



ISSN Print: 2664-844X
ISSN Online: 2664-8458
NAAS Rating (2026): 4.97
IJAFA 2026; 8(9): 92-97
www.agriculturaljournals.com
Received: 07-06-2026
Accepted: 11-07-2026

Pranjal Raut
P.G. Scholar, Department of
Genetics and Plant Breeding,
GHRU, Saikheda, Madhya
Pradesh, India

Deepak Sapkal
Associate Professor,
Department of Genetics and
Plant Breeding, GHRU,
Saikheda, Madhya Pradesh,
India

Kashiwar G
P.G. Scholar, Department of
horticulture (fruit science),
GHRU, Saikheda, Madhya
Pradesh, India

Genetic Evaluation of Field Pea (*Pisum sativum* var. *arvense* L.) for Yield and Yield Components

Pranjal Raut, Deepak Sapkal and Kashiwar G

DOI: <https://www.doi.org/10.33545/2664844X.2026.v8.i9b.1861>

Abstract

The present investigation, “Genetic Evaluation of Field Pea for Yield and Yield Components,” was conducted during Rabi 2025–26 at G. H. Raisoni University, Saikheda, Madhya Pradesh. Twenty genotypes were evaluated in an RBD with three replications for eleven yield and yield-related traits. Significant differences were observed among all genotypes, indicating high genetic variability. KDP-27 recorded the highest grain yield (16.61 q/ha), followed by Uttara (16.00 q/ha) and Pant-243 (15.86 q/ha). High heritability and favourable genetic advance were observed for grain yield, plant height, and branching traits. Pods per plant, secondary branches, pod length, seeds per pod, and 100-seed weight showed strong positive associations with grain yield, whereas days to flowering and maturity showed negative correlations. Overall, KDP-27 was identified as the most promising genotype, and simultaneous selection for important yield components can effectively improve field pea productivity.

Keywords: *Pisum sativum* var. *arvense*, genetic variability, heritability, genetic advance, correlation, path coefficient analysis, grain yield, KDP-27

Introduction

Field pea (*Pisum sativum* subsp. *arvense* L.) is one of the most important pulse crops grown worldwide. It is also known as dun pea, Austrian winter pea, or grey pea and is among the oldest domesticated food legumes cultivated by humans for more than 7,000 years. Field pea belongs to the family Fabaceae and is widely cultivated in temperate and subtropical regions for human consumption, livestock feed and soil fertility improvement. Owing to its high nutritional value, nitrogen-fixing ability and adaptability to diverse agro-climatic conditions, field pea occupies an important position among grain legumes [15]. Field pea is cultivated in many countries across the world for both food and feed purposes. Several cultivars differing in seed size, shape and colour are available, including white, green, brown and blue-seeded types. According to recent FAOSTAT estimates, dry pea occupies approximately 7.3 million hectares globally with an annual production of about 14.1 million tonnes and an average productivity of nearly 1.9 t ha⁻¹. India is one of the major producers of field pea among pulse-growing countries, and the crop occupies about 0.77 million hectares with an annual production of approximately 1.07 million tonnes and productivity of around 1.39 t ha⁻¹. Uttar Pradesh, Madhya Pradesh, Bihar, Rajasthan, and West Bengal are the major field pea-growing states of the country [1]. Field pea is a climbing, annual, herbaceous legume with weak, succulent, and viny stems. The plant generally attains a height of 45–150 cm, depending upon genotype and environmental conditions. Leaves are compound, consisting of one or more pairs of leaflets terminating in tendrils that assist the plant in climbing. Flowers are borne singly or in clusters and may be white, pink, purple or bluish in colour. Pods contain several seeds that vary in colour, shape and size. The root system is relatively shallow but highly efficient at forming nodules through symbiosis with *Rhizobium* bacteria, enabling biological nitrogen fixation and improving soil fertility. Field pea is a self-pollinated diploid species with chromosome number 2n = 14. It is considered one of the most valuable cool-season pulse crops because of its high nutritional quality. The seeds contain approximately 20–25 per cent protein, substantial amounts of carbohydrates, vitamins and minerals. They are particularly rich in lysine and tryptophan, amino acids that are generally deficient in cereal grains. Due to its high digestibility and nutritional composition, field pea serves as an excellent source of protein for human diets and livestock feeding systems.

