–2149 kg ha^{-1}). According to principal component analysis (PCA), PC1 and PC2 accounted for 73.50% of the overall variability, with the first four principal components explaining 89.80%. A correlation study found that yield was highly impacted by PPP, PH, HSW, and YPP, although HSW exhibited a negative correlation with phenological duration. The genotypes were divided into five different groups using hierarchical clustering, which showed significant inter-cluster divergence and plenty of room for parent selection during hybridization. Genotypic divergence and trait relationships were further confirmed by heatmap-based clustering. Genotypes containing favorable qualities for earliness, PPP, HSW, and yield were effectively rated using MGIDI analysis. Among all genotypes, BFPX41, BFPX1, BFPX23, BFPX30, and BFPX16 emerged as prospective high-yielding and extra-early candidates appropriate for rice–rice systems. The future breeding of short-duration, high-yielding field peas appropriate for intensive cropping systems will be firmly established due to the identified genetic diversity and improved genotypes.

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1 | Introduction

Field pea (*Pisum sativum* L.) is one of the most important winter-season grain legumes cultivated worldwide, contributing over 14 million tons from more than 7 million hectares (FAO 2025). It is a self-pollinated diploid (2n = 14) annual winter-season pulse crop (Kindie et al. 2019; SAREP 2026) and is commonly used as both a vegetable and pulse and offers an economical source of digestible protein, essential amino acids, carbs, vitamins, and minerals for resource-poor families (Abha et al. 2019; Getachew 2019). Its nitrogen-fixing capacity enhances soil fertility and makes it an environmentally viable alternative for crop rotation (Gebremichael et al. 2025; Keneni et al. 2013). However, despite its promise, the crop's productivity is typically hampered by terminal heat, soil moisture stress, and disease challenges in short-season conditions, underlining the significance of producing extra-early and stable cultivars (Islam et al. 2025).

Field pea must achieve early maturation to mitigate heat, drought, and disease stress in semiarid and rice-dominated areas (Parihar et al. 2022; Thomas et al. 2026). Early maturing field pea varieties help fit the crop into intensive farming systems and increase yield in a shorter time because they complete their lifecycle in 80–90 days (Endres and Kandel 2021; Kadžiulienė et al. 2025). These early varieties are important for rice-fallow, rice-rice, and traditional agricultural landscapes (TAL) because long-duration types suffer from heat stress and late planting. Extra-early field pea genotypes work best in rice-fallow and rice-rice systems where the cropping window is very short. Long-duration varieties face heat and drought stress or delay the next crop, reducing production (Nath et al. 2023; Parihar et al. 2021; Sansa et al. 2025). Therefore, identifying extra-early field pea genotypes is important to support continuous crop production in rice-based systems.

In the Indo-Gangetic Plains (IGP), rice-based farming systems are very important for food security (Ray et al. 2020). These systems use a lot of energy and affect the environment, so making them more sustainable is necessary (Kumawat et al. 2025). Diversifying the cropping system and improving energy use can help make rice-based farming more efficient (Ray et al. 2020), because land, water, and energy are becoming limited. Improving resource-use efficiency is now a major concern for rice-based systems (Kumawat et al. 2025). In Bangladesh, rice is the main food, and replacing it is very difficult, especially in the rainy season due to soil and climate conditions (Kumar et al. 2022). In lowland areas of the IGP, fully replacing rice with other crops is not possible (Biswas et al. 2024; Ranjan et al. 2024). However, farmers can diversify the rice–wheat system by adding oilseeds, legumes, vegetables, and fodder crops, especially in integrated farming systems (Liu et al. 2025; Saha et al. 2022). To improve the environment and farm income, sustainable cropping systems are needed to replace rice–fallow areas in the IGP (Reddy et al. 2025; Sahoo et al. 2024).

Field pea breeding is a crucial process for improving yield and quality and depends on understanding genetic variation, heritability, and genetic advance (GA) for key agronomic traits. Biometric tools like genotype coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h_2b), and GA help breeders see how effective selection will be in early generations (Akter et al. 2020; Castro-Urrea et al. 2023; Viradiya et al. 2025). These measures, GCV, PCV, heritability, and GA, are useful for studying genetic diversity and the ability of plants to adapt (Azam et al. 2020). By using new genetic materials and selecting plants with good yield traits, breeding programs aim to improve field pea productivity (Akter et al. 2020; Azam et al. 2020). The correlation studies assist plant breeders in making more precise selections. Due to the increased relevance of agricultural growth, the current understanding of trait linkages assists. Due to the expanding relevance of crop growth, current understanding of trait linkages supports the right selection process (Gonçalves et al. 2017).

Moreover, multivariate techniques are important for genotype identification, as they help researchers understand complex phenotypic data that cannot be explained by single-trait methods. Cluster analysis groups genotypes based on similarity and helps identify natural variation patterns, outliers, and relationships with ecological or geographic origins (Bashir et al. 2025; Dhanda and Munjal 2017; Farid et al. 2021; Mohi-Ud-din et al. 2021). These cluster differences are useful for choosing genetically diverse parents to improve the breeding pool and increase genetic gain in future breeding cycles (Dhanda and Munjal 2017). Principal component analysis (PCA) helps identify genotypes by converting many correlated traits into fewer uncorrelated components that explain the main variation in the dataset (Cozzolino et al. 2019; Ullah et al. 2022). This reduction makes data easier to interpret while still keeping most of the original variability (Cozzolino et al. 2019). Using both cluster analysis and PCA together gives a clearer and stronger understanding of diversity patterns (Aslam et al. 2017; Koij and Saba 2015). Biplots and component loadings help confirm the clusters and improve the accuracy of genotype classification (Aslam et al. 2017). Together, these methods help breeders understand trait relationships, find hidden patterns, and select the best genotypes for breeding (Koij and Saba 2015).

A diverse germplasm pool provides the basic material needed to select superior genotypes and develop climate-resilient varieties for fragile environments (Bhanu 2017; Salgotra and Chauhan 2023). Climate change, irregular rainfall, shorter growing seasons, and rising food demand make the protection and improvement of diverse breeding lines more important than ever (Daszkiewicz 2022; Diouf et al. 2021). Although field pea is an important crop worldwide, studies focusing on extra-early genotypes are very limited (Abha et al. 2019; Getachew 2019). Few studies have compared genetic diversity among different plant types, such as dwarf, semi-dwarf, determinate, and indeterminate, within extra-early maturity groups (Azam et al. 2020; Azam et al. 2024). There is also little information comparing regular and semi-leafless plant types in terms of genetic diversity (Getachew 2019). Because of this lack of knowledge, the present study aimed to examine genetic diversity in field pea genotypes using key morpho-agronomic traits (Abha et al. 2019).

The multi-trait genotype–ideotype distance index (MGIDI) index, developed by Olivoto and Nardino (2021), is an important advancement in plant breeding because it overcomes the limitations of selecting genotypes based on a single trait.

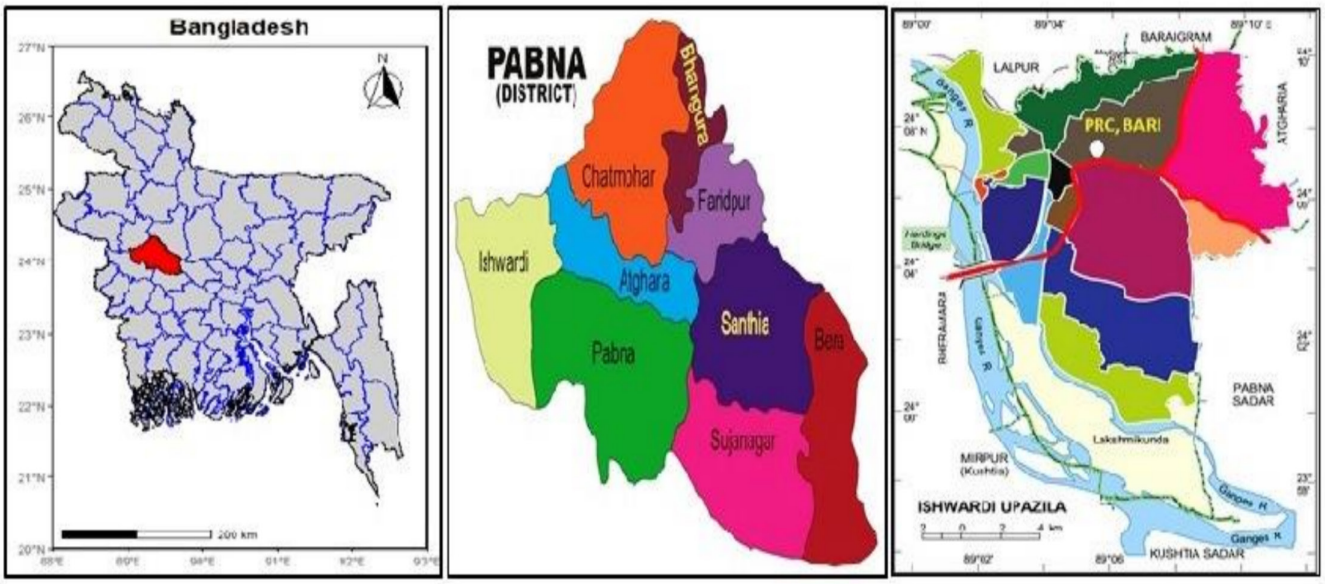


FIGURE 1 | Location map at Pulses Research Centre, Ishwardi, Pabna.

Single-trait selection often gives biased results and causes unbalanced genetic improvement. MGIDI evaluates many traits at the same time and calculates the Euclidean distance between each genotype and an ideal ideotype with the best values for all traits (Olivoto and Nardino 2021). This method improves selection accuracy and shows both strengths and weaknesses of each genotype. It helps breeders identify which traits need improvement while keeping the desirable traits (Olivoto et al. 2022). MGIDI is especially useful when breeders must consider several traits at once, such as early maturity, high yield, stability, and wide adaptability (Olivoto et al. 2022; Olivoto and Lúcio 2020). This tool is very helpful for field pea breeding in rice–rice cropping systems, where varieties must mature early, fit short sowing windows, and maintain good yield (Olivoto and Nardino 2021).

In rice-based systems with short planting windows and many environmental challenges, identifying extra-early, high-yielding, and stable field pea genotypes is crucial for improving productivity and cropping intensity. However, the genetic diversity of extra-early field pea suitable for rice-fallow and intensive rice systems remains insufficiently explored. Understanding genetic diversity and heritable traits is essential for effective selection and long-term crop improvement, especially under climate change and limited resource conditions. Therefore, this study hypothesizes that significant genetic variability exists among extra-early field peas that can effectively identify superior genotypes combining early maturity, high yield potential, and desirable agronomic traits. In this context, the present study evaluates the genetic diversity, variability, heritability, and overall performance of 43 extra-early field pea genotypes using multivariate statistical tools, including PCA, cluster analysis, and the MGIDI index. The objective of this study is to identify promising genotypes and key traits that can support breeding programs within rice-rice and rice-fallow cropping systems.

2 | Materials and Methods

2.1 | Experimental Site

This experiment was undertaken in two separate years (2023–2024 and 2024–2025) in Bangladesh, each falling under identical agroclimatic zones. The trial was held in the Pulses Research Centre (PRC), Bangladesh Agricultural Research Institute (BARI) (latitude: 24°08′ 60.00″N, longitude: 89°04′ 0.12″E, 13 m above sea level), which is located in the AEZ 11, corresponding to the High Ganges River Floodplain in Bangladesh (Figure 1).

2.2 | Climatic Conditions

Table 1 displays the monthly mean temperatures, wind speed, and precipitation data throughout the duration of the experiment. The soil was clay loam soil, with a pH of 7.1. The first-year trial was carried out from November 2023 to March 2024, with temperatures between 10.6 and 30.1°C, 5.1 mm of total rainfall, and 80.15% humidity during the cropping season. This second-year study was done from November 2024 to March 2025. During the cropping season, temperatures varied from 11.6°C to 30.4°C, with a total rainfall of 8.5 mm.

