Principal Component Analysis of Field Pea (*Pisum sativum* L.Var. *arvense*) Genotypes

Abstract

Field pea is one of the important rabi pulse crops that requires improvement to enhance productivity due to its growing demand. PCA was employed to assess variability among fifty-seven field pea genotypes, including two checks Pant P 554 and JM 6, evaluated at the Seed Breeding Farm, JNKVV, Jabalpur during *rabi* 2024–25 in a Randomized Complete Block Design with two replications. Sixteen quantitative traits were studied (Days to 50% flowering and maturity, Number of primary branches per plant, Number of secondary branches per plant, Number of nodes per plant, Number of effective nodes per plant, Pod length, Pod bearing length, Number of pods per plant, Number of effective pods per plant, Plant height, Numbers of seeds per pod, Hundred seed weight, Seed yield per plant, Biological yield per plant, Harvest index) out of which five PCs with eigenvalues >1 explained 69.143% of total variability. PC1 was mainly influenced by plant height, number of nodes per plant, pod bearing length, number of pods per plant, number of effective pods per plant, biological yield and seed yield per plant. PC2 was defined by harvest index and number of seeds per pod, while days to 50% flowering, days to maturity, number of primary branches per plant and number of effective nodes per plant were the dominant traits in PC3. PC4 was mostly affected by the trait weight of 100 seeds. Pod length was the main trait in PC5. Genotypes Pant P-243, Ambika, Adarsh, Pant P-554 and IPFD 11-5 were identified as promising.

Keywords: Field pea, Principal Component Analysis, principal components, eigenvalue

Abbreviations: PCA- Principal Component Analysis; PCs- Principal components

INTRODUCTION-

Field pea (*Pisum sativum* L. var. *arvense*) is one of the most important pulse crops cultivated in India, primarily during the winter season. It is an annual, herbaceous, self-pollinating legume extensively grown across temperate regions. Field pea has a diploid chromosome number of 2n = 14 and a genome size of approximately 4.5 Gb (Arumuganathan and Earle, 1991). The crop belongs to the family Fabaceae, the largest family of flowering plants, which comprises about 450 genera and 1200 species (Luitel *et al*.,2021). The genus *Pisum* includes two species: *Pisum fulvum* Sibth. and *Pisum sativum*. According to Vavilov (1949), the primary centres of origin of field pea are Ethiopia, the Mediterranean, and Central Asia.

Globally, field pea is cultivated across a wide range of agro-climatic regions, with major producers including Canada, Russia, China, and India. In India, it is primarily grown in Uttar Pradesh, Madhya Pradesh, and Bihar, with Uttar Pradesh being the leading producer. Due to its high nutritional value and wide adaptability, field pea is gaining importance as a food legume; however, its yield potential remains constrained by multiple production and breeding challenges.

One of the key limitations in field pea improvement is the narrow genetic base, resulting from domestication and reliance on a few cultivars. This restricts the introduction of novel traits such as resistance to diseases, tolerance to abiotic stresses, and improved agronomic performance. In addition, problems such as lodging, pod shattering, and poor synchronization in flowering and maturity reduce harvest efficiency and limit yield stability. These challenges highlight the need for systematic genetic improvement to develop superior varieties with high yield potential, resilience and better marketability.

The success of any crop improvement programme depends on the effective assessment and utilization of genetic variability. Studies on variability not only provide insights into the extent of diversity present in germplasm but also help identify promising genotypes for use in breeding. Principal component analysis (PCA) is a multivariate statistical tool that reduces a large set of correlated variables into a smaller set of uncorrelated principal components, thereby capturing most of the variability in the dataset. In crop breeding, PCA is widely used for the evaluation of genetic diversity based on agro-morphological traits. This approach facilitates the identification of trait associations, classification of genotypes, and selection of potential parents for hybridization, thus strengthening decision-making in breeding programmes aimed at developing improved field pea cultivars.