Corresponding Author:
Pranjal Raut
P.G. Scholar, Department of
Genetics and Plant Breeding,
GHRU, Saikheda, Madhya
Pradesh, India

The crop is also utilized in crop rotations where it improves soil health, reduces fertilizer requirements and contributes to sustainable agricultural production^[16]. The genetic diversity present in crop species results from natural selection acting on wild progenitors, combined with centuries of human intervention through domestication, selection, and breeding. The genomes of modern cultivars, landraces, ecotypes and wild relatives reflect the cumulative effects of mutation, recombination, selection and adaptation to diverse environments. Such diversity provides valuable information regarding species evolution and offers opportunities for crop improvement through the utilization of useful alleles present in diverse germplasm resources^[10]. The genetic diversity of a species is the outcome of cumulative mutation, recombination and natural selection. In crop plants, this diversity has been further shaped by thousands of years of conscious and unconscious selection by farmers and breeders. Early domestication involved selecting wild plants with desirable agronomic traits, leading to the development of locally adapted landraces. During this process, several undesirable characteristics, such as pod shattering and seed dormancy, were eliminated, whereas desirable traits, such as larger seed size and improved yield, were retained^[2, 17]. Modern breeding programmes have continued this process through systematic hybridisation and selection, leading to substantial gains in productivity and adaptation. However, intensive selection has also narrowed the genetic base of many cultivated crops, highlighting the need for continuous evaluation and utilisation of diverse germplasm resources^[3, 17]. Morphological characterisation is generally considered the first step in the description, classification and identification of germplasm resources. It facilitates the assessment of diversity and provides useful information for plant breeding programmes. Characterisation of germplasm enables the identification of desirable traits and assists breeders in selecting suitable parental lines for hybridisation programmes. The significance of morphological and genetic characterisation in crop improvement has been emphasised by several researchers^[4, 5, 6, 7].

Yield is a complex quantitative character resulting from the combined effects of several component traits and environmental factors. In field pea, seed yield is influenced by plant height, number of branches per plant, pods per plant, seeds per pod, biological yield, harvest index, seed weight and other related traits. Since yield is polygenically inherited and strongly influenced by the environment, direct selection based solely on yield may not always be effective. Therefore, a detailed understanding of the magnitude of genetic variability and the nature of association among yield-contributing characters is essential for designing efficient breeding strategies.

Genetic variability serves as the foundation of any crop improvement programme. The effectiveness of selection depends upon the amount of heritable variation present in the population. Assessment of variability enables breeders to identify promising genotypes and estimate the scope of improvement through selection. The magnitude of variability is commonly measured using the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV). The phenotypic coefficient of variation represents total observable variation, whereas the genotypic coefficient of variation estimates the portion attributable to genetic causes.

A comparison of these parameters provides valuable insights into how environmental factors influence trait expression. Heritability is another important genetic parameter that measures the proportion of total phenotypic variance attributable to genetic factors. Knowledge of heritability helps breeders assess the reliability of phenotypic selection. However, heritability alone cannot predict the expected progress from selection. Therefore, it is generally considered together with genetic advances. High heritability coupled with high genetic advance indicates the predominance of additive gene action and suggests that substantial improvement can be achieved through simple selection procedures. Conversely, high heritability associated with low genetic advance often indicates the involvement of non-additive gene effects and environmental influences^[10, 12].

Correlation analysis provides valuable information regarding the degree and direction of association among different characters. Since seed yield is determined by several interrelated traits, understanding their relationships is important for formulating effective selection criteria. Positive correlations between yield and component traits facilitate simultaneous improvement of multiple characters, whereas negative associations may create constraints during breeding. Estimation of both genotypic and phenotypic correlations helps distinguish genetic associations from environmental effects and provides a better understanding of trait relationships^[12].