2.3 | Plant-Based Materials

All the lines, or genotypes, were picked from the prior observation trail (OT) in 2022 at the PRC breeding field. For this investigation, 43 field pea genotypes were acquired from PRC, BARI. The released variety BARI Motor-2 (BFPX26) was utilized as a check for early investigated genotypes. The list and description of the materials utilized for the study and their sources are presented in Table 2.

TABLE 1 | Monthly mean agroclimatic data during the field experiment period in 2023 and 2024 at PRC, BARI, Ishwardi, Pabna.

Years	Months	Min (°C)	Max (°C)	Wind (km/h)	Rainfall (mm)	Humidity (%)	Cloud (%)	Pressure (mb)	Sunshine hours
2023–2024	November	18.6	30.1	11.4	0	84.5	0	1004.4	7.0
	December	14.6	26.1	9.80	3.8	82.2	49.7	1010.5	6.7
	January	10.8	22.2	10.90	0	81.5	10.7	1009.7	6.1
	February	13.8	27.4	12.80	1.3	72.4	31.5	1011.4	5.9
	March	14.6	29.5	15.40	3.3	75.2	30.5	1016.8	6.2
2024–2025	November	19.0	30.4	10.00	0	84.0	0	1010.7	7.5
	December	12.7	25.9	9.50	0	81.5	5.7	1009.8	6.3
	January	11.6	24.5	9.20	0	79.5	6.2	1008.6	5.8
	February	14.0	28.8	12.20	8.5	72.4	53.0	1006.9	5.7
	March	14.9	30.4	14.60	0	77.2	31.5	1020.2	6.0

TABLE 2 | Description of 43 field pea genotype name, code, and sources of seed.

Acc. code	Genotype name	Seed source	Acc. code	Genotype name	Seed source
BFPX1	BFPX-17007-2	OT	BFPX23	BFPX-17008-5	OT
BFPX2	BFPX-17003-2	OT	BFPX24	BFPX-17006–5	OT
BFPX3	BFPX-17001-2	OT	BFPX25	BFPX-17007-4	OT
BFPX4	BFPX-17006-3	OT	BFPX26	BARI Motor-2	Breeder
BFPX5	BFPX-17008-1	OT	BFPX27	BARI Motor-3	Breeder
BFPX6	BFPX-17001–1	OT	BFPX28	BFPX 1700 3–10	PYT
BFPX7	BFPX-17003-1	OT	BFPX29	BFPX 17005–1	PYT
BFPX8	BFPX-17008-8	OT	BFPX30	BFPX 1700 3–5	PYT
BFPX9	BFPX-17004-2	OT	BFPX31	BARI Motor-4	PYT
BFPX10	BFPX-17004-1	OT	BFPX32	BRPX 17002–12	Breeder
BFPX11	BFPX-17007-3	OT	BFPX33	BFPX 17002–13	PYT
BFPX12	BFPX-17006-2	OT	BFPX34	BFPX 17001–11	PYT
BFPX13	BFPX-17008-9	OT	BFPX35	BFPX 17005–7	PYT
BFPX14	BFPX-17008-6	OT	BFPX36	BFPX 17005–4	PYT
BFPX15	BFPX-17008-7	OT	BFPX37	BFPX 17003–8	PYT
BFPX16	BFPX-17006-1	OT	BFPX38	BFPX 17001–3	PYT
BFPX17	BFPX-17005-1	OT	BFPX39	BFPX 17002–7	PYT
BFPX18	BFPX-17007-1	OT	BFPX40	BARI Motor-1	Breeder
BFPX19	BFPX-17008-2	OT	BFPX41	BFPX-16003	RYT
BFPX20	BFPX-17006-6	OT	BFPX42	BFPX-16005	RYT
BFPX21	BFPX-17008-3	OT	BFPX43	BFPX-16008	RYT
BFPX22	BFPX-17008-4	OT	—	—	—

Abbreviations: Acc., accessions; OT, observation yield trail; PYT, preliminary yield trail; RYT, regional yield trail.

2.4 | Experimental Design and Crop Husbandry

A randomized complete block design (RCBD) with three replications was utilized to set up the research for two consecutive years (2023–2024 and 2024–2025). A plot size of $4 \times 2\,m^2$ ($8\,m^2$) was employed in this study, where each plot was composed of four rows with 80 plants inside each row, with an inter-row spacing of 50 cm and 5–7 cm between plants within the row. The spacing between plots and block distances was 1.0 and 1.5 m, respectively. The application of pre-sowing irrigation helps achieve good germination. The experimental plots were well-prepared before planting, and we applied farm yard manure (FYM). The prescribed quantities of fertilizer and manure were used during field pea growing (Azam et al. 2020). Before being sown, the seeds were treated with 2.5 g/kg of Provex, a mixture of carboxin and thiram. Weeds were regularly pulled from the experiment, and irrigation was applied as needed. All agronomic management methods were applied equitably and appropriately as per the guidelines of Azam et al. (2024).

2.5 | Collected Data

Data were obtained on a single plant and plot basis. Five randomly chosen plants from each genotype in each replication were used to gather plant-specific data, including plant height (PH) (cm), number of pods per plant (NPPP) (number), and yield per plant (YPP) (gram). While the data on a plot basis were gathered, they include days to 80% flowering (DF), days to 90% maturity (DM), hundred seed weight (HSW) (grams), and seed yield per hectare (YPH) (kilogram per hectare).

2.5.1 | DF

DF is the number of days that passed between the date of sowing and the point at which about 80% of the plants in a plot displayed flowering on roughly 80% of their flower buds.

2.5.2 | DM

The number of days from the date of planting to a stage where 90% of plants have completed their physiological maturity was determined by yellowish leaf color and shedding starting on the lower stem, and hardened pods and seeds.

2.5.3 | PH and Other Plant-Related Data

The average height of five randomly selected plants in each plot was measured (centimeter) from the ground surface to the top of the main stem at physiological maturity (when the color of their pods changed from green to lemon yellow). The average number of mature pods per plant (PPP) was counted during harvest on five randomly chosen plants. YPP was also counted at harvest on five randomly picked plants, in five randomly taken yields per plant. The weight in grams of 100 seeds was randomly chosen from each plot. And lastly, the net plot grain yield adjusted at 10% moisture content was translated into yield per hectare in kilograms.

2.6 | Statistical Analysis

Researchers chose the graphical depiction using boxplots to demonstrate the influence of field pea on yield and yield-associated characteristics. Boxplots summarize numerous variable distributions, help discover correlations, compare central tendency and variability, and aid in exploratory data analysis and hypothesis testing (Morales et al. 2021). They conducted the multivariate analysis using the R (v4.1.2) and R Studio software (v1.4.1717). They created the boxplot with the R packages "ggplot2," "ggpubr," and "reshape2" (Morales et al. 2021). PCA, a versatile tool of multivariate analysis, offers insights into the structure of complex datasets not only by reducing the dimensionality of the datasets while retaining most of the variability but also by identifying the key components driving the variation (Gewers et al. 2022). The eigenvalue was extracted, and the PCA variable plot was shown using the R packages "ggplot2," "gridExtra," "factoextra," "ggbiplot," and "corrplot" (Bouras et al. 2022). The data were utilized to produce a heatmap and hierarchical clusters with Euclidean distance and Ward's minimal variance approach (Ward.D2) using the "pheatmap" and "ggplot2" packages (Walasek-Janusz et al. 2022). Mahalanobis distance is an important matrix in multivariate analysis, offering insights into data relationships, distributions, similarity between points, and clustering observations. The genotypes were grouped into distinct clusters with clear dissimilarities in the generated cluster heatmap, and the genotypes within the clusters showed a high degree of similarity (Lahav et al. 2019). A cluster validation software called "clv" was used to measure the Mahalanobis squared distance (D2) between the clusters (Ambachew et al. 2023). Mean values were discriminated using the least significant difference (LSD) technique at a significance threshold of 5%. Various genetic parameters, including genotypic variance (GV, $\sigma^2 g$), phenotypic variance ($\sigma^2 p$), environmental variance ($\sigma^2 e$), the genotypic coefficient of variation (GCV), the PCV, the environmental coefficient of variation (ECV), heritability (h2), and GA as a percentage of the mean (GAPM), were calculated using the variability package. To analyze the phenotypic and genotypic variation (PV and CV), researchers examined and marked GCV and PCV to employ the formula proposed by Johnson et al. (1955). Allard (1999) provided the equation used to calculate the broad-sense heritability ($h_2 b$) of all desired traits. Burton and DeVane (1953) classed heritability as low (0%–10%), moderate (10–20%), and high (above 20%). Singh and Chaudhury (1985) interpreted the equation used to estimate GA. The statistical analysis for the MGIDI was done utilizing the R Package "metan" version 1.19.0 (https://github.com/TiagoOlivoto/metan) in R version 4.1.2 (http://www.r-project.org/) (Olivoto et al. 2022).

3 | Results

3.1 | Variability and Mean Performance Among the Traits

A box plot was used to visualize the descriptive statistics of 43 field pea genotypes on the yield and yield-contributing traits (Figure 2).

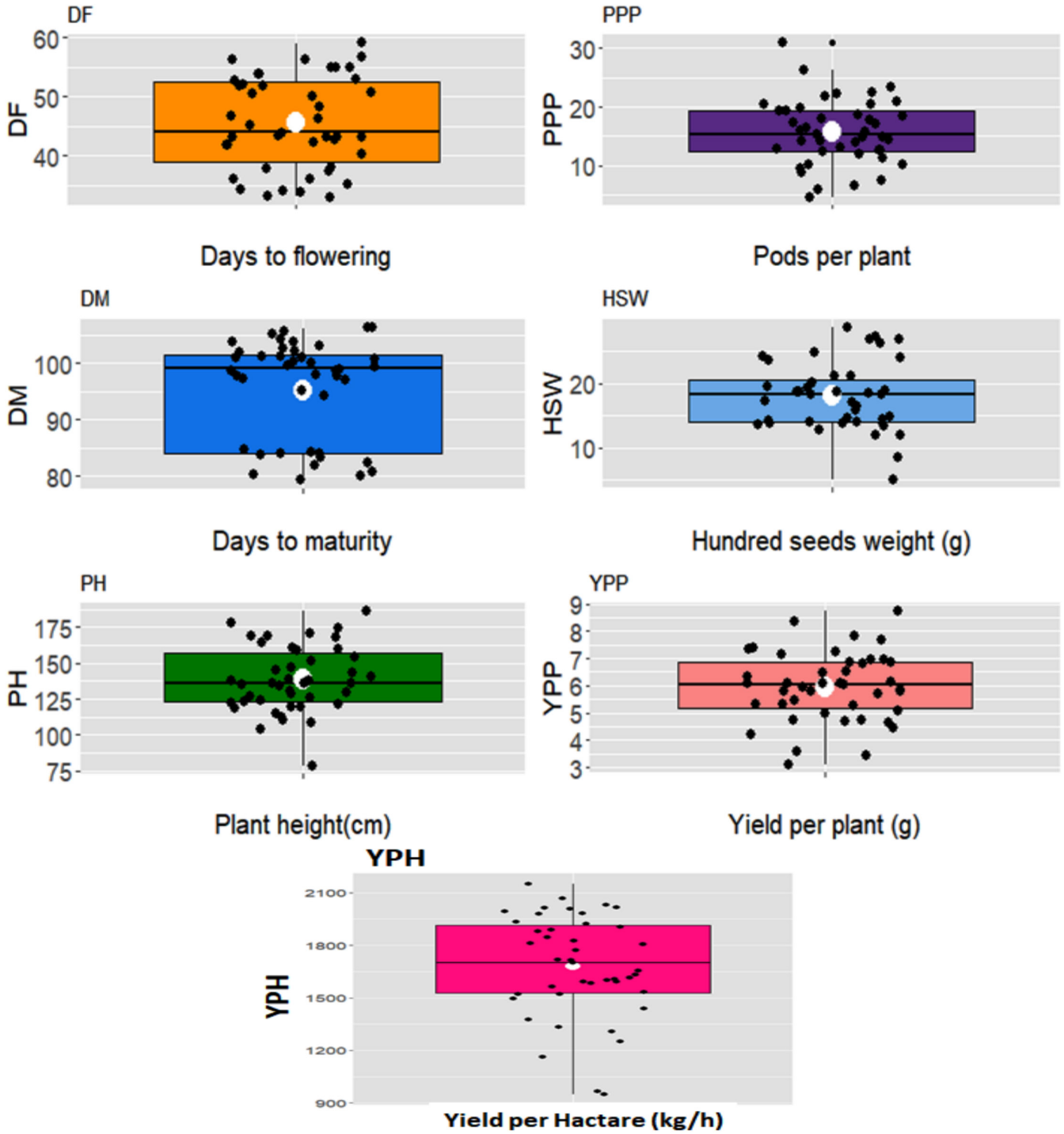


FIGURE 2 | The box plots show the descriptive statistics of the field pea genotypes' yield and yield-contributing attributes. The white circle represents the corresponding trait mean, and the horizontal line inside the box represents the median. Q1 (first quartile/25th percentile), Q3 (third quartile/75th percentile), (Q1–1.5IQR), and (Q3 + 1.5IQR) are indicated by the box's lower and upper boundaries, lower and upper whisker, respectively. Interquartile range or IQR. The black dots in the boxes represent the distribution of the 43 genotypes. DF, days to 80% flowering; DM, days to 90% maturity; HSW, the weight of 100 seeds (g); PH, plant height (cm); PPP, the number of pods per plant (number); YPH, seed yield (kg/h); YPP, yield per plant.

