

## Principal Components Analysis for Yield and Quality Contributing Traits in Field Pea (*Pisum sativum* L.) Genotypes

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**ABSTRACT:** The study involved the examination of 43 field pea genotypes, focusing on their yield, and quality traits, and employed Principal Component Analysis. Field pea genotypes were evaluated in Randomized Complete Block Design (RCBD) in three replications along with three different dates of sowing at BSP Soybean Unit, Department of Genetics & Plant Breeding, College of Agriculture, JNKVV, Jabalpur during Rabi Season 2022-2023. The Principal Components Analysis was applied on 19 different yield and quality traits pooled under various environmental conditions. Out of nineteen, only 7 principal components (PCs) exhibited more than 1 eigen value and showed 79.34 % variability among the traits studied. The PC1 accounted the highest of total variability 24.548%, whereas, PC2, PC3, PC4, PC5, PC6 and PC7 exhibited 15.31%, 11.13%, 9.65%, 7.36%, 5.94% & 5.44% respectively. Rotated component matrix revealed that the PC1, PC2 and PC3 accounted for yield related traits. PC4, PC5 and PC7 contributed yield and quality with traits. Highest PC score was recorded in PC1 HFP 94-12 (4.268) & in PC2 Kalamatar (4.582), PC3 Tall Green (Hybrid) (2.560), PC4 HUP 2 (2.908), PC5 Batana Moolchand (2.63) and PC7 KFP 151 (2.398). The identified genotypes IPFD 99-25, Kalasona, Batana Moolchand and Gol Batra Tenduna showed their presence in two or more than two principal components. The genotypes contributing to the higher PC value will be of great importance as parental lines for the transfer of these traits to the recipients. The genotypes contributing high PC scores with sharing their presence in more than one component will be utilized as breeding line for hybridization programme to identify the transgressive segregation in the population.

**Keywords:** PCA, Yield and Quality, Variability, Field Pea.

### INTRODUCTION

The genus *Pisum* of the family Fabaceae includes the two species of pea, *Pisum fulvum* and *Pisum sativum*, as well as various wild subspecies (abyssinicum) of *Pisum sativum*. Garden peas (*Pisum sativum* var. *hortense*) and field peas (*Pisum sativum* var. *arvense*) are the two species of cultivated peas. One species of the genus *Pisum*, *Pisum sativum* ssp. *Abyssinicum*, is thought to be a progenitor and closely resembles the cultivated pea (Jing *et al.*, 2010). This is self-pollinating rabi pulse crop with the chromosome number  $2n=14$  is the field pea. Pea is in the Mediterranean region and grown at higher altitudes in tropical regions where the temperature ranges from 7 to 30 degrees Celsius.

Garden peas are used for food; thus, they are harvested when the pods are still green and boiled grains are used for later uses as vegetables Slade and others dietary purposes. For a variety of cuisine recipes, field peas are utilized as dried, whole or split dals or as flour (besan). The nutritional value of pea seeds is the primary

measure used to assess it. It has a high nutritional value and is a significant source of protein (between 21 and 25 percent) with high quantities of lysine and tryptophan amino acids (Bhat *et al.*, 2013; Gregory *et al.*, 2016) although it contains relatively low cysteine and methionine amino acids (Cheyhan and Avci 2005). This is regarded as the most affordable source of protein in the diet. Since it is herbaceous plant, it is frequently cultivated for food and fodder. Including the essential vitamins B1 and B5, dry pea seeds have 56.5% carbohydrates, 1.1% fat, 2.2% minerals, and 4.5% fiber. Animal feed is made from the stalks, broken cotyledons, and seed coat.

Due to day by day increasing of world population, more and more food availability will be required in coming years to fulfill the daily caloric needs. Regarding this prospect, there is urgent need for the development high yielding varieties of field pea having good quality seed for the multiplication and utilization for cultivation purposes. Inception of the genetic improvement programme for seed yield and its component traits, it

requires identification of suitable genotypes for a particular agro-climatic zone. These sources will be utilized as base material for further improvement in order to break the existing yield plateau. The study on principal component analysis serves the purpose of unveiling underlying patterns within data sets and minimizing redundancy. The objective of this study was to pinpoint the primary components with the highest variability, making them crucial for genotype selection based on specific traits.