Although correlation coefficients indicate associations among characters, they do not reveal the direct and indirect contributions of individual traits to yield. To overcome this limitation, path coefficient analysis is employed. Path analysis partitions correlation coefficients into direct and indirect effects, thereby providing a more precise understanding of cause-and-effect relationships among traits. This technique enables breeders to identify characters that exert a substantial direct influence on yield, thereby helping formulate efficient selection strategies. Consequently, correlation and path coefficient analyses have become indispensable tools in plant breeding programmes aimed at yield improvement^[12, 13, 15].

The growing demand for protein-rich foods, coupled with the need for sustainable agricultural systems, has heightened the importance of pulse crops such as field peas. Developing high-yielding, stable cultivars requires a comprehensive understanding of genetic variability and the relationships among yield-contributing traits. Evaluation of field pea germplasm for quantitative traits provides opportunities to identify superior genotypes and formulate effective breeding strategies for future crop improvement programmes.

Materials and Methods

Experimental site and plant material

The present investigation was carried out during the rabi season of 2025-26 at the Research Farm, School of Agricultural Sciences, G. H. Rasoni University, Saikheda, Madhya Pradesh, India, situated at 21.514862° N latitude and 78.76364° E longitude. The experimental material comprised 20 Field pea genotypes from diverse sources, namely IPFD18-14, IPFD18-16, IPFD18-17, IPFD18-11, IPFD18-13, Rachna, Uttara, Jayanti, Shikha, IPFD18-20, Pant pea-5, KPMR 485, HFP94-12, Pant-243, KDP-27, IPCL-4-17, IPC2010-134, IPCK2013-163, Aman, and Prakash.

Experimental design and crop management

The 20 genotypes were tested in a Randomised Block Design (RBD), replicated three times, resulting in 60 single-row plots. The experimental area was laid out in plots, each measuring 2.0 m x 3.00 m (row length 4.0 m; row-to-row spacing 30 cm; plant-to-plant spacing 10 cm; 20 plants per row), leaving 288 m² excluding borders and paths. The crop was fertilised with the recommended dose of 20:60:20 kg N:P₂O₅:K₂O ha⁻¹, and the standard agronomic package of practices recommended for the rabi Field pea region was adhered to across all plots.

The meteorological observations recorded on weekly basis during crop growing period (Standard Meteorological Weeks 46 of 2025 to 13 of 2026) revealed that rainfall ranged from 0.0 to 5.0 mm, with the maximum temperature ranged from 24.8 to 35.0 °C and minimum temperature ranged from 11.2 to 21.2 °C, and relative humidity ranged from 30 to 52%, signifying that the crop was produced under typical dry, cool to warm weather conditions of the rabi season with no significant weather aberration.

Observations recorded

Observations were recorded on five randomly selected and tagged plants in each plot of every replication for eleven quantitative yield and yield attributing traits viz., Days to 50% Flowering (DF50), Days to Maturity (DM), Plant Height (PH), Number of Primary Branches per Plant (PB), Number of Secondary Branches per Plant (SB), Number of Pods per Plant (PPP), Number of Pods per Axil (PPA), Pod Length (PL), Number of Seeds per Pod (SPP), 100-Seed Weight (SW), and Grain Yield (Yha) following [10, 12]. Days to 50 per cent flowering and days to maturity were recorded on a plot basis, while the remaining nine traits were recorded on the five tagged plants and averaged to obtain the plot mean.

Statistical analysis

All of the data for the 11 quantitative traits were collected and statistically analysed by R software (Version 4.5.1). Analysis of variance for the Randomised Block Design, along with estimation of the genotypic and phenotypic coefficients of variation, broad-sense heritability, and genetic advance (both as an absolute value and as a percentage of the mean, worked out at 5% selection intensity), was carried out using the R package 'variability',

which partitions the observed phenotypic variance into its genotypic, environmental and error components and derives the associated genetic parameters directly from the fitted model. GCV and PCV were categorised as low, moderate or high following [10, 11, 12, 14] broad-sense heritability was categorised following [8, 10] and genetic advance as a percentage of the mean was likewise categorised following [8, 12].