3.1.1 | Phenological Traits

The box plot for DF reveals a considerable spread, showing substantial variance among the genotypes (Figure 2). The median is centrally positioned within the interquartile range (IQR), suggesting a generally symmetric distribution. A few genotypes emerge as outliers, meaning that some lines bloomed substantially earlier or later than the rest. Genetic variety, which is essential for choosing early- or late-flowering genotypes appropriate for various habitats or cropping patterns, is suggested by this variation in flowering time. DM also exhibits a relatively broad range, demonstrating substantial diversity in physiological maturity among the genotypes. The box is modestly tilted toward the lower end, showing that most genotypes developed

within a reasonably narrow range, with a few late-maturing outliers. The observed difference in maturity length matches the blooming data, showing that earliness might be utilized in breeding for short-duration cultivars. PH exhibits a wide IQR, suggesting significant genetic variation (Figure 2). Tall and dwarf outliers are shown by a few extreme numbers above and below the whiskers, respectively. Such diversity is helpful for choosing genotypes adapted to different cropping methods (e.g., intercrop or sole crop) or for mechanized harvesting. The reasonably uniform dispersion shows that PH is impacted by both hereditary and environmental factors.

3.1.2 | Yield-related Qualities

Strong genetic variety for this attribute is implied by the PPP distribution's large variability and several outliers (Figure 2). The median is somewhat below the center, suggesting a modestly right-skewed distribution, where most genotypes have moderate pod numbers and a few genotypes have extraordinarily high pod counts. HSW has very limited variance compared with other variables, showing that seed size is more constant across genotypes. YPH has significant genotype variability, which reflects the combined impact of yield components (Figure 2). The box plot displays a few lower and higher outliers, showing that both low- and high-yielding lineages exist in the population. A significant opportunity for selection and yield enhancement is indicated by the spread. The data are not significantly skewed, as indicated by the tight alignment of the mean and median values.

3.1.3 | Field Pea Genotype's Descriptive Performance

The mean performance of 43 field pea genotypes for seven yield and yield-contributing variables is shown in Table 3. Substantial variance was seen across the genotypes for all recorded variables, demonstrating the presence of substantial genetic variety in the experimental materials.

3.1.4 | Phenology and Growth Characteristics

The population mean was 46 days, while the genotypes' DF varied from 33 to 59 days (Table 3). The coefficient of variation (CV) was low (8.66%), demonstrating steady expression of this feature under the experimental circumstances. The earliest blooming genotype was BFPX26 (33 days), followed closely by BFPX5 and BFPX2, while BFPX40 was the slowest to flower (59 days). The observed diversity points to the existence of both late-flowering and early-flowering varieties that are appropriate for certain agro-ecological zones or cropping sequences. DM varied from 74 to 106 days, with an average of 95 days and a CV of 7.79%, demonstrating generally equal performance among genotypes. BFPX26 matured earliest (74 days), while BFPX28, BFPX37, BFPX38, and BFPX40 took the longest time (106 days). Breeding projects aimed at short-duration variations for rice-based cropping systems may benefit from the difference between early and late maturing genotypes. PH varied widely among genotypes, ranging from 78.47 cm (BFPX26) to 185.85 cm (BFPX14), with a mean of 138.41 cm and a CV of 7.97%. Such a large range shows great genetic variation for plant architecture. While shorter genotypes like BFPX26 could provide superior lodging resistance, taller genotypes like BFPX14, BFPX5, and BFPX9 might be beneficial for biomass output (Table 3).

3.1.5 | Seed Yield and Yield Components

With a mean of 15.69 and a CV of 4.80%, the PPP showed significant variance, ranging from 4.62 to 31.00 (Table 3). BFPX41 has the most pods (31.00), followed by BFPX23 (26.26) and BFPX25 (23.31). Conversely, BFPX26 generated the fewest pods (4.62). The large variability in pod number implies that this feature strongly contributes to yield variance among genotypes. HSW ranged from 4.93 to 28.80 g, with a mean of 18.01 g and a CV of 5.79%, demonstrating considerable variability. BFPX40 produced the smallest seeds (4.93 g), whereas BFPX16 produced the heaviest (28.80 g). Both small-seeded and bold-seeded genotypes suggest the possibility of selection based on processing suitability and market preference. YPP varied from 3.10 to 8.33 g, with a mean of 6.07 g and a low CV (5.98%), reflecting high experimental accuracy. BFPX41 (8.33 g) produced the maximum YPP, closely followed by BFPX1 (8.72 g) and BFPX16 (7.80 g). The lowest yield was achieved by BFPX26 (3.10 g).

These data reveal a broad range of production potential among genotypes. YPH varied from 950 to 2149 kg ha^{-1}, with an overall mean of 1678 kg ha^{-1} and a CV of 5.11%, suggesting substantial variance among genotypes. The maximum yield was produced from BFPX41 (2149 kg ha^{-1}), followed by BFPX1 (2030 kg ha^{-1}), BFPX23 (2014 kg ha^{-1}), and BFPX30 (2017 kg ha^{-1}), while BFPX26 and BFPX40 were the lowest yielders (950 and 967 kg ha^{-1}, respectively). The large yield range suggests considerable genotypic effect and opportunity for selection of high-yielding lines.

3.2 | Range, Genetic Parameters and Coefficients of Variation

3.2.1 | Genetic variance

A significant range of variance was identified across the 43 field pea genotypes for all examined characteristics, indicating high genetic variety within the germplasm. There is sufficient variety for selection in the population, as indicated by the range values, which ranged from 4.4 (PPP) to 690 (YPH) (Table 4). The phenotypic variation (PV) was greater than the GV for each variable, indicating that environmental factors affect the expression of these traits. Nonetheless, the little discrepancies between PV and GV for most traits suggest that hereditary factors predominantly influenced trait performance rather than environmental factors. The phenotypic (PCV) and genotypic (GCV) coefficients of variation ranged from 9.95% to 37.15% and 2.67% to 34.07%, respectively. The GCV and PCV were highest for PPP (GCV = 34.07%; PCV = 37.15%), then for HSW (GCV = 29.03%; PCV = 29.61%), and finally for YPP (GCV = 25.53%; PCV = 30.53%). The wide range of these attributes indicates a significant opportunity for effective selection. On the other hand, DF (GCV = 17.01%; PCV = 17.22%), DM (GCV = 9.95%; PCV = 10.11%), and PH (GCV = 15.76%; PCV = 17.67%) showed a lot of variation. YPH

TABLE 3 | Mean performance of 43 field pea genotypes for yield components and seed yield evaluated at PRC in during 2023 and 2024 (Pooled data).

Genotypes	DF	DM	PH	PPP	HSW	YPP	YPH
BFPX1	37	102	177.49	18.68	21.22	8.72	2030
BFPX2	34	82	108.56	12.98	15.88	6.15	1615
BFPX3	38	97	147.01	19.77	18.57	6.31	1656
BFPX4	42	81	103.94	14.26	26.97	5.70	1497
BFPX5	33	97	170.61	20.45	19.40	7.33	1923
BFPX6	36	84	119.77	10.13	17.18	4.76	1250
BFPX7	34	79	126.46	12.88	18.35	5.80	1523
BFPX8	48	99	136.29	19.37	18.63	4.43	1162
BFPX9	50	99	173.95	15.73	19.53	7.26	1906
BFPX10	35	80	115.44	8.85	16.51	6.10	1602
BFPX11	34	82	134.37	11.31	19.84	7.16	1880
BFPX12	43	84	126.06	15.93	26.98	6.07	1593
BFPX13	43	103	167.66	14.95	18.68	5.48	1440
BFPX14	40	99	185.85	14.26	18.90	6.53	1715
BFPX15	43	100	164.12	12.59	18.27	6.88	1805
BFPX16	43	85	118.79	7.47	28.80	7.80	2007
BFPX17	42	84	124.20	10.23	23.58	5.95	1563
BFPX18	46	95	143.67	13.87	21.13	6.03	1584
BFPX19	43	94	159.89	18.09	20.06	4.98	1307
BFPX20	42	84	123.31	6.69	24.83	5.08	1334
BFPX21	44	101	168.94	14.95	24.23	6.96	1826
BFPX22	36	80	119.38	9.54	26.36	5.84	1533
BFPX23	38	99	168.74	26.26	18.77	7.67	2014
BFPX24	43	83	121.64	6.00	27.23	5.25	1377
BFPX25	45	98	159.10	23.31	18.70	6.07	1593
BFPX26	33	74	78.47	4.62	23.99	3.10	950
BFPX27	52	101	140.53	17.80	12.82	3.59	1607
BFPX28	57	106	154.60	21.87	13.57	7.38	1520
BFPX29	52	104	135.33	20.47	14.07	4.72	1935
BFPX30	54	104	160.60	22.20	13.72	5.32	2017
BFPX31	47	98	110.47	11.93	11.89	4.22	1717
BFPX32	55	105	130.33	14.47	14.03	6.84	1633
BFPX33	53	100	128.27	12.47	13.82	6.47	1980
BFPX34	55	104	138.93	15.33	14.68	5.82	1982
BFPX35	51	101	136.27	18.47	13.73	5.78	2067
BFPX36	52	101	144.87	16.33	13.46	6.82	1993
BFPX37	54	106	136.13	19.27	14.14	6.95	1887

(Continues)

TABLE 3 | (Continued)

Genotypes	DF	DM	PH	PPP	HSW	YPP	YPH
BFPX38	55	106	151.13	12.53	17.01	4.71	1772
BFPX39	53	101	138.07	17.00	14.93	4.62	1700
BFPX40	59	103	122.73	20.87	4.93	3.47	967
BFPX41	51	98	137.73	31.00	12.02	8.33	2149
BFPX42	56	102	112.27	22.47	14.48	5.33	1813
BFPX43	56	100	129.47	17.27	8.49	6.07	1847
Min	33	74	78.47	4.62	4.93	3.10	950
Max	59	106	185.85	31.00	28.80	8.33	2149
Mean	46	95	138.41	15.69	18.01	6.07	1678
SE of mean	0.70	0.99	6.37	1.34	0.60	0.59	49.40
CV	8.66	7.79	7.97	4.8	5.79	5.98	5.11
LSD	1.97	2.77	17.92	3.77	1.69	1.64	138.93

Abbreviations: DF, days to 80% flowering; DM, days to 90% maturity; HSW, hundred seed weight (g); PH, plant height (cm); PPP, number of pods per plant (number); YPH, seed yield (kg/h); YPP, yield per plant.

(GCV = 17.54%; PCV = 18.27%) also showed a lot of variation that was acceptable for selection (Table 4).