Principal component analysis, basically a well-known data reduction technique, initially floated by Pearson (1901) and later developed by Hotelling (1933). PCA is a non-parametric, multivariate technique that analyzes a data table in which several inter-correlated quantitative dependent variables describe observations to extract important information (Nachimuthu *et al.*, 2014). So, intensive selection procedures can be designed to bring about rapid improvement of yield and quality attributing traits.

## MATERIAL AND METHODS

Experimental material consisted of 43 field pea genotypes were obtained from Field Pea Improvement Project, Department of Genetics & Plant Breeding, College of Agriculture, JNKVV, Jabalpur. The experiment was laid out in Randomized Complete Block Design (RCBD) in three replications along with three different dates of sowing (5<sup>th</sup> November 2022 – (normal), 5<sup>th</sup> December 2022 – (late) and 5<sup>th</sup> January 2023 – (extra late). All the genotypes were sown in four rows pattern keeping 30.0 cm row to row and 10.0 cm plant to plant distance. A total of 19 yield and quality attributing trait based observations were made. Further, Observations for days to fifty percent flowering (days), days to maturity (days), number of primary branches per plant, number of secondary branches per plant,

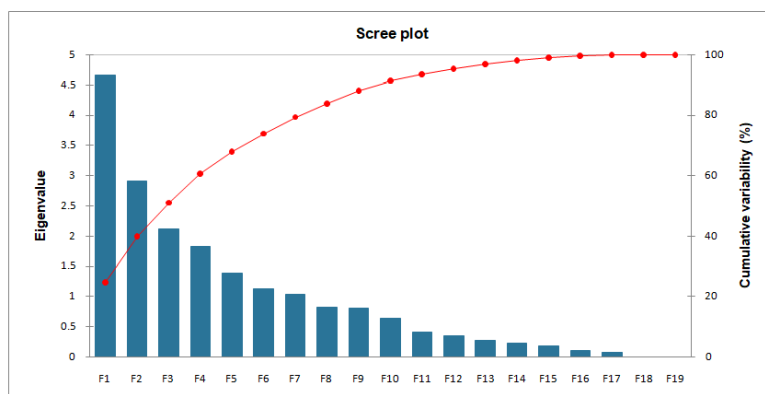
plant height (cm), number of nodes per plant, number of effective nodes per plant, pod bearing length (cm), number of pods per plant, number of effective pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), biological yield per plant (g), harvest index (%), seed yield per plant (g), total sugar content (%), protein content (%) and carbohydrate content (%) were recorded each of the three environments individually. The observations based on mean of the five individual plants was statistically analysed to find out Principal Component Analysis present in the experimental material for each traits. Principal Component Analysis (PCA) is a widely recognized technique for reducing the dimensionality of data. It allows the transformation of a large number of variables into a more concise set that retains most of the essential information. The methodology for PCA is based on the principles outlined by Massy (1965); Jolliffe (1986). By employing PCA, one can obtain a reduced number of linearly uncorrelated variables from a larger set of correlated variables. These derived linear variables, known as principal components, serve as crucial criteria for the selection of plants.

## RESULTS AND DISCUSSION

Principal components analysis was applied on 43 field pea genotypes using pooled data of all the three environments. Out of nineteen, only 7 principal components (PCs) exhibited more than 1 eigen value and showed about 79.34 % variability among the traits studied. The PC1 accounted for 24.548 % of total variability, whereas, PC2, PC3, PC4, PC5, PC6 and PC7 exhibited 15.31%, 11.13%, 9.65%, 7.36%, 5.94% & 5.44% respectively (Table 1). Similar result exhibited by Hanci and Cebeci (2019); Shukla (2015) also finding is in agreement where PC1 accounted for 29.784% of the total variability.