Results and Discussion

Analysis of variance

The analysis of variance revealed significant differences ($p < 0.001$) among the genotypes for all the characters studied (Table 1), indicating substantial and exploitable genetic variability within the experimental material. The mean sum of squares due to genotypes was highly significant for all the studied traits viz, days to 50% flowering (26.5360), days to maturity (27.4833), plant height (99.3850), number of primary branches (3.1149), number of secondary branches (17.7047), pods per plant (3.7768), pods per axil (0.1428), pod length (0.6932), seeds per pod (0.2222), 100-seed weight (3.1852) and yield (5.8960). The mean sum of squares due to replication was comparatively low for all the characters, ranging from 0.0086 for pods per axil to 1.8500 for days to maturity. The error mean squares ranged from 0.0122 for seeds per pod to 4.6610 for plant height. The highly significant genotype effects for all characters indicated considerable genetic variability among the 20 genotypes evaluated. Thus, the material used in the present investigation possessed sufficient variability for further genetic analysis and selection for desirable traits, particularly yield and its contributing characters.

Significant variation is present across all studied traits. This is an essential prerequisite for any crop improvement programme, as the existence of significant genotypic variation confirms that selection and hybridisation can be effectively deployed to develop superior recombinants or varieties. The mean sum of squares due to replications was non-significant or small for all traits, confirming the adequacy of experimental management and the reliability of the data collected. The error mean squares were also small relative to the genotypic mean squares across all traits, further reflecting the precision and homogeneity of the experimental environment. Similar results were also reported by [9, 10, 15].

Table 1: Analysis of Variance for eleven yield and yield-contributing traits in twenty field pea genotypes evaluated in RBD with three replications

S. No.	Source of Variation / Trait	Mean Sum of Squares (MSS) (Degrees of Freedom)		
		Replication (df = 2)	Genotype (df = 19)	Error (df = 38)
1	Days to 50% Flowering (DF50)	0.2167	26.5360***	1.7254
2	Days to Maturity (DM)	1.8500	27.4833***	3.0781
3	Plant Height – cm (PH)	0.7240	99.3850***	4.6610
4	No. of Primary Branches (PB)	0.0350	3.1149***	0.2213
5	No. of Secondary Branches (SB)	0.6013	17.7047***	1.1336
6	Pods per Plant (PPP)	0.0918	3.7768***	0.3005
7	Pods per Axil (PPA)	0.0086	0.1428***	0.0146
8	Pod Length – cm (PL)	0.0281	0.6932***	0.0255
9	Seeds per Pod (SPP)	0.0380	0.2222***	0.0122
10	100-Seed Weight – g (SW)	0.1880	3.1852***	0.1346
11	Yield – q/ha (Yha)	0.1054	5.8960***	0.2341

*** Significant at $p < 0.001$; ** Significant at $p < 0.01$; * Significant at $p < 0.05$; ns = Non-significant

Genetic variability, heritability and genetic advance

Genetic parameters of yield and their components are given in Table 2. Results showed that percentage of PCV was higher than the percentage of GCV for all the traits under study. At 50% flowering, GCV and PCV were estimated at 4.90% and 5.38%, respectively, both in the low range (<10%), indicating that this trait is relatively less variable among the tested genotypes. Similar low GCV and PCV were observed for days to maturity (GCV = 2.46%, PCV = 2.89%) and seeds per pod (GCV = 5.24%, PCV = 5.68%). Moderate GCV and PCV were recorded for pod length (GCV = 6.46%, PCV = 6.82%), pods per axis (GCV =

7.10%, PCV = 8.23%), plant height (GCV = 7.71%, PCV = 8.25%), seed weight (GCV = 5.42%, PCV = 5.77%), and seed yield (GCV = 9.69%, PCV = 10.27%). Among these, plant height exhibited a relatively higher GCV (7.71%), reflecting the wide morphological variation present in the germplasm for this trait. The highest GCV and PCV values were recorded for primary branches (GCV = 9.55%, PCV = 10.59%), secondary branches (GCV = 9.50%, PCV = 10.43%), and seed yield (GCV = 9.69%, PCV = 10.27%), all approaching the moderate boundary. Similar finding also reported in *Pisum* and other Fabaceae [9, 14, 15].