MATERIAL AND METHODS

The Experimental materials consist of fifty-seven field pea genotypes including two checks received from Department of Genetics and Plant Breeding, College of Agriculture, JNKVV, Jabalpur and IIPR, Kanpur. The experiment took place during the *Rabi* season of 2024-25 at the Seed breeding farm, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh in Randomized Complete Block Design with two replications. Each genotype had been sown in 5 meters row while plant to plant distance was 8-10 cm and row to row distance was 45 cm. From each replication, five plants were chosen to record observations on various traits, including days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height, number of nodes per plant, number of effective nodes per plant, pod bearing length, number of pods per plant, number of effective pods per plant, pod length, number of seeds per pod, 100-seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g). Principal Component Analysis based on Pearson’s correlation matrix cluster analysis and a scree plot was performed using a demo version of XLSTAT.

3. RESULTS AND DISCUSSION

Fifty-seven genotypes of field pea were analysed quantitatively using PCA in the current study program. Only five of the sixteen Principal components (PCs) had an Eigen value greater than one, indicating variation among the variables being examined (Aman *et al*. 2021; Bishnoi *et al*. 2025). It showed that these five PCs under investigation varied by around 69.143%. PC1 (22.86%) had the highest variability, followed by PC2 (15.428%), PC3 (12.075%), PC4 (11.081%) and PC5 (7.699%). Eigenvalues, % variance and cumulative % are mentioned in Table 1. The semi-curved line beyond the fifth principal component showed only minimal variation, indicating that the majority of variation was concentrated in PC1 (Kommineni Jagadeesh *et al*. 2024). Hence, selecting genotypes based on the traits grouped under PC1 would be most desirable, as illustrated in Fig. 1.

Out of all the components, PC1 explained the most percentage of variability (22.86%), according to the rotated component matrix. Plant height, number of nodes per plant, pod bearing length, number of pods per plant, number of effective pods per plant, biological yield per plant and seed yield per plant were the dominant traits in PC1 (Azam *et al*. 2024; Singh BK *et al*. 2017; Shabbir *et al*. 2025). Traits like harvest index and number of seeds per pod were the main traits of PC2 (Luitel *et al*. 2021; Singh SK *et al*. 2020). Days to 50% flowering, days to maturity, number of primary branches per plant and number of effective nodes per plant were the dominant traits in PC3 (Aman *et al*. 2021; Shrestha *et al*. 2023). PC4 was mostly affected by the trait weight of 100 seeds (Singh H. *et al*. 2025). Pod length was the main trait in PC5 (Zhao *et al.* 2020) (Table 3).

Table 1: Principal Components of different traits

S. No.	Traits	Principal Components	Eigen values	Variability %	Cumulative %
1.	Days to 50% flowering	PC1	3.652	22.86	22.86
2.	Days to maturity	PC2	2.468	15.428	38.254

3.	Number of primary branches per plant	PC3	1.932	12.075	50.329
4.	Number of secondary branches per plant	PC4	1.773	11.081	61.410
5.	Plant height (cm)	PC5	1.232	7.699	69.109
6.	Number of nodes per plant	PC6	1.000	6.763	75.872
7.	Number of effective nodes per plant	PC7	0.847	5.292	81.164
8.	Pod bearing length (cm)	PC8	0.810	5.064	86.228
9.	Number of pods per plant	PC9	0.661	4.131	90.359
10.	Number of effective pods per plant	PC10	0.452	2.825	93.184
11.	Pod length (cm)	PC11	0.361	2.255	95.439
12.	Number of seeds per pod	PC12	0.273	1.709	97.147
13.	100 seed weight (g)	PC13	0.231	1.442	98.589
14	Biological yield per plant (g)	PC14	0.120	0.747	99.336
15	Seed yield per plant (g)	PC15	0.081	0.505	99.842
16	Harvest index	PC16	0.025	0.158	100.00