**Table 1: Eigen values, variability and cumulative percentage for nineteen traits in field pea genotypes.**

Characters	Principal Component (PC)	Eigen value	Variability (%)	Cumulative Variability (%)
DFP	PC1	4.664	24.548	24.548
DM	PC2	2.910	15.317	39.865
NPBPP	PC3	2.115	11.130	50.994
NSBPP	PC4	1.835	9.657	60.652
PH	PC5	1.388	7.306	67.957
NNPP	PC6	1.129	5.941	73.898
NENPP	PC7	1.035	5.448	79.346
PBL	PC8	0.829	4.364	83.710
NPPP	PC9	0.815	4.288	87.998
NEPPP	PC10	0.635	3.343	91.341
PL	PC11	0.418	2.201	93.542
NSPP	PC12	0.356	1.872	95.414
100SW	PC13	0.275	1.447	96.861
BYPP	PC14	0.228	1.202	98.063
HI	PC15	0.183	0.962	99.026
SYPP	PC16	0.102	0.539	99.565
TSC	PC17	0.073	0.382	99.947
PC	PC18	0.006	0.030	99.977
CC	PC19	0.04	0.023	100.000



**Fig. 1.** Scree plot of field pea genotypes showing eigen values among various principal components (F1-F19) and Cumulative variability (%).

Scree plot explained the percentage of variance associated with each principal component obtained by drawing a graph between Eigen values and principal component number. PC1 showed 24.548% variability with Eigen value 4.664 which then declined gradually (Fig. 1). Semi curve line is obtained after sixteen PC

tended to become straight with little variance observed in each PC. From the graph, it is clear that the maximum variation was observed in PC1 in compare to other nineteen PCs. So, selection of lines from this PC will be desirable.

**Table 2: PC values for nineteen phenological, yield and quality traits of field pea genotypes.**

Traits	Principal components						
	PC1	PC2	PC3	PC4	PC5	PC6	PC7
DFF	<b>0.661</b>	-0.499	-0.224	-0.307	0.096	-0.002	0.030
DM	<b>0.669</b>	-0.355	-0.212	-0.381	0.296	0.018	0.061
NPBPP	0.338	-0.287	0.186	<b>0.380</b>	-0.126	0.331	0.300
NSBPP	0.089	-0.097	-0.112	0.365	0.323	-0.397	<b>0.713</b>
PH	0.456	<b>0.603</b>	0.019	-0.423	0.137	-0.062	0.046
NNPP	<b>0.658</b>	-0.019	-0.149	-0.470	0.162	-0.157	0.032
NENPP	0.112	<b>0.865</b>	0.162	-0.104	0.011	0.032	-0.058
PBL	0.238	<b>0.876</b>	0.191	-0.141	-0.038	-0.053	0.073
NPPP	<b>0.762</b>	0.337	-0.136	0.388	-0.122	-0.149	0.036
NEPPP	<b>0.767</b>	0.336	-0.145	0.392	-0.087	-0.124	0.035
PL	-0.564	0.201	<b>0.523</b>	0.047	0.290	-0.179	0.172
NSPP	-0.614	0.121	-0.097	0.156	<b>0.379</b>	-0.393	-0.192
100 SW	-0.238	-0.066	<b>0.589</b>	-0.309	0.186	0.132	0.085
BYPP	<b>0.710</b>	-0.053	0.456	0.015	0.333	0.114	-0.122
HI	0.309	-0.348	<b>0.541</b>	0.252	-0.269	-0.380	-0.236
SYPP	0.620	-0.247	<b>0.644</b>	0.171	0.016	-0.178	-0.240
TSC	0.196	0.295	-0.293	<b>0.474</b>	0.049	0.346	-0.182
PC	0.019	0.060	0.395	-0.250	-0.570	0.170	<b>0.425</b>
CC	0.052	0.034	0.244	0.283	<b>0.574</b>	0.500	0.044