Table 2: Estimates of genetic parameters for eleven quantitative traits in twenty field pea genotypes

Traits	GCV (%)	PCV (%)	Heritability (Broad Sense h ²)	Genetic Advance (GA)	GA as % of Mean
Days to 50% Flowering	4.90	5.38	82.74	5.39	9.18
Days to Maturity	2.46	2.89	72.55	5.00	4.32
Plant Height (cm)	7.71	8.25	87.14	10.81	14.82
Primary Branches	9.55	10.59	81.34	1.82	17.74
Secondary Branches	9.50	10.43	82.97	4.41	17.82
Pods Per Plant	8.70	9.76	79.41	1.98	15.96
Pod Per Axis	7.10	8.23	74.52	0.37	12.63
Pod Length (cm)	6.46	6.82	89.72	0.92	12.60
Seeds Per Pod	5.24	5.68	85.16	0.50	9.96
Seed Weight (g)	5.42	5.77	88.31	1.95	10.49
Yield (q/ha)	9.69	10.27	88.96	2.67	18.83

PCV = phenotypic coefficient of variation; GCV = genotypic coefficient of variation; h²b = broad-sense heritability; GA = genetic advance; GAM = genetic advance as a percentage of the mean.

Correlation analysis

Significance was tested at the 5% (*) and 1% (***) levels of probability. In the present investigation, genotypic and phenotypic correlation coefficients were computed for all possible pairs among eleven traits in twenty genotypes of field pea (*Pisum sativum* var. *arvense* L.), namely: Days to 50% flowering (DF50) exhibited a significant and strongly negative correlation with grain yield (Yha) at both the genotypic ($r_g = -0.895^{***}$) and phenotypic ($r_p = -0.800^{***}$) levels. A non-significant positive correlation was observed with Plant Height (PH; $r_g = 0.311$; $r_p = 0.256^*$), with the phenotypic estimate marginally significant at the 5% level, suggesting only a weak positive association between flowering duration and plant stature. In contrast, DF50 was significantly and strongly negatively correlated with all yield-contributing traits: PB ($r_g = -0.927^{***}$; $r_p = -0.745^{***}$), SB ($r_g = -0.953^{***}$; $r_p = -0.770^{***}$), PPP ($r_g = -0.903^{***}$; $r_p = -0.744^{***}$), PPA ($r_g = -0.946^{***}$; $r_p = -0.718^{***}$), PL ($r_g = -0.915^{***}$; $r_p = -0.798^{***}$), SPP ($r_g = -0.959^{***}$; $r_p = -0.758^{***}$), and SW ($r_g = -0.930^{***}$; $r_p = -0.828^{***}$). (Tables 3 and 4) respectively. The results are presented and discussed trait-wise below. Similar findings have already been reported in pea and other legumes [9, 12, 13, 14].

Path Coefficient Analysis

Path coefficient analysis was computed at both the genotypic and phenotypic levels using the ten yield-contributing traits (DF50, DM, PH, PB, SB, PPP, PPA, PL, SPP, SW) as causal variables and Grain Yield (Yha) as the criterion variable (Tables 5 and 6), respectively. Trait-wise results are discussed below, with both genotypic and phenotypic direct and indirect effects presented together for each trait.