3.2.2 | Heritability (h_2b)

Broad-sense heritability estimates show that most traits are very heritable, with values ranging from 70 to 98. The highest heritability was found for DF (98), next DM (97), and finally HSW (96). YPP (70) exhibited moderate heritability, although PH (80) and YPH (92) showed strong heritability as well. The high heritability of most traits indicates that additive gene effects mostly govern their inheritance, suggesting that phenotype-based selection might be effective for genetic enhancement (Table 4).

3.2.3 | GA and GAPM

The GA ranged from 2.67 (YPP) to 582.13 (YPH), illustrating the anticipated enhancement under selection pressure. The GAPM ranged from 20.17% for DM to 64.36% for PPP. The highest GAPM was achieved for PPP at 64.36%, with HSW at 58.65%, YPP at 43.97%, and YPH at 34.70%. This indicates that these traits are primarily influenced by additive genes and can be effectively improved through selection. Furthermore, traits exhibiting modest genetic improvement, like DF (34.62%) and PH (28.98%), suggest a reasonable potential for enhancement. DM had the lowest GAPM (20.17%), suggesting that selection for this trait has produced little genetic gain (Table 4).

3.3 | PCA

PCA, a possible method of multivariate data analysis, is purposely utilized to investigate and reduce difficult and considerable datasets. In order to improve the discriminatory ability for classifying the measured features according to their correlations under typical growth conditions, the PCA was calculated in our study. Six principal components (PCs) were obtained for the current investigation; however, only the first four PCs with eigenvalues greater than one were deemed significant (Figure 3). These four PCs accounted for around 89.8% of the genotypic variability, as impacted by observable characteristics. Among the significant PCs, the first two components accounted for around 73.5% of the overall variability (Figure 3). In the PCA-variable plot, the first PC (PC1) represented approximately 46.8% of the total variability. All characteristics contributed favorably to PC1, but attributes such as HSW contributed negatively to PC1 (Figure 3). The second PC (PC2) accounted for around 26.7% of total variability and was largely explained by the qualities like DF, DM, and PPP on the path to positive direction. PC2 was adversely affected by other characteristics (Figure 3). To acquire an overall knowledge, the contributions of seedling attributes to the first six important PCs were analyzed. After that, traits that contributed more than 5% of the total variability were chosen for further multivariate analysis.

3.4 | Correlation Analysis

DF demonstrated a substantial positive correlation with days to maturity ($r = 0.74^*$), implying that genotypes that bloomed sooner tended to mature earlier as well (Figure 4). However, DF revealed a substantial negative correlation with HSW ($r = -0.62^*$), indicating that late-flowering genotypes tended to yield smaller seeds. The association of DF with other features such as PH, PPP, and YPP was modest and nonsignificant, showing little direct effect on yield components. DM revealed positive relationships with PH ($r = 0.58^*$) and PPP ($r = 0.64^{***}$), showing that late-maturing genotypes often had taller plants and greater PPP. Conversely, DM showed a significant negative correlation ($r = -0.63$) with HSW, suggesting that bolder seeds are typically associated with early-maturing genotypes (Figure 4). The strong correlation observed between DF and DM indicates their

TABLE 4 | Range, genotypic variance, phenotypic variance, phenotypic coefficient of variability (%), genotypic coefficient of variability (%), broad sense heritability (h_2), genetic advance (GA), and genetic advance percent of mean (GAMP) of field pea (pooled data).

Traits	Range		EV	GV	PV	ECV	GCV	PCV	h_2b	GA	GAPM
DF	31.83	60	1.48	60.11	61.58	2.67	17.01	17.22	98	15.78	34.62
DM	71.25	107	2.91	89.18	92.10	1.80	9.95	10.11	97	19.14	20.17
PH	75.81	213.8	121.89	476.03	597.92	7.98	15.76	17.67	80	40.10	28.98
PPP	4.40	38	5.40	28.59	33.99	14.81	34.07	37.15	84	10.10	64.36
HSW	4.43	29.30	1.09	27.34	28.43	5.80	29.03	29.61	96	10.56	58.65
YPP	1.12	17	1.03	2.40	3.43	16.74	25.53	30.53	70	2.67	43.97
YPH	690	2175	7321.99	86606.41	93928.4	5.10	17.54	18.27	92	582.13	34.70

Note: Details of traits are presented in Figure 2.
Abbreviations: ECV, environmental coefficient of variance; EV, environmental variance; GA, genetic advance; GAPM, genetic advance as percentage of mean; GCV, genotypic coefficient of variance; GV, genotypic variance; h_2b, heritability (broad sense); PCV, phenotypic coefficient of variance; PV, phenotypic variance.

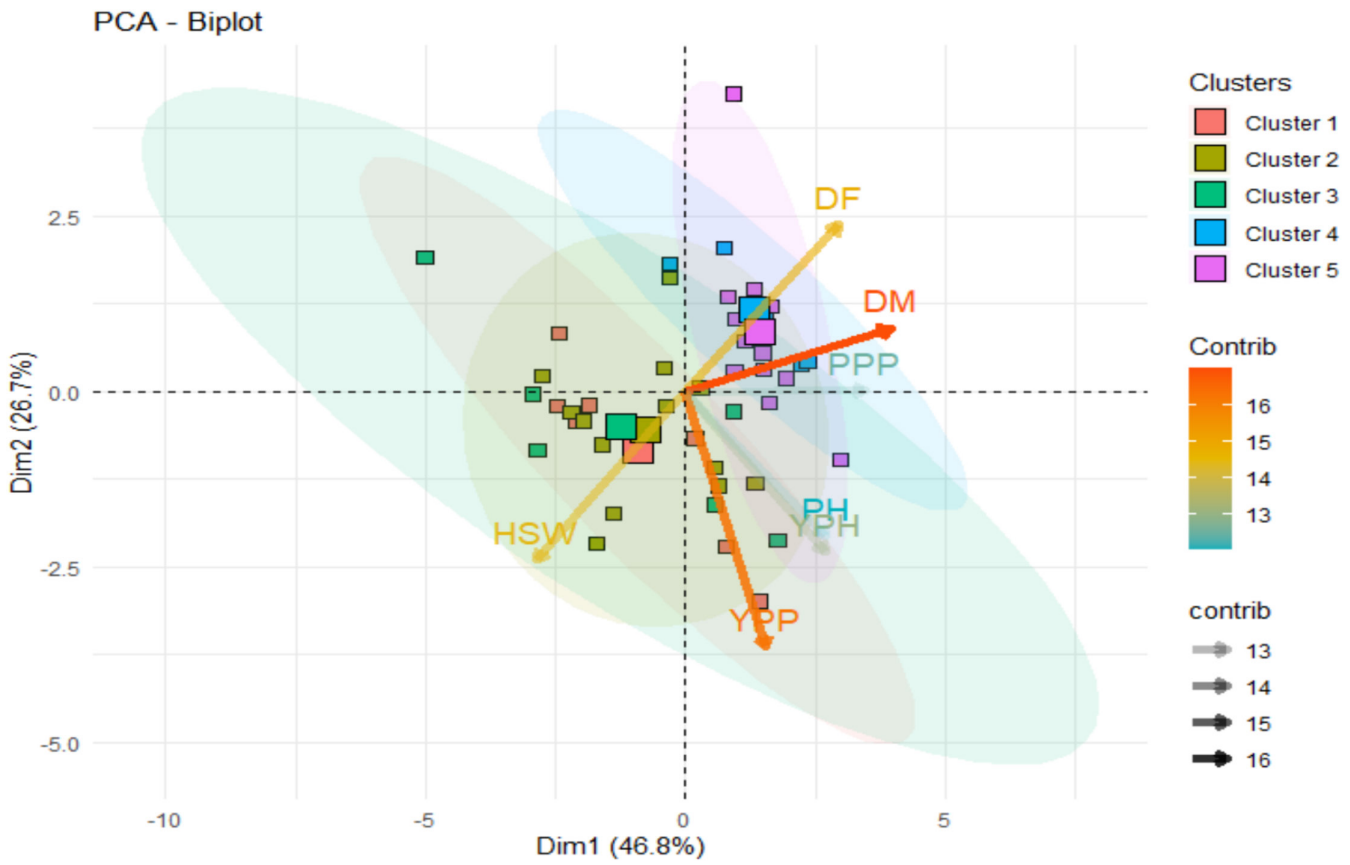


FIGURE 3 | Yield traits are displayed in a PCA-variable plot. The length and color intensity of a vector in the plot indicate the quality of the representation and the contribution of the attributes to the principal components, respectively. The angles between the vectors created from the plot's central point show whether the seedling traits interact positively or negatively. Figure 2 shows specifics of seedling characteristics (for an explanation of how this figure legend's color references should be interpreted).

physiological relationship throughout the crop's growth period. Positive associations were found by PH with PPP ($r=0.46$) and DM ($r=0.58$), indicating that taller genotypes are likely to possess more pods and a longer duration of maturity. Taller plants may improve yield potential by increasing pod-bearing capacity, as indicated by the positive but non-significant correlation with YPH ($r=0.41$) (Figure 4). Longer growth length and taller plants increase pod formation, supported by PPP's strong positive associations with DM ($r=0.64$) and PH ($r=0.46$). However, a negative correlation ($r=-0.52$) exists between PPP and HSW, suggesting a compensatory relationship between pod quantity and seed size. Genotypes that generate more pods often have relatively smaller seeds (Figure 4). HSW exhibits substantial negative correlations with DF ($r=-0.62$), DM ($r=-0.63$), and PPP ($r=-0.52$). This inverse relationship suggests that genotypes characterized by larger seeds often flower and mature

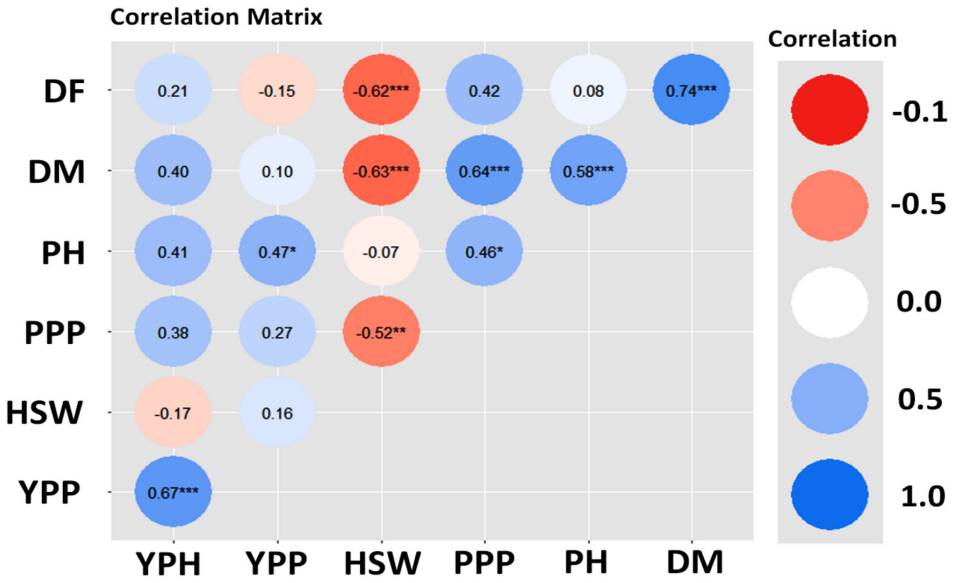


FIGURE 4 | The Pearson correlation coefficient values are displayed in the correlation heatmap for the selected study traits. The blue values are positive, and the red ones are negative. It has a range of −1 to 1, whereby −1 denotes an absolute negative linear relationship, +1 indicates a perfect positive linear relationship, and 0 specifies no relationship at all between studied variables. Details of traits are presented in Figure 2.

sooner, resulting in a lower number of pods produced. The relationship between HSW and YPH ($r = -0.17$) is negative and nonsignificant, indicating that merely increasing seed weight does not guarantee greater yields. The association between YPP and YPH is notably strong ($r = 0.67$), suggesting that individual plant productivity plays a significant role in total yield performance. Relationships with yield components were positive; however, they were not significant. This indicates that YPP incorporates multiple features instead of relying on a single factor. YPH was favorably linked with most characteristics, notably YPP ($r = 0.67$***), PH ($r = 0.41$), DM ($r = 0.40$), and PPP ($r = 0.38$). These relationships imply that yield improvement is substantially driven by the collective performance of multiple yield components. Field pea production growth is more dependent on pod quantity and plant stature than on individual seed size, according to the non-significant association with HSW ($r = -0.17$).