Note: DFF= Days to fifty percent flowering, DM= Days to maturity, NPBPP= Number of primary branches per plant, NSBPP= Number of secondary branches per plant, PH= Plant height (cm), NNPP= Number of nodes per plant, NENPP= Number of effective nodes per plant, PBL= Pod bearing length (cm), NPPP= Number of pods per plant, NEPPP= Number of effective pods per plant, PL= Pod length (cm), NSPP= Number of seeds per pod, 100 SW= 100-seed weight (g), BYPP= Biological yield per plant (g), HI= Harvest index (%), SYPP= Seed yield per plant, TSC= Total sugar content, PC= Protein content, CC= Carbohydrate content.

Rotated component matrix revealed that the PC1 accounted for the highest variability (24.548%) among the other components. On the basis of principal component analysis, two types of components were identified i.e. yield and quality related components. PC1, PC2 and PC3 accounted for yield related traits. PC4, PC5 and PC7 contributed yield and quality related traits. The traits which are dominated by PC1 are days to fifty percent flowering, days to maturity, number of nodes per plant, number of pods per plant, number of effective pods per plant and biological yield per plant. PC2 was also dominated by yield related traits i.e., plant height, number of effective nodes per plant and

pod bearing length. PC3 contributed yield related traits i.e., pod length, hundred seed weight and harvest index. PC4 dominated by number of primary branches per plant and one quality trait i.e., Total sugar content. PC5 dominated by number of seeds per pod and one quality trait i.e., Carbohydrate content. PC6 is not dominated by any trait. PC7 was dominated by number of secondary branches per plant and quality trait i.e., Protein content. The highest PC scores of all the traits were estimated in seven principal components and are displayed in Table 3. Similar findings have been reported by Shukla (2015); Kanoj (2016); Singh *et al.* (2017) for different yield related traits of field pea.

**Table 3: Interpretation of rotated matrix for the traits having maximum values in each PC.**

Traits	PC1	PC2	PC3	PC4	PC5	PC7
	Days to 50% flowering	Plant height	Pod length	Number of primary branches per plant	Number of seeds per pod	Number of secondary branches per plant
	Days to Maturity	Number of effective nodes per plant	Hundred seed weight	Total sugar content	Carbohydrate content	Protein content
	Number of nodes per plant	Pod bearing length	Harvest index			
	Number of pods per plant		Seed yield per plant			
	Number of effective pods per plant					
	Biological yield per plant					

**PC scores for field pea genotypes-** In 43 genotypes of field pea, high PC scores for all nineteen traits were estimated in 7 principal components and presented in Table 4. PC1 covered 12 genotypes having scored greater than one, which range from HFP 94-12 (4.268) to KPMR-402 (1.120). PC2 covered 12 genotypes having scored greater than one, which range from Kalamatar (4.582) to VL 3(1.036). PC3 covered 13 genotypes having scored greater than one, which range

from Tall Green (Hybrid) (2.560) to KPMR 486 (1.065). PC4 covered 9 genotypes having scored greater than one, which range from HUP 2 (2.908) to IPFD 12-2 (1.123). PC5 covered 10 genotypes having scored greater than one, which range from Batana Moolchand (2.63) to IPFD 11-5 (1.027). PC7 covered 6 genotypes having scored greater than one, which range from KFP 151 (2.398) to Kalasona (1.358).