The adequacy of the path model is assessed through the residual effect (R), computed as $R = \sqrt{1 - R^2}$, where R^2 is the coefficient of determination. A low residual effect indicates that the causal traits included in the model collectively explain a large proportion of the total variation in grain yield, and that no major contributing traits have been omitted. In the present study, the residual effect was 0.0005 at the genotypic level and 0.2797 ($\sqrt{0.0783}$) at the phenotypic level. The near-zero genotypic residual (0.0005) confirms that the ten traits included in the genotypic path model account for virtually all ($\approx 99.95\%$) of the genetic variation in grain yield, indicating that the genotypic model is highly adequate. The phenotypic residual of 0.2797, while somewhat higher, is still acceptable and indicates that the phenotypic model explains approximately 92.2% of the total phenotypic variation in yield, the additional unexplained portion attributable to micro-environmental variation not captured by the measured traits.

Table 3: Genotypic Correlation Coefficients among Quantitative Traits in 20 Field Pea (*Pisum sativum* L.) Genotypes

Genotypic correlation											
Traits	DF50	DM	PH	PB	SB	PPP	PPA	PL	SPP	SW	Yha
DF50	1										
DM	0.943***	1									
PH	0.311	0.292	1								
PB	-0.927***	-0.879***	-0.222	1							
SB	-0.953***	-0.952***	-0.034	0.953***	1						
PPP	-0.903***	-0.888***	0.056	0.943***	0.985***	1					
PPA	-0.946***	-0.899***	-0.317	0.976***	0.98***	0.981***	1				
PL	-0.915***	-0.844***	-0.085	0.962***	0.995***	0.998***	0.971***	1			
SPP	-0.959***	-0.903***	-0.208	0.997***	0.978***	0.995***	0.981***	0.981***	1		
SW	-0.93***	-0.872***	-0.163	0.96***	0.967***	0.996***	0.963***	0.987***	0.982***	1	
Yha	-0.895***	-0.841***	0.007	0.918***	0.985***	0.994***	0.966***	0.982***	0.986***	0.985***	1

Table 4: Phenotypic Correlation Coefficients among Quantitative Traits in 20 Field Pea (*Pisum sativum* L.) Genotypes

Phenotypic correlation											
	DF50	DM	PH	PB	SB	PPP	PPA	PL	SPP	SW	Yha
DF50	1										
DM	0.81***	1									
PH	0.256*	0.25	1								
PB	-0.745***	-0.664***	-0.218	1							
SB	-0.77***	-0.73***	-0.048	0.858***	1						
PPP	-0.744***	-0.732***	0.011	0.756***	0.808***	1					
PPA	-0.718***	-0.621***	-0.211	0.765***	0.729***	0.719***	1				
PL	-0.798***	-0.646***	-0.046	0.786***	0.838***	0.837***	0.792***	1			
SPP	-0.758***	-0.686***	-0.138	0.786***	0.825***	0.796***	0.833***	0.879***	1		
SW	-0.828***	-0.694***	-0.134	0.819***	0.794***	0.801***	0.828***	0.89***	0.873***	1	
Yha	-0.8***	-0.73***	0.012	0.795***	0.887***	0.897***	0.733***	0.883***	0.859***	0.878***	1

Table 5: Genotypic path coefficient analysis showing direct and indirect effects of component traits on seed yield in field pea

Genotypic Path										
	DF50	DM	PH	PB	SB	PPP	PPA	PL	SPP	SW
DF50	1.55272	-1.52872	-0.15892	-0.44595	0.15333	1.33223	3.42439	-5.67805	-0.11797	0.57007
DM	1.4631	-1.62236	-0.14808	-0.42372	0.15263	1.30519	3.23715	-5.22411	-0.11175	0.53232
PH	0.48547	-0.47264	-0.50828	-0.10619	0.00545	-0.08394	1.14859	-0.53679	-0.02559	0.10036
PB	-1.44319	1.43275	0.11249	0.47979	-0.15276	-1.38937	-3.62349	5.96725	0.12311	-0.58746
SB	-1.48566	1.54515	0.01728	0.45735	-0.16025	-1.53485	-3.5501	6.17248	0.11977	-0.59392
PPP	-1.40692	1.44018	-0.02902	0.45339	-0.16729	-1.47029	-3.55215	6.26853	0.12743	-0.62868
PPA	-1.47581	1.45769	0.16204	0.48254	-0.15791	-1.44961	-3.60284	6.02224	0.12249	-0.5908
PL	-1.42366	1.36859	0.04406	0.46232	-0.15973	-1.48827	-3.50362	6.19279	0.12319	-0.6053
SPP	-1.48572	1.47042	0.1055	0.4791	-0.15567	-1.51968	-3.5795	6.18765	0.12329	-0.61781
SW	-1.44558	1.4104	0.08331	0.46032	-0.15544	-1.50959	-3.47624	6.12182	0.1244	-0.61232