3.5 | Heatmap-Based Cluster Analysis

A combined heatmap and hierarchical clustering analysis (Figure 5) utilized PCA-selected traits to assess the pattern of genotypic variability and the relationships between seedling and agro-morphological features. Clustering based on the Ward.D2 agglomerative method, along with Euclidean distance, resulted in the identification of five distinct genotype clusters (Clusters 1–5), highlighting significant variations in phenotypic expression across the evaluated genotypes. The genotype clusters differed markedly in their relative performance patterns across the measured traits, as indicated by the contrasting color gradients on the heatmap. The list of genotypes categorized under each cluster is shown in Table 2. The examined characteristics were divided by the dendrogram into three main clusters at the trait level, labeled as characteristics Cluster 1, Cluster 2, and Cluster 3. These clusters represent groups of attributes that show similar expression patterns and covariation among genotypes. Unlike trait Cluster 2, which encompassed qualities exhibiting significant negative or positive deviations (blue–orange extremes), trait Cluster 1 primarily showcased generally uniform or moderate expressions. Features associated with pod and yield qualities were included in Trait Cluster 3, showcasing distinct variability patterns in contrast to early growth traits. Blue tones represent values that are higher than average for each genotype × trait combination, while orange tones signify values that are lower than average. The heatmap color scale, which ranges from −2 to +2, clearly illustrates the intensity and direction of relative standardized values.

3.6 | Cluster Dendrogram Interpretation

The hierarchical cluster analysis classified the 43 field pea genotypes into five separate groups based on their performance in yield and yield-contributing characteristics (Table 5 and Figure 6). The dendrogram produced using the genetic divergence data demonstrated considerable separation across genotypes, demonstrating a large range of genetic diversity within the analyzed population.

3.6.1 | Cluster Composition and Size

Seven genotypes (BFPX1, BFPX5, BFPX9, BFPX14, BFPX15, BFPX21, and BFPX23) made up this cluster 1 (Table 5 and Figure 6). The very modest cluster size shows these genotypes have comparable morphological and agronomic traits. They are presumably medium-duration and high-yielding kinds with greater plant stature, as evidenced by their cluster mean values. Cluster 2, the biggest group, has 13 genotypes (BFPX2, BFPX4, BFPX6, BFPX7, BFPX10, BFPX11, BFPX12, BFPX16, BFPX17, BFPX20, BFPX22, BFPX24, and BFPX26). The significant number of genotypes in this cluster shows a high degree of similarity among these accessions. Cluster 3 consists of six genotypes (BFPX3, BFPX8, BFPX13, BFPX18, BFPX19,

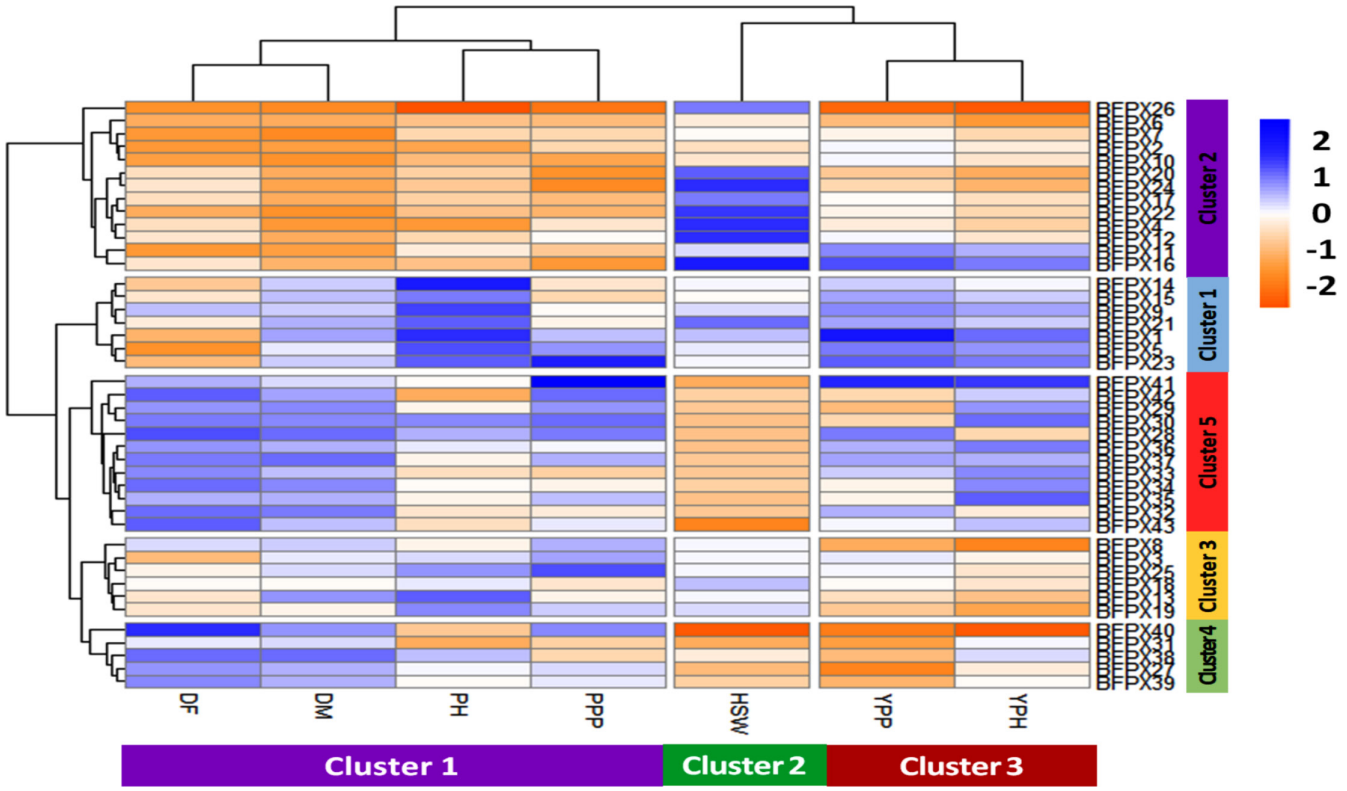


FIGURE 5 | Heatmap and cluster analysis (method = ward. D2 and distance = Euclidean) based on PCA-selected traits influencing genotypic variability between genotypes and seedling traits. Five clusters were acquired at the genotype level (Clusters 1, 2, 3, 4, and 5), and three clusters (Clusters 1, 2, and 3) were obtained at the trait level. The intensity of the relative values for the studied attributes is expressed by various color tones. Table 2 displays the genotype list for each cluster. Details of traits are presented in Figure 2.

TABLE 5 | Cluster grouping of 43 field pea genotypes based on the Ward.D2 method and Euclidean distance analysis.

Clusters	No. of genotypes	Genotype code
Cluster 1	7	BFPX1, BFPX5, BFPX9, BFPX14, BFPX15, BFPX21, BFPX23
Cluster 2	13	BFPX2, BFPX4, BFPX6, BFPX7, BFPX10, BFPX11, BFPX12, BFPX16, BFPX17, BFPX20, BFPX22, BFPX24, BFPX26
Cluster 3	6	BFPX3, BFPX8, BFPX13, BFPX18, BFPX19, BFPX25
Cluster 4	5	BFPX27, BFPX31, BFPX38, BFPX39, BFPX40
Cluster 5	12	BFPX28, BFPX29, BFPX30, BFPX32, BFPX33, BFPX34, BFPX35, BFPX36, BFPX37, BFPX41, BFPX42, BFPX43

and BFPX25). Cluster 4 had five genotypes (BFPX27, BFPX31, BFPX38, BFPX39, and BFPX40). Cluster 5 comprises 12 genotypes: BFPX28, BFPX29, BFPX30, BFPX32, BFPX33, BFPX34, BFPX35, BFPX36, BFPX37, BFPX41, BFPX42, and BFPX43. This cluster is characterized by high-yielding genotypes that exhibit late blooming and maturity, moderate PH, and a large NPPP. This cluster represents a promising opportunity for projects aimed at yield improvement, given its high yield per hectare and favorable yield components.

3.6.2 | Dendrogram Architecture

The dendrogram clearly showed significant genetic variation among the field pea genotypes under study, as it separated the genotypes into several distinct groups (Figure 6). Clusters 2 and 4 exhibited the highest inter-cluster distances, as did Clusters 2 and 3. This indicates that these pairings are the most divergent and may act as potential parents for hybridization aimed at enhancing heterosis. The existence of clusters that mature both early and late, along with groups that yield high and low, further highlights the presence of significant genetic diversity, which is crucial for breeding programs. The moderate distances within clusters indicate that the genotypes in each cluster are predominantly similar.

3.6.3 | Cluster Mean Analysis of Field Pea Genotypes

Table 6 shows the average performance of 43 field pea genotypes divided into five clusters for seven quantitative variables. The clustering pattern indicated high inter-cluster variability,

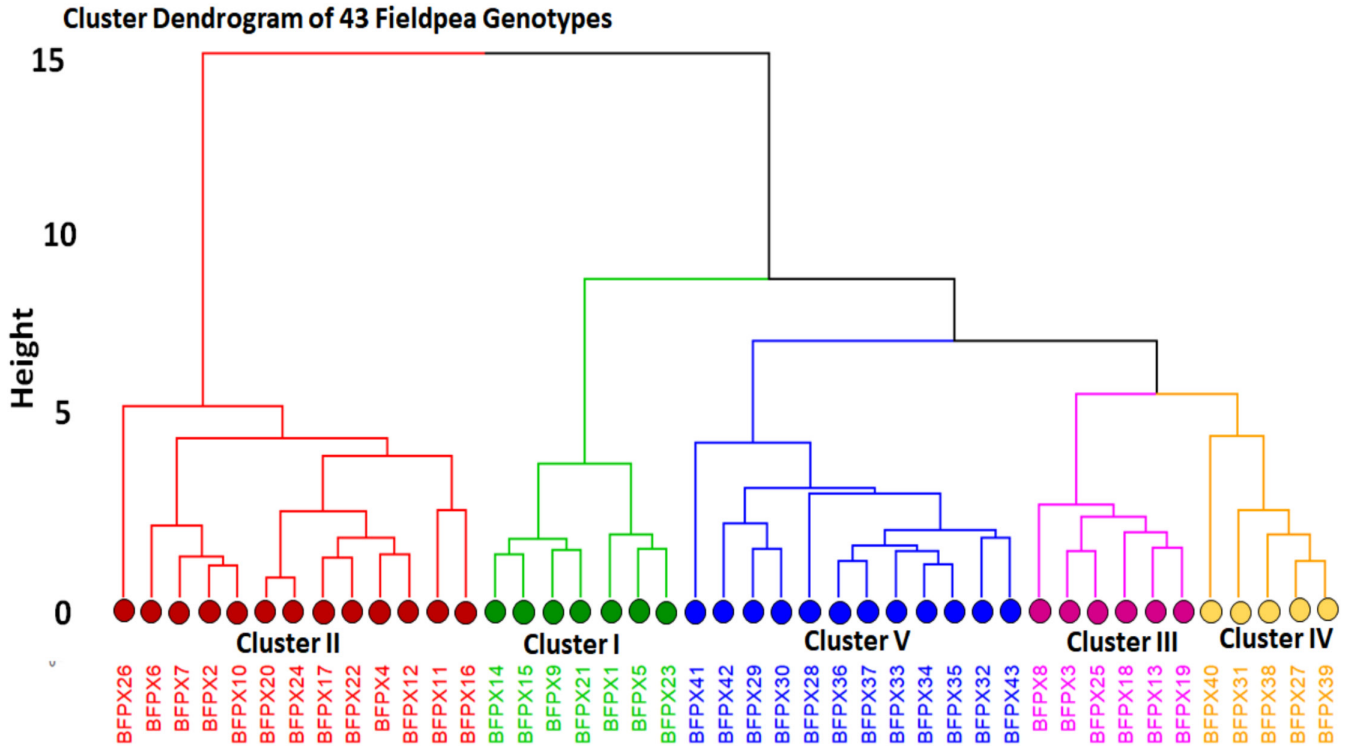


FIGURE 6 | Dendrogram of 43 early field pea genotypes derived from squared Euclidean linkage cluster and Ward method analysis.