Fig 1: Scree Plot between Eigen Value and Principal Components

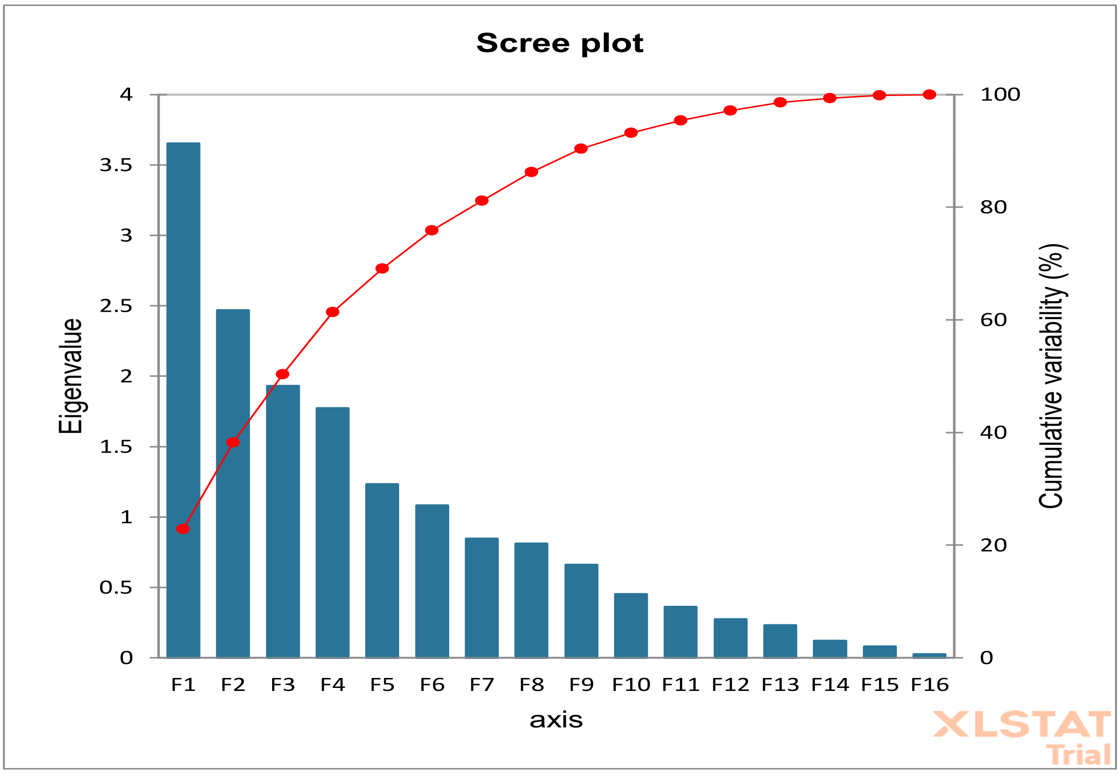


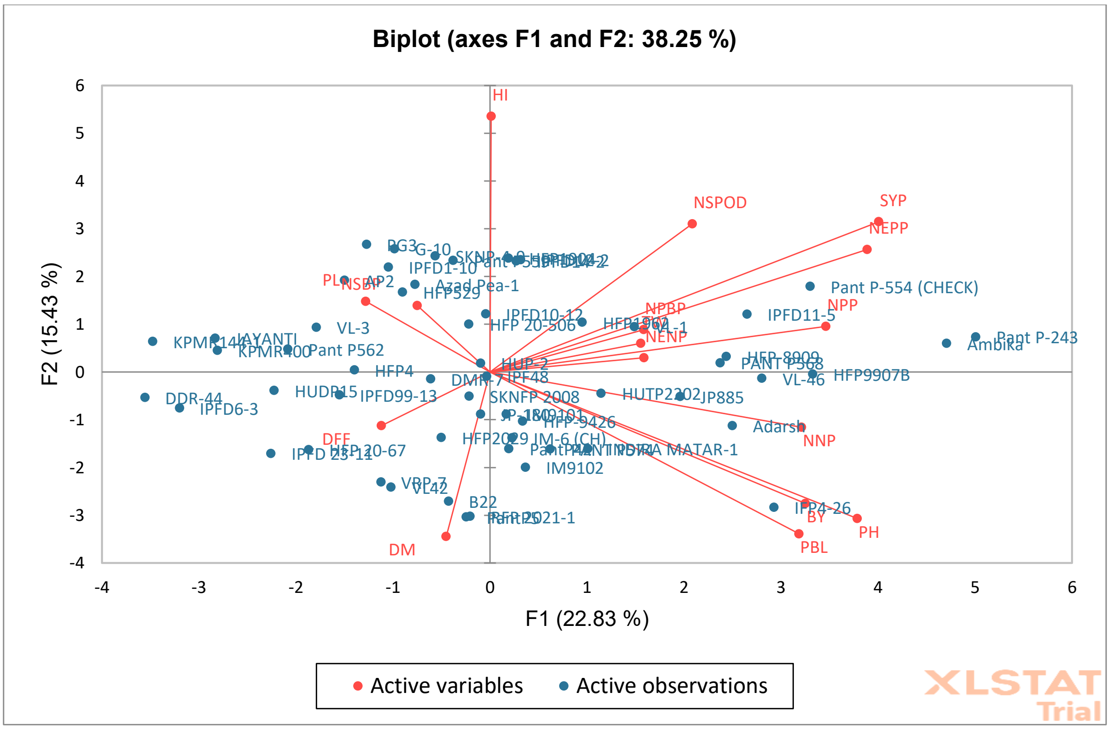
Table 2: Principal Components Values of Rotation Component Matrix (>0.25)

Traits	Principal components				
	PC1	**PC2**	**PC3**	**PC4**	**PC5**
Days to 50% flowering	0.000	-0.173	**0.638**	-0.105	0.129
Days to maturity	-0.084	-0.530	**0.511**	-0.215	-0.341
Number of primary branches per plant	0.297	0.136	**0.554**	-0.191	0.382
Number of secondary branches per plant	-0.141	0.215	-0.371	-0.252	-0.400
Plant height (cm)	**0.710**	-0.473	-0.286	0.205	0.043
Number of nodes per plant	**0.602**	-0.178	-0.206	0.265	0.134
Number of effective nodes per plant	0.297	0.046	**0.523**	0.415	-0.271

Pod bearing length (cm)	**0.597**	-0.522	-0.285	0.249	0.108
Number of pods per plant	**0.649**	0.147	0.356	-0.372	-0.215
Number of effective pods per plant	**0.729**	0.395	0.162	-0.239	-0.290
Pod length (cm)	-0.240	0.228	0.043	-0.303	**0.661**
Number of seeds per pod	0.391	**0.478**	-0.278	-0.417	0.152
100 seed weight (g)	0.291	0.092	0.327	**0.633**	0.265
Biological yield per plant (g)	**0.609**	-0.424	-0.024	-0.453	0.137
Seed yield per plant (g)	**0.751**	0.484	-0.012	-0.001	0.032
Harvest index (%)	0.002	**0.825**	0.015	0.449	-0.086

Table 3: Rotated Matrix results of different traits (> 0.25)

	PC 1	**PC 2**	**PC 3**	**PC 4**	**PC 5**
Traits	Plant height	Number of seeds per pod	Days to 50% flowering	100 seed weight	Pod Length
	Number of nodes per plant	Harvest index	Days to maturity		
	Pod bearing length		Number of primary branches per plant		
	Number of pods per plant		Number of effective nodes per plant		
	Number of effective pods per plant				
	Biological yield per plant				
	Seed yield per plant				



Biplot (axes F1 and F2: 38.25 %)

Fig. 2: Biplot

PC Scores of Genotypes for Field pea Genotypes

The genotype PANT P-243 recorded the highest PC1 score, indicating its overall superiority in the traits such as plant height, number of nodes per plant, pod bearing length, number of pods per plant, number of effective pods per plant, biological yield per plant and seed yield per plant (Parveen *et al*. 2025; Bishnoi *et al*. 2025). Other genotypes with notable PC1 scores included Ambika, Adarsh, Pant P-554, IPFD 11-5, PANT P568, JP885, HFP-8909, VL-46, HFP9907B and IFP4-26 also showing considerable influence from these traits.