Residual= 0.0005

Table 6: Phenotypic path coefficient analysis showing direct and indirect effects of component traits on seed yield in field pea

Phenotypic path										
	DF50	DM	PH	PB	SB	PPP	PPA	PL	SPP	SW
DF50	-0.06515	0.00773	0.0146	0.06132	-0.25967	-0.25604	0.09304	-0.0223	-0.10587	-0.26727
DM	-0.05305	0.00949	0.01439	0.05458	-0.24821	-0.25356	0.08155	-0.0182	-0.09478	-0.22682
PH	-0.01667	0.00239	0.05709	0.01794	-0.01621	0.00375	0.02731	-0.00123	-0.01944	-0.04284
PB	0.04862	-0.00631	-0.01246	-0.08219	0.29048	0.26086	-0.09932	0.02201	0.1088	0.26582
SB	0.05019	-0.00699	-0.00275	-0.07081	0.33714	0.27817	-0.09431	0.02346	0.1161	0.2564
PPP	0.04847	-0.00699	0.00062	-0.06228	0.27245	0.34412	-0.09311	0.02346	0.11163	0.25904
PPA	0.04683	-0.00598	-0.01205	-0.06306	0.24561	0.24757	-0.13102	0.02223	0.11669	0.26746
PL	0.0521	-0.00619	-0.00251	-0.06485	0.2836	0.2895	-0.10315	0.02789	0.12282	0.2873
SPP	0.04995	-0.00652	-0.00804	-0.06475	0.28344	0.27824	-0.10939	0.02481	0.13775	0.2862
SW	0.05399	-0.00668	-0.00758	-0.06772	0.26796	0.27642	-0.10733	0.02484	0.12252	0.32268

Residual= 0.0783

Conclusion

The present study showed that the twenty field pea genotypes differed considerably for all the characters studied, indicating the presence of useful genetic variation for crop improvement. The high heritability recorded for

different traits suggested that selection based on observable performance may be effective. Important yield-related characters such as number of pods per plant, seeds per pod, number of secondary branches, pod length, and 100-seed weight showed a positive relationship with grain yield. In

contrast, early flowering and early maturity were found to be favourable for achieving better grain production. The path coefficient analysis further indicated the importance of pod length, secondary branches, pods per plant, and seed weight in determining grain yield. Therefore, improvement in these traits can help breeders develop higher-yielding field pea varieties. Among the genotypes evaluated, KDP-27 performed best for grain yield and several important yield components. Other promising genotypes, including Uttara, Pant-243, Jayanti, and Rachna, also showed good performance and may be useful in future breeding programmes. The results suggest that simultaneous selection for earliness, better branching, higher pod number, longer pods, more seeds, and heavier seeds would be beneficial. These traits can be considered together while selecting superior plants. The available genetic variation provides good opportunities for further crop improvement. Promising genotypes can also be used as parents in hybridisation programmes. Such breeding approaches may help combine desirable characters in new progenies. Overall, the findings provide useful information for selecting superior material and developing productive and early-maturing varieties of field pea.