TABLE 6 | Cluster mean values of seven traits of field pea genotypes (pooled data).

	Clusters				
Traits	**Cluster 1**	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**
DF	41	38	44	53	54
DM	100	82	98	102	103
PH	172.81	116.95	152.27	132.59	137.07
PPP	17.56	10.07	18.23	16.03	19.30
HSW	20.05	22.81	19.30	12.32	13.35
YPP	7.34	5.75	5.55	4.12	6.32
YPH	1888	1517	1457	1553	1902

Note: Details of traits are presented in Figure 2.

demonstrating the presence of extensive genetic variation among the genotypes for the examined variables.

Cluster 1 had the tallest plants (172.81 cm) of all the clusters, with somewhat early blooming (41 days) and late maturity (100 days). Genotypes in this cluster observed high PPP (17.56) and somewhat high HSW (20.05 g) (Table 6). The YPP (7.34 g) and YPH (1888 kg ha^{-1}) were likewise high, demonstrating that Cluster 1 genotypes combine beneficial features for both production and plant stature. Thus, this cluster represents high-yielding and tall genotypes with excellent agronomic traits. Cluster 2 contained early-flowering (38 days) and early-maturing (82 days) genotypes with shorter plants (116.95 cm) and the lowest PPP (10.07). These genotypes, however, showed the greatest HSW (22.81 g), suggesting bold-seeded varieties. Despite early development and bold seeds, the YPP (5.75 g) and YPH (1517 kg ha^{-1}) were considerably lower. Hence, Cluster 2 comprises early, short-statured, bold-seeded genotypes ideal for short-duration cultivation but with low production potential. Cluster 3 genotypes had medium PH (152.27 cm), moderate blooming (44 days), and maturity length (98 days). This cluster observed high PPP (18.23) and moderate HSW (19.30 g). The YPP (5.55 g) and YPH (1457 kg ha^{-1}) ranked among the lowest, indicating that despite a substantial number of pods, the yield potential was constrained, possibly due to smaller seed size or decreased seed filling. Cluster 3 includes cultivars that are of moderate duration, fairly tall, and medium-yielding. In Cluster 4, genotypes that are late-flowering (53 days) and late-maturing (102 days) were identified, exhibiting an intermediate PH of 132.59 cm. The HSW for this group was the lowest at 12.32 g, while the PPP was significant at 16.03. The YPP (4.12 g) and YPH (1553 kg ha^{-1}) were likewise low, suggesting that the genotypes in this cluster are

TABLE 7 | Inter- and intra-cluster distance for five clusters.

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	**1.922**				
Cluster 2	4.352	**2.447**			
Cluster 3	2.783	3.536	**1.856**		
Cluster 4	4.349	4.549	3.066	**2.493**	
Cluster 5	3.347	4.725	3.118	2.952	**2.036**

Note: Bold values indicates intra-cluster distances (diagonal elements).

small-seeded, late-maturing, low-yielding varieties that could be useful for breeding for lateness or specialized environmental adaptation but less appropriate for high-yield production. Cluster 5 consisted of late-flowering (54 days) and late-maturing (103 days) genotypes with intermediate PH (137.07 cm). The highest YPH (1902 kg ha^{-1}) and PPP (19.30) were produced by these genotypes. They had significantly lower HSW at 13.35 g and a moderate YPP of 6.32 g. The combination of a large number of pods and a moderate seed weight resulted in enhanced yield potential. Therefore, high-yielding, late-maturing genotypes with abundant pod-bearing potential are represented by Cluster 5.

3.6.4 | Inter- and Intra-Cluster Distance Analysis

Table 7 shows the distances between and within the five groups of 43 field pea genotypes. The inter-cluster distance indicates genetic divergence between clusters, whereas the intra-cluster distance reflects genetic divergence within a cluster. A larger inter-cluster distance indicates increased genetic divergence, suggesting that hybridization between genotypes from these clusters may yield maximum heterosis and enhance diversity in the segregating generations.

3.6.5 | Intra-Cluster Separation

The intra-cluster distances indicated varying levels of genetic homogeneity within the clusters, ranging from 1.856 in Cluster 3 to 2.493 in Cluster 4. The lowest intra-cluster distance for Cluster 3, measured at 1.856, suggests that the genotypes within this cluster exhibit less diversity and greater similarity. Cluster 4 exhibited the greatest intra-cluster distance at 2.493, indicating a broader genetic base within this cluster and a notable level of genotype variability. Cluster 1 (1.922), Cluster 2 (2.447), and Cluster 4 (2.493) exhibit moderate intra-cluster distances, which suggest a significant level of internal genetic variability. The overall intra-cluster distances were smaller than the inter-cluster distances, confirming the effectiveness of clustering in assembling genetically related genotypes.

3.6.6 | Inter-Cluster Distance

The inter-cluster distances revealed a significant genetic difference among the clusters, ranging from 2.783 between Clusters 1 and 3 to 4.725 between Clusters 2 and 5. Clusters 2 and 5 exhibited the largest inter-cluster distance at 4.725. This was closely followed by the distance between Clusters 4 and 2, which measured 4.549, and the distance between Clusters 1 and 2, recorded at 4.352. This indicates that the genotypes within these clusters exhibit the greatest genetic differences from each other and that the pairs of these clusters show the highest levels of genetic divergence. Clusters 1 and 3 exhibited the lowest inter-cluster distance of 2.783, suggesting a notable similarity in their genetic backgrounds. Intermediate levels of genetic divergence were observed between Clusters 3 and 4 (3.066) as well as between Clusters 3 and 5 (3.118).

3.7 | Path Analysis of Yield-Attributing Traits in Field Pea Genotypes

Path coefficient analysis was conducted using pooled data to examine the direct and indirect effects of yield-contributing characteristics on YPH across 43 field pea genotypes (Figure 7). The structural simulation model indicates that YPP exerted the largest positive direct effect on YPH, quantified at 0.43, highlighting its essential role as the primary yield determinant. PPP exhibited a slight negative direct effect of −0.03 on yield, whereas PH showed a low negative direct effect of −0.11. DF and DM influenced yield indirectly via YPP and PPP, yet they exhibited strong positive correlations with various phenological parameters.

The significance of these pathways in yield generation was underscored by the indirect effects, showing that PH and DM mainly contributed to yield via YPP (0.74) and PPP (0.06). According to HSW's moderately negative correlation with DF (−0.62) and PPP (−0.52), increased seed size might be linked to a reduction in the number of pods and a delay in flowering. It appears that taller plants and a slight delay in flowering contribute to increased yield by enhancing YPP, as indicated by the strong positive correlations observed between PH and YPP (0.72) and between DF and YPP (0.16).

The model explained a considerable portion of the variance in yield potential. YPP emerged as the strongest direct predictor of yield, while PH, DM, and PPP influenced yield indirectly by affecting YPP. The results illustrate the interaction between morphological and phenological characteristics in determining field pea productivity, providing valuable insights for selection techniques focused on enhancing yield in the studied ecosystems.

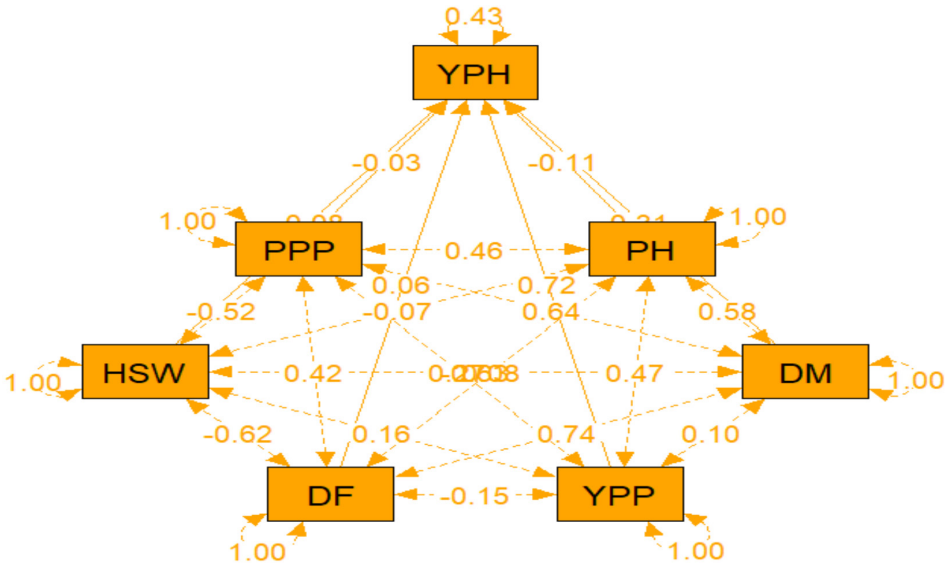


FIGURE 7 | Path analysis of yield-attributing traits in 43 field pea genotypes during 2023 and 2024 (pooled data).

TABLE 8 | Original value (Xo), selected value (Xs), selection differential in percentage (SD%), heritability (h2), and selection gain in percent (SG%) for yield and yield contributing traits of 43 field pea genotypes, based on 2 years of pooled data from the MGIDI.

Factorial loadings after rotation	VAR	DF	DM	PH	PPP	HSW	YPP	YPH
	FA1	−0.88	−0.85	0.22	0.61	−0.86	−0.15	0.17
	FA2	−0.01	0.40	−0.71	−0.55	−0.01	−0.86	−0.80
	Communality	0.78	0.88	0.56	0.67	0.73	0.76	0.66
	Uniquenesses	0.22	0.12	0.44	0.33	0.27	0.24	0.34
Selection differential	Factor	FA1	FA1	FA1	FA1	FA2	FA2	FA2
	Xo	45.6	94.90	15.70	18	138	6.07	1681
	Xs	41.1	97.10	19.60	20.70	156	8.31	1984
	SD	−4.46	2.19	3.86	2.69	17.2	2.25	304
	SD%	−9.78	2.30	24.60	15	12.4	37	18.10
	h_2b	99.2	98.90	94.10	98.70	92.1	87.5	97.70
	SG	−4.42	2.16	3.63	2.66	15.8	1.96	297
	SG (%)	−9.70	2.28	23.20	14.80	11.40	32.40	17.70
	Sense	Decrease	Decrease	Increase	Increase	Increase	Increase	Increase
	Goal	100	0	100	100	100	100	100

Note: VAR = the trait's name; Factor = the factor that traits where grouped into; Xo = the original population mean; Xs = the mean of selected genotypes; SD and SDperc = the selection differential and selection differential in percentage, respectively; h_2b = the broad-sense heritability; SG and SGperc = the selection gains and selection gains in percentage, respectively; Sense = the desired selection sense; Goal: selection gains match desired sense? 100 for yes and 0 for no.

3.8 | Selection of Short-Duration Genotypes Using MGIDI

Based on 2 years of pooled data, superior field pea genotypes for yield and yield-contributing characteristics were identified using the MGIDI. After applying varimax rotation, the factor analysis revealed two main factors (FA1 and FA2) that together explained a substantial portion of the overall variability in the attributes. Factor loadings indicated that PH, YPP, and YPH were mainly connected to FA2, while DF, DM, PPP, and HSW exhibited a strong association with FA1. The communalities varied from 0.56 (PH) to 0.88 (DM), suggesting that the retrieved components adequately reflected the majority of the trait variation (Table 8).