PC2 was mainly governed by the harvest index and number of seeds per pod, PG3 showed the highest PC2 score, prominent genotypes in PC2 included Pant P-554, IPFD12-2, IPFD14-2, HFP1904, Pant P559, AP2, G-10, SKNP-4-9 and IPFD1-10 (Luitel *et al*. 2021).

The highest PC3 score was observed in IPFD 23-11, reflecting it's associated with the days to 50% flowering, days to maturity, number of primary branches per plant and number of effective nodes per plant. Genotypes such as Ambika, Pant P-243, IPFD

11-5, HFP 20-67 and RFP 2021-1 also showed strong association under PC3 (Aman *et al.* 2021).

The genotype PANT P568 had the highest PC4 score, highlighting its excellence in 100-seed weight. Other genotypes with high PC4 scores included Pant P-554, PANT P574, HFP529, KPMR144-1, PG3, INDIRA MATAR-1, DMR-7 and IPFD1-10 (Singh H. *et al.* 2025).

PC5 characterized by pod length. HFP9907B emerged with the highest PC5 score, other genotypes include Pant P-243, IPFD10-12, VL-3 and HFP-9426 (Zhao *et al.* 2020).

Table 4: PC scores of Field pea Genotypes (>1.50)

S. No.	Genotypes	PC1	PC2	PC3	PC4	PC5
1	Ambika	**4.707**	0.598	**2.661**	-0.301	-1.966
2	Pant P-243	**5.009**	0.737	**1.508**	-1.105	-1.586
3	Adarsh	**2.499**	-1.122	1.376	1.249	0.816
4	Pant P-554	**3.301**	**1.792**	-0.036	**1.851**	-1.431
5	IPFD 11-5	**2.651**	1.208	**2.325**	-0.971	-0.318
6	IPFD12-2	0.317	**2.351**	-0.511	-0.662	-1.234
7	IPFD10-12	-0.044	1.217	1.742	-0.018	1.577
8	IPFD14-2	0.272	**2.325**	-0.523	-0.818	0.510
9	HFP1904	0.190	**2.382**	-0.686	-0.186	-0.541
10	PANT P574	0.622	-1.615	0.468	**2.443**	1.219
11	PANT P568	**2.374**	0.192	-0.328	**2.906**	-0.314
12	HFP 20-506	-0.217	1.004	1.433	0.949	1.341
13	HFP 20-67	-1.867	-1.628	**2.370**	1.284	-0.348
14	RFP 2021-1	-0.204	-3.026	**1.550**	-0.070	-0.748
15	HUTP2202	1.147	-0.445	-0.788	1.359	0.690
16	Pant P562	-2.083	0.482	0.519	0.386	-0.740
17	Pant P559	-0.379	**2.336**	0.620	-1.220	0.247
18	IPFD 23-11	-2.257	-1.705	**2.939**	-2.726	0.963
19	HFP1962	0.950	1.039	0.797	-2.032	0.941
20	SKNFP2008	-0.214	-0.509	-1.889	-0.126	-1.548