References

- Food and Agriculture Organization of the United Nations. FAOSTAT database. Rome: FAO; 2024.
- Zohary D, Harlan JR, Ashri A. Origin and evolution of cultivated plants. Science. 1973;182:441-443.
- Tanksley SD, McCouch SR. Seed banks and molecular maps: unlocking genetic potential from the wild. Science. 1997;277(5329):1063-1066.
- Smith JSC, *et al.* The use of plant genetic resources. In: Brown ADH, *et al.*, editors. The use of plant genetic resources. Cambridge: Cambridge University Press; 1989. p. 76-88.
- Naghavi MR, Jahansouza MR. Variation in the agronomic and morphological traits of Iranian chickpea accessions. J Integr Plant Biol. 2005;47(3):375-379.
- Able JA, Langridge P, Milligan AS. Capturing diversity in the cereals: many options but little promiscuity. Trends Plant Sci. 2007;12(2):71-79.
- Muhammad AA, Nawab NN, Khan AA, Ashraf M, Niaz S, Mahmood K. Estimation of genetic diversity in pea (*Pisum sativum* L.) germplasm using numerical taxonomy. Pak J Bot. 2009;41(5):2439-2448.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47(7):314-318. doi:10.2134/agronj1955.00021962004700070009x
- Kumar V, Bharti B, Nath S, Pratap J, Prasad S, Kumar D. Genetic divergence, variability and association analysis for seed yield and its contributing traits in selected germplasm of field pea (*Pisum sativum* L.). Legume Res. 2025;48(12):1979-1986. doi:10.18805/LR-5413
- Vivek K, Rabiya J, Gawande AB, Sandeep N, Vaidurya PS. Assessing genetic diversity in the 3K mini-core collection of rice (*Oryza sativa* L.) using standardised Euclidean distance and Ward's hierarchical clustering. Plant Sci Today. 2026. doi:10.14719/pst.15766
- Kumari J, Kumar V, Masih SA, Maxton A. Effect of phytohormonal seed priming with indole acetic acid and salicylic acid on yield and yield component traits in green gram. Plant Arch. 2025;25(2). doi:10.51470/PLANTARCHIVES.2025.v25.no.2.046
- Kumari J, Maxton A. Genetic variability and trait association in 20 diverse genotypes of greengram (*Vigna radiata* L.) under field conditions. Environ Conserv J. 2025;26(3):976-983. doi:10.36953/ECJ.33033093
- Yadav M, Kumari J, Gantait A, Kumar V, Maxton A. Assessment of genetic diversity for yield component traits and grain yield of blackgram [*Vigna mungo* (L.) Hepper]. J Exp Agric Int [Internet]. 2024 Sep 3 [cited 2026 Aug 30];46(9):426-433. Available from: <https://journaljeai.com/index.php/JEAI/article/view/2839>
- Yadav KK, Kumari J, Mamatha A, Kumar V, Gantait A, Maxton A. Study of genetic variability and path analysis for yield in greengram (*Vigna radiata* L. Wilczek). J Exp Agric Int [Internet]. 2024 Aug 28 [cited 2026 Aug 30];46(9):130-141. Available from: <https://journaljeai.com/index.php/JEAI/article/view/2812>
- Yadav A, Upadhyay DK, Jha A, Ram CN, Tiwari C, Srivastava A. Estimates of genetic variability, heritability and genetic advance in garden pea (*Pisum sativum* L. var. hortense) for yield and quality attributes. J Adv Biol Biotechnol [Internet]. 2026 Jun 10 [cited 2026 Aug 30];29(6):458-466. Available from: <https://journaljabb.com/index.php/JABB/article/view/4027>
- Sadras VO, Calderini DF, editors. Crop physiology: case histories for major crops. London: Academic Press; 2020.
- Noru RSR, Thomas B, Maraskole SK, S VP, Panotra N, Rajesh J, *et al.* Participatory plant breeding: a pathway to sustainable and resilient agriculture. J Adv Biol Biotechnol [Internet]. 2024 Aug 10 [cited 2026 Aug 30];27(8):1293-1306. Available from: <https://journaljabb.com/index.php/JABB/article/view/1253>