Using MGIDI scores, the anticipated improvement following selection was measured by calculating selection gain (SG) and selection difference (SD). Discernible shifts in the intended directions were observed for most attributes when comparing the original population mean (Xo) to the mean of selected genotypes

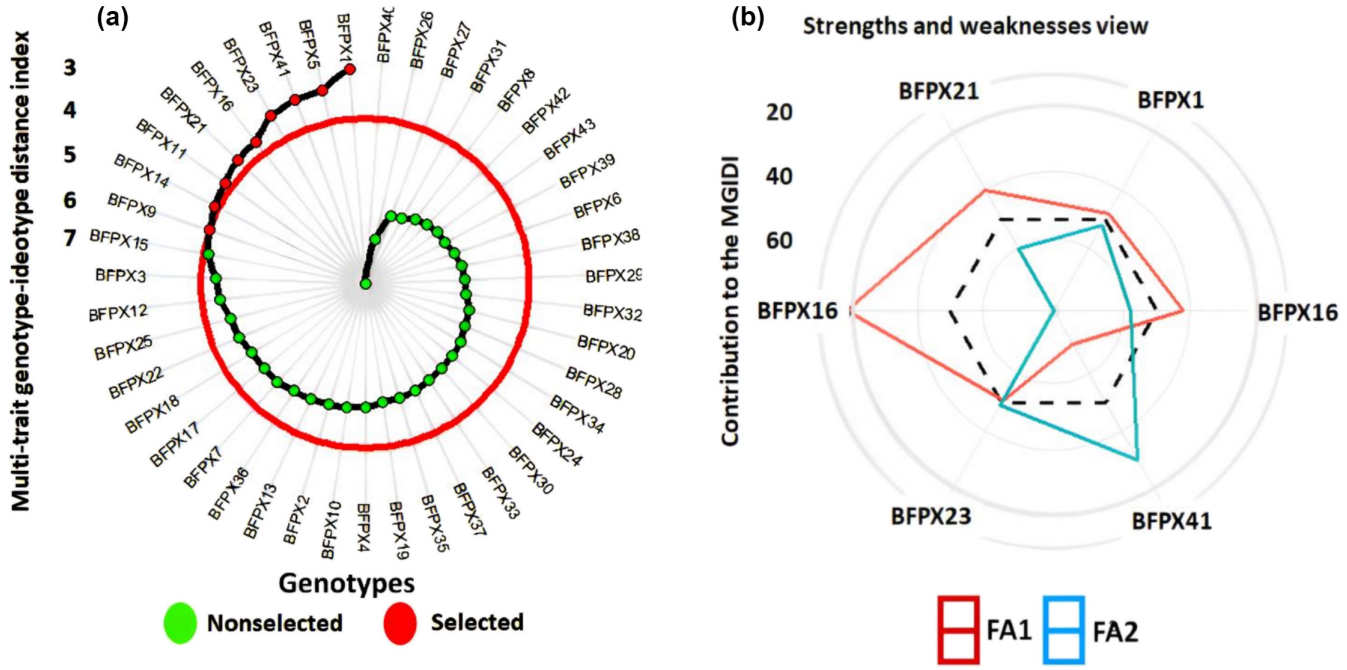


FIGURE 8 | (a) The MGIDI selection index ranking of genotypes and the top field pea genotypes are displayed in the circular preview. The top-ranked and chosen genotypes are highlighted in red. The central red circle represents the cut point based on the selection pressure. (b) The percentage of each component on the calculated MGIDI index is shown in the strengths and weaknesses view of the chosen genotypes. The proportion of a factor's explanation decreases with the degree to which its traits approximate the ideotype (nearer the outer boundary). The dashed line represents the theoretical value, assuming equal contributions from each component. (The reader is directed to the online version of this article for an explanation of the color references in this figure legend.)

(Xs) (Table 8). Conversely, days to maturity (−2.30%) and days to blooming (−9.78%) exhibited a satisfactory reduction, suggesting early maturity in the selected genotypes. The highest positive SD% was observed in PH (+24.6%), yield per hectare (YPH, +18.1%), and HSW (+37%).

The broad-sense heritability (h_2b) values ranged from 87.5% (YPP) to 99.2% (DF), showing a consistent high across the variables. The trends in SD% were closely aligned with the projected SGs in percentage (SG%), which were highest for HSW at +32.4%, followed by PH at +23.2%, and YPH at +17.7%. The qualities linked to earliness showed a negative SG% in accordance with the intended reduction target. The MGIDI-based selection typically resulted in the anticipated genetic advancement across all traits, achieving a complete alignment between the selection target and the intended perception of improvement. The findings indicate that high-yielding, early-maturing field pea genotypes with enhanced yield-attributing traits were effectively identified through simultaneous selection using the MGIDI technique.

In Figure 8a, the ranking of 43 field pea genotypes is presented through the MGIDI. The circular plot clearly distinguishes the MGIDI values of both the selected and non-selected genotypes. Genotypes closer to the center of the plot exhibited smaller MGIDI scores, indicating a greater degree of ideotype similarity and, as a result, enhanced performance in yield and yield-contributing traits. On the other hand, genotypes situated closer to the periphery exhibited larger MGIDI values, which indicate poorer multi-trait performance.

The most desirable genotypes identified based on the MGIDI ranking include BFPX1, BFPX5, BFPX16, BFPX23, and BFPX41, as they are in close proximity to the ideotype. Table 8 presents the selection differential and gain estimates, indicating that these genotypes exhibited beneficial combinations of early blooming and maturity, an increased pod number, enhanced seed weight, and greater yield potential. The remaining genotypes, located around the outer circle, were categorized as non-selected due to their higher MGIDI values and relatively lower multi-trait performance. A radar map illustrated and compared the performance profiles of two variables, FA1 and FA2, across six different axes: BFPIX16, BFPIX21, BFPIX23, BFPIX41, and contribution to the MGIDI index (Figure 8b). The evaluation of the percentage of each component on the calculated MGIDI index helped identify strengths and weaknesses. FA1 consistently displayed higher values across multiple axes, particularly in BFPIX16, BFPIX21, BFPIX23, and its contribution to the MGIDI index. FA1 appears to possess a generally superior performance profile in these domains. FA2 displayed greater inconsistency, achieving its highest value at BFPIX41. FA2, while significantly stronger in BFPIX41, exhibited generally lower values than FA1 across all other examined axes (Figure 8b). These comparison profiles reveal the distinct contributions and performance traits of FA1 and FA2 within the assessed context.

4 | Discussion

The successful intensification of rice-based cropping systems in South Asia depends largely on the incorporation of

short-duration and climate-resilient legumes such as field pea. The 43 extra-early genotypes assessed in this study showed significant variation in yield-attributing and phenological traits, indicating a high potential for identifying ideotypes appropriate for rice–rice and rice–fallow systems. Combining genetic information, different types of analysis, MGIDI-based selection, and path modeling gives a complete view of the breeding possibilities for extra-early field peas.

Substantial phenotypic variability among the 43 field pea genotypes is revealed by the box plots across all traits. The highest variation in PH, PPP, and YPH was observed, highlighting these as the most discriminating traits for genotypic differentiation (Figure 2 and Table 3). Researchers suggest that variations in PH and PPP may stem from genetic factors and regional climate and soil conditions (Kanwar et al. 2020; Patidar et al. 2023; Sirwaiya and Kushwah 2018). Differences in the number of seeds per pod in field pea varieties were also reported by the studies (Bhushan et al. 2025; Devi et al. 2021; Kanwar et al. 2020; Raj et al. 2020; Sirwaiya and Kushwah 2018). The difference in yield may be attributed mainly to the difference in PPP, SPP, and YPP. These results were supported by Kanwar et al. (2020). Traits like HSW and DM exhibited comparatively narrow variability, indicating relative uniformity. Outliers in traits indicate that some genotypes show extreme phenotypic expressions, making them potential breeding parents for yield, earliness, or environmental adaptation (Figure 2 and Table 3). The data distribution suggests a diverse genetic base among the evaluated field pea genotypes, allowing for selection and improvement through breeding.

4.1 | Genetic Variability and Implications for Selection

The wide range of variation observed among the 43 extra-early field pea genotypes across all agro-morphological traits clearly demonstrates the presence of substantial genetic diversity within the evaluated germplasm (Table 4). Such diversity is essential for effective selection, particularly for breeding programs targeting highly intensive rice–rice cropping systems where early maturity, high seed weight, and yield efficiency are crucial.

Significant genetic variation was observed in traits such as flowering, PH, pod shape, and yield components. The genotypes examined indicate their potential as a valuable breeding pool. Genetic and PV exists extensively in traits such as PH, the number of effective pods, SPP, and seed yield. This indicates that a significant amount of inherent variety exists, which is essential for selection to function effectively. Various types of peas and other legumes exhibit similar patterns (Shubham et al. 2025; Yumkhaibam et al. 2019).

Traits with high heritability and significant genetic progress, such as DF, plant population per hectare (PPP), and harvest index (HSW), are primarily influenced by additive gene action (Table 4). These traits respond effectively to direct selection in the early generations (Allard 1999; Falconer 1996). Similar findings in field pea confirm that additive effects play a major role in determining productivity traits in short-duration genotypes (Pallavi et al. 2024; SinghRathore et al. 2019). This is particularly important for developing extra-early cultivars, where a short growth period should not reduce the effectiveness of selection. Although the comparatively slight variations between PV and GV for the majority of traits indicated that environmental impact was not dominating, the consistently larger phenotypic variance compared with GV across traits implies that environmental variables influenced trait expression. Other pulse crops also show comparable outcomes. Good genetic control makes early-generation selection easier in short seasons. The GCV and PCV values confirm these observations. Traits including PPP, HSW, and YPP have high GCV and PCV in this study. This shows they have a lot of natural variety. It also suggests these features have good potential for improvement. This large variance is necessary for extra-early breeding. These features affect yield when the growing time is short. Traits like DF, DM, and PH exhibit modest variance. Moderate variation is helpful because these traits affect crop longevity. They also help plants establish effectively in rice-fallow environments. These data suggest that the genotypes have various maturity groups. At the same time, they retain a constant plant structure. This structure is excellent for high-density planting.

Johnson et al. (1955) suggested that heritability values are low (< 30%), moderate (30%–60%), and high (> 60%), and genetic progress as a percent of the mean is classed as low (< 10%), moderate (10%–20%), and high (> 20%). Heritability estimates were high for most traits, ranging from 70 to 98, which indicates that additive genetic effects predominantly influence trait expression (Table 4). The high broad-sense heritability values for DF, DM, and HSW indicate that these traits can be effectively enhanced through direct selection. The combination of high heritability along with moderate-to-high GCV and PCV enhances the reliability of phenotype-based improvement in early segregating generations. The heritability observed for YPP suggests that while genetic factors are significant, environmental influences are also important, indicating that assessing multiple environments could enhance selection accuracy. Yimam et al. (2024) have reported similar findings, highlighting significant heterogeneity in the phenological characteristics and seed quality of field pea.

Insights into prospective GAs are provided by GA and GAPM. The highest GAPM values for PPP (64.36%), HSW (58.65%), YPP (43.97%), and YPH (34.70%) indicate that these traits are primarily influenced by additive gene action and could be significantly improved through selection (Table 4). The total yield is significantly influenced by these features, highlighting their importance for developing ideotypes of extra-early field pea that are suitable for rice-based systems. In contrast, traits like DM exhibited lower genetic progress (20.17%), indicating that enhancing crop duration might require either significant selection pressure or the introduction of genes from various maturity sources. Studies in field pea have reported similar findings, revealing significant heritability estimates for yield and yield-contributing variables (Barcchiya et al. 2018; Viradiya et al. 2025). According to the study, the most promising features for attaining genetic gain in field pea breeding programs are PPP, HSW, YPP, and YPH.

4.2 | PCA Analysis

Substantial genetic variation exists among the genotypes, as revealed by the PCA groups. Clear correlations between attributes are also shown. This information proves beneficial for targeted breeding of field peas. PCA is effective in comprehending complex characteristic patterns. Breeders are assisted in generating sturdy and high-yielding cultivars of field peas. The PCA biplot, along with the trait-based PCA plot, distinctly highlights the most significant features. The majority of the differences among genotypes are explained by these features. Past investigations by the studies support this strategy (Chiquet et al. 2018; Tiruneh et al. 2018). The biplot indicates that strong connections exist between phenotypic traits based on genotype proximity; however, traits located closer to the origin contribute minimally to the overall variation (Kose et al. 2018; H. K. Sharma et al. 2016).