S. No.	**Genotypes**	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**
21	HFP2029	-0.502	-1.372	-1.214	0.407	0.658
22	B22	-0.427	-2.704	-1.840	1.005	-1.299
23	JP885	**1.961**	-0.516	-1.443	-1.572	-1.930
24	AP2	-1.500	**1.919**	-4.115	-0.406	-0.026
25	G-10	-0.983	**2.581**	-2.118	-0.531	0.513
26	HUP-2	-0.097	0.183	-1.750	-0.715	1.121
27	Azad Pea-1	-0.774	1.832	-0.662	-1.939	**1.549**
28	VRP-7	-1.123	-2.305	-0.880	-2.120	-0.339
29	HFP-8909	**2.437**	0.321	-1.690	-0.633	-1.182
30	JP-180	-0.095	-0.884	-1.923	-1.539	-0.773
31	VL-3	-1.788	0.937	-0.943	0.115	**1.618**
32	PantP42	0.195	-1.605	-1.317	-0.016	-1.579
33	IM9102	0.367	-1.995	-0.624	1.373	1.413
34	VL42	-1.020	-2.410	-1.506	-1.454	-1.451
35	PantP5	-0.245	-3.038	-0.067	0.054	0.291
36	HFP529	-0.900	1.670	-0.338	**1.739**	-1.493
37	KPMR144-1	-3.476	0.641	1.141	**2.450**	-1.003
38	PG3	-1.272	**2.671**	0.309	**2.253**	-0.028
39	SKNP-4-9	-0.564	**2.428**	1.444	-1.556	-0.237
40	KPMR400	-2.810	0.449	0.811	0.879	-0.049
41	VL-1	1.490	0.948	-0.110	1.023	0.618
42	VL-46	**2.803**	-0.135	-0.635	-0.229	0.201
43	JM-6	0.229	-1.382	0.350	0.624	-0.021
44	INDIRA MATAR-1	1.009	-1.608	-0.850	**1.593**	0.583
45	DMR-7	-0.612	-0.146	-0.277	**1.744**	-0.376
46	HFP9907B	**3.326**	-0.041	-0.240	-1.463	**3.087**
47	IFP4-26	**2.927**	-2.834	1.204	-0.421	1.039
48	HFP-9426	0.337	-1.032	-2.137	0.136	**1.630**
49	IM9101	0.168	-0.886	-0.742	0.822	1.096
50	IPFD99-13	-1.550	-0.483	0.320	-1.137	-0.321
51	HUDP15	-2.224	-0.388	1.855	-1.729	-0.903
52	DDR-44	-3.555	-0.536	1.194	0.689	-0.107

S. No.	Genotypes	PC1	PC2	PC3	PC4	PC5
53	IPF48	-0.032	-0.091	-0.006	-1.561	1.791
54	IPFD6-3	-3.200	-0.752	1.126	-0.839	-0.496
55	JAYANTI	-2.832	0.708	0.147	-0.724	-0.447
56	HFP4	-1.396	0.044	1.007	-0.690	-1.446
57	IPFD1-10	-1.047	**2.197**	0.972	**2.175**	0.768

Table 5: Promising genotypes on the basis of scores of Principal Components

PC 1	PC 2	PC 3	PC 4	PC 5
Ambika	Pant P-554	Ambika	Pant P-554	Azad Pea-1
Pant P-243	IPFD12-2	IPFD 23-11	PANT P574	VL-3
Adarsh	IPFD14-2	IPFD 11-5	PANT P568	HFP9907B
Pant P-554	HFP1904	Pant P-243	HFP529	HFP-9426
IPFD 11-5	Pant P559	RFP 2021-1	KPMR144-1	
PANT P568	AP2	HFP 20-67	PG3	
JP885	G-10		INDIRA MATAR-1	
HFP-8909	PG3		DMR-7	
VL-46	SKNP-4-9		IPFD1-10	
HFP9907B	IPFD1-10			
IFP4-26				

Conclusion

On the basis of principal component analysis, Pant P-243, Ambika, Adarsh, Pant P-554, IPFD 11-5, PANT P568, JP885, HFP-8909, VL-46, HFP9907B and IFP4-26, are designated as putative genotypes for field pea breeding for yield and attributing traits. These genotypes may be utilized in field pea breeding programmes to develop robust donors for future.

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