4.3 | Correlation Analysis

The correlation matrix revealed a complex relationship between yield and its component features (Panwar et al. 2023). By utilizing correlation studies, plant breeders can select desirable varieties that exhibit preferred features, as these studies reveal the nature and strength of relationships between different attributes (Azam et al. 2020; Uhlarik et al. 2022). The analysis revealed that the strongest positive relationships were found among DF, DM, PH, and PPP, indicating that these traits develop in harmony and together enhance yield potential (Figure 4). HSW showed negative correlations with the duration of growth and the number of pods. This indicates that larger seeds often result in a reduced number of pods or a shorter growth period. There is a strong positive association between YPP and YPH. This means that plants with high YPP also give high yield per hectare. So, selecting plants with good individual performance can boost overall production. The traits most closely associated with yield were PPP, PH, and DM. HSW showed a contrary or adverse impact on these yield traits. The findings align with the research conducted in the studies (Devi et al. 2018; Gautam et al. 2017). It was also found by researchers that an increase in pod yield correlates with a greater NPPP, longer pod lengths, a higher seed count per pod, an increased shelling percentage, and elevated total soluble solids (Devi et al. 2017). These qualities significantly contribute to yield. We conducted a heatmap analysis to more thoroughly assess the association between genotype and trait, identifying the top-performing genotypes based on the evaluated characteristics of field pea. According to the heatmap analysis, the yield performance of field pea varieties Cluster 2 and Cluster 5 surpassed that of all other varieties.

4.4 | Genetic Difference and Breeding Value of Clusters

Hierarchical clustering split the genotypes into five categories. These groups demonstrate considerable genetic differences among the genotypes. Such genetic distance is significant for hybridization efforts. Genotypes from distant clusters can form powerful heterotic combinations (Azam et al. 2024; Jyothireddy et al. 2018; Oussama et al. 2025). These pairings may cause additional variance in the future generation. For breeding early and high-yielding varieties, clusters with strong pod characteristics and a high harvest index are highly significant. The divergence pattern in this study matches past worldwide pea research (Ouafi et al. 2016; A. Sharma et al. 2025). Those studies also demonstrated that reproductive factors predominantly distinguish the groups. Breeders can choose parents based on genetic variations and high trait performance. Trait-specific clusters assist in finding the optimal parents for breeding.

4.5 | Analysis of Cluster Mean

Multivariate approaches are beneficial for evaluating genetic differences in germplasm. They enable breeders to identify good genotypes and design breeding strategies (Das et al. 2024). Like other studies, PCA indicated that traits with positive loadings explained most of the variation (Gerrano et al. 2019). PCA and cluster analysis are often employed to analyze quantitative attributes and to uncover high-performing genotypes (Das et al. 2024). Cluster 2 (early, bold-seeded) and Cluster 5 (high-yielding, late-maturing) were the most distinct groups. Crossing these clusters may combine early maturity with good yield (Table 5 and Figure 6). Cluster 1 and Cluster 3 exhibited moderate performance. These clusters can serve as bridge parents for transferring features among distant groups. The unusual clustering pattern presents promising opportunities for forming heterotic groups. This pattern assists breeders in selecting parents to enhance yield and increase genetic diversity. These clusters' genotypes can be utilized in hybridization processes to generate the desired types. Strong heterotic offspring can be produced by crossing genetically distant parents (Yadav et al. 2023). According to Sharma et al. (2023), their research indicated that pea genotypes clustered into four or five distinct groups. This study reveals significant genetic variation among the 43 field pea genotypes. The distances between clusters were greater than the distances within clusters. This means the clustering grouped the genotypes efficiently. The most distant clusters were Clusters 2 and 5, followed by Clusters 2 and 4, and Clusters 1 and 2. These cluster couples give very good alternatives for breeding. Similar findings were reported by the studies (Assen 2020; Azam et al. 2024; Upadhyay and Raghubanshi 2020). It is anticipated that crossing genotypes from these clusters will result in significant heterosis and vigorous recombination. Intriguing directions for future pea breeding research are also offered by the high inter-cluster distances.

Studying genetic diversity is made easier through the use of cluster analysis. It illustrates the relationship between genotypes according to their traits (Alam et al. 2024). The study also showed that genotypes from different species and origins can appear in the same cluster. This means that trait differences do not always reflect genetic differences. Field pea breeding should focus on genetic diversity within and between species and sources (Assen et al. 2024). This approach can help develop better and more successful breeding strategies in the future. The cluster mean analysis demonstrated clear divergence among the five groups for most of the yield and yield-contributing attributes (Table 6).

Clusters 1 and 5 were recognized as superior clusters for yield performance, having high mean values for YPP and YPH. Cluster 4 was characterized by late-maturing, small-seeded, and low-yielding genotypes, whereas Cluster 2 stood out due to its bold seed size and early maturity. Crosses involving genotypes from Cluster 2 (early, bold-seeded) with those from Cluster 4 (high-yielding, late-maturing) or Cluster 3 (tall, productive) are expected to produce transgressive segregants that integrate earliness, bold seed, and high yield (Table 6). The current study revealed that genotypes from various plant types, conditions, and resource origins were spread throughout each cluster, indicating phenotypic diversity. In line with these findings, the researchers reported similar results (Yumkhaibam et al. 2019).

4.6 | Path Analysis: Determining Yield's Direct and Indirect Contributors

The number of effective pods, seeds per pod, pod length, thousand-grain weight, and harvest index have a major impact on grain yield, as demonstrated by the route analysis. Improving reproductive efficiency and assimilate partitioning is essential for increasing yields in extra-early genotypes. These findings align with earlier studies indicating that PPP and seed weight serve as key determinants of production in peas (Azam et al. 2020; N. Kumar et al. 2021; Pratap et al. 2021; D. Sharma et al. 2023). Yield is indirectly influenced by traits such as PH and leaf quality (Kumar et al. 2025; Shferaw and Tarekegne 2024). Their influence on yield operates via reproductive characteristics. Understanding the interaction of traits is essential for developing selection indices. Broad beans (Shferaw and Tarekegne 2024) and peas (Kumar et al. 2025) also exhibited similar indirect effects, particularly in environments that are short-season or prone to stress.

4.7 | MGIDI Multi-Trait Selection: Identifying Balanced Ideotypes

The MGIDI index is now widely employed in legume breeding (Koura et al. 2025; Olivoto and Lúcio 2020). It evaluates maturity, yield, physiology, and plant architecture simultaneously. Genotypes that exhibit low MGIDI scores demonstrate strong performance across various characteristics. These genotypes represent balanced ideotypes characterized by early maturity, a large number of pods, good seed size, a high harvest index, and improved physiological features. MGIDI has been successfully employed in lentil, chickpea and pea (Basavaraj et al. 2025) (Debnath et al. 2024). It recognizes complicated trait trade-offs in short growth periods, which helps selection suit rice–fallow systems.

4.8 | Implications for Rice–Rice And Rice–Fallow Cropping Systems

This study focuses on extra-early field pea genotypes that fit well into rice-intensive cropping systems (Shubham et al. 2025). Most previous studies did not examine extra-early field pea specifically for these systems. The selected genotypes have extra-early maturity, many pods, good seed weight, a high harvest index, and strong yield. These traits help the crop grow quickly without reducing yield, which is important in rice–fallow areas facing heat, drought, or weed pressure (Kaul et al. 2024). Adding field pea to rice systems improves soil nitrogen and residue quality and reduces the need for chemical fertilizers. Field pea also increases whole-system productivity and supports long-term sustainability (Islam et al. 2023; Jena et al. 2022).

4.9 | Summary of Key Findings

The assessment of 43 extra-early field pea genotypes showed significant phenotypic and genetic variability in all phenological, morphological, and yield-related traits, indicating a wide genetic foundation appropriate for breeding development. Significant variations were noted in flowering (33–59 days), maturity (74–106 days), PH (78–186 cm), PPP (4.6–31.0), seed weight (4.9–28.8 g), and yield (950–2149 kg/ha), highlighting considerable potential for selection. Moreover, high heritability estimates (70%–98%) and significant genetic progress for essential traits like PPP, seed weight, YPP, and seed yield suggest that additive gene action is the main influence, resulting in these traits being very receptive to selection.

Multivariate analyses (PCA, clustering, heatmap) reliably identified distinct genotype groups, indicating high levels of genetic divergence. Five genotype clusters were identified, with Clusters 1 and 5 demonstrating higher yield potential, whereas Cluster 2 consisted of early, bold-seeded types that are well-suited for short-duration environments. Correlation and path analyses revealed that YPP is the most significant direct factor affecting seed yield, whereas PPP, PH, and maturity have an indirect impact on yield through their influence on YPP.

The MGIDI multi-trait selection index successfully pinpointed well-rounded ideotypes that integrate earliness, a high pod count, preferred seed weight, and exceptional yield. The most promising genotypes—BFPX41, BFPX1, BFPX23, BFPX30, and BFPX16—ranked closely to the ideotype and showed robust multi-trait performance appropriate for rice–rice and rice–fallow systems. The genotypes present substantial potential for creating short-duration, high-yielding field pea cultivars that align well with the limited planting windows of intensive rice-based cropping systems.

5 | Conclusions

The study revealed substantial genetic variability among 43 field pea genotypes concerning phenology, morphology, and yield parameters. The considerable potential for genetic improvement in rice–rice cropping systems is suggested by this diversity. Flowering and maturity periods show significant variation. This enables the identification of genotypes that can thrive during short fallow periods, particularly those that emerge very early. Examples of multivariate techniques that have proven useful in characterizing genotypic divergence and identifying necessary trait connections for focused breeding include PCA, heatmap-based clustering, and Mahalanobis distances.

High heritability estimates and significant genetic advancement for important characteristics further demonstrate the efficiency of selection. The MGIDI demonstrated significant effectiveness

in integrating numerous desired features and selecting superior genotypes. In intensive rice-based systems, genotypes such as BFPX41, BFPX1, BFPX23, and BFPX30 serve as excellent candidates for varietal development. These genotypes consistently demonstrate superior performance in yield and yield components, all while maintaining early maturity. Overall, the integration of variability evaluation, multivariate statistics, and MGIDI-based selection presents a strong framework for expediting breeding of extra-early, high-yielding field pea genotypes appropriate for rice-fallow and rice–rice agro-ecologies.

Author Contributions

Md. Golam Azam: conceptualization, methodology, investigation, software, validation, formal analysis, visualization, writing – original draft, writing – review and editing. **Md. Rafiqul Islam:** data curation, visualization. **Mohammad Mamunur Rashid Sarker:** software, visualization, writing – original draft, writing – review and editing. **Md. Hasan Waliullah:** visualization, writing – review and editing. **H. M. Khairul Bashar:** visualization, writing – review and editing. **Md. Kamrul Islam:** visualization, writing – original draft, writing – review and editing. **Md. Bazlur Rahman:** visualization, writing – original draft, writing – review and editing. **Md Mashiur Rahman:** data curation, formal analysis, visualization, writing – original draft, writing – review and editing. **Umakanta Sarker:** conceptualization, supervision, investigation, software, validation, writing – review and editing.

Acknowledgments

The authors would like to acknowledge the research facilities provided by the Pulses Research Centre, Bangladesh Agricultural Research Institute, Ishwardi, Pabna 6620, Bangladesh.

Funding

This work was supported and funded by the Pulses Research Centre, Bangladesh Agricultural Research Institute (BARI) under the regular research programme for sustainable production systems.

Ethics Statement

According to institutional and municipal regulations, the study involving human subjects did not require ethical review and permission. According to both institutional and national regulations, participants in this study were not required to provide written informed consent.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The datasets generated during the current investigation are accessible from the corresponding author upon reasonable request. Requests to access the datasets should be made to azamprcbari@gmail.com.

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