**Table 4: Principal component scores of different field pea genotypes.**

Sr. No.	Genotype	PC1	PC2	PC3	PC4	PC5	PC6	PC7
1.	Shikha	0.811	-0.645	<b>2.161</b>	0.837	-0.951	-0.390	0.677
2.	Rachna	0.701	-3.425	<b>1.556</b>	0.041	<b>1.441</b>	-0.557	-1.541
3.	Jayanti	<b>1.608</b>	-2.031	0.837	-1.126	-0.216	-1.159	0.243
4.	Double Branching	-1.998	-1.927	0.945	0.879	-2.447	2.178	0.061
5.	VL 1	-2.530	-0.922	-0.299	<b>1.890</b>	-0.802	-0.013	-1.080
6.	DDR 39	0.221	-1.331	-1.314	<b>2.297</b>	-1.601	-0.230	0.809
7.	VL 3	0.272	<b>1.036</b>	-0.024	-0.173	-1.305	-0.260	-0.287
8.	PP 14	<b>3.143</b>	-0.837	0.180	0.764	-0.306	1.352	-1.872
9.	DDR 52	-3.297	-0.237	<b>1.510</b>	0.406	-0.483	-1.039	<b>2.110</b>
10.	RP 3	-1.692	-1.235	<b>1.051</b>	<b>2.161</b>	-0.130	-1.107	-1.821
11.	IPFD 12-2	-1.237	-1.445	0.318	<b>1.123</b>	-0.333	-0.230	-1.891
12.	Triple Branching	-2.159	0.305	0.648	0.058	0.356	0.601	0.030
13.	Aman	0.900	-1.996	-1.339	-1.144	<b>1.686</b>	0.099	0.283
14.	DDR 54	-0.708	0.257	-2.155	0.710	-0.100	-0.826	0.676
15.	JP 885(Purple)	-6.581	-0.896	-2.190	0.011	-1.367	-0.073	-0.542
16.	HUP 2	<b>3.170</b>	<b>1.124</b>	-2.014	<b>2.908</b>	-1.062	-0.635	0.636
17.	KPMR 302	0.299	-3.803	-0.142	-1.667	0.817	0.562	<b>1.554</b>
18.	KPMR 423	0.094	-2.021	0.290	-0.481	-0.311	-0.829	0.106
19.	KPMR 486	-0.953	0.508	<b>1.065</b>	-0.645	0.921	0.284	-0.357
20.	KPMR 327	0.516	0.161	-0.098	<b>1.407</b>	<b>1.680</b>	0.158	-0.317
21.	KPF 151	-1.841	-0.006	0.803	0.229	0.711	-0.238	<b>2.398</b>
22.	KPMR 485	<b>3.238</b>	0.880	<b>1.070</b>	-0.066	-1.552	-0.604	-1.673
23.	PP 86	<b>1.346</b>	-0.388	<b>1.411</b>	-1.034	-0.748	1.485	-0.230
24.	KPMR 503	-0.119	-0.717	-0.731	-0.592	-1.468	0.754	<b>1.539</b>
25.	HFP 94-12	<b>4.268</b>	-1.262	<b>1.806</b>	0.537	<b>1.276</b>	-0.601	0.789
26.	Kalamatar	-1.879	<b>4.582</b>	0.896	-0.381	-0.929	1.015	0.132
27.	IPFD 11-5	0.832	-0.112	-0.497	<b>1.582</b>	<b>1.027</b>	1.089	-0.258
28.	DDR 94-14	-2.321	-0.542	-1.819	-1.763	<b>1.491</b>	0.612	-0.326
29.	KPMR 502	-0.613	<b>1.735</b>	-0.656	-0.396	0.840	-0.893	-0.105
30.	HUVP 12	-1.479	0.114	0.031	-2.640	<b>2.242</b>	1.540	-1.161
31.	HFP 94-13	-0.558	<b>1.706</b>	-0.064	-2.758	-0.891	-1.444	-0.383
32.	KPMR 402	<b>1.120</b>	-0.660	-1.445	-2.599	-0.808	1.434	-0.056
33.	Safed Batri Gudda	<b>1.769</b>	<b>1.128</b>	-2.144	0.436	-0.514	0.576	-1.060
34.	Batana moolchand	<b>1.923</b>	<b>2.645</b>	-3.006	<b>2.555</b>	<b>2.631</b>	1.131	0.894
35.	Matar Rangpur	-0.017	-0.690	-3.338	-1.139	-1.123	-0.353	0.960
36.	Kashi Samriddhi	0.354	<b>1.506</b>	0.871	0.565	<b>1.576</b>	-1.817	0.423
37.	Kali batri	0.504	0.452	-1.421	-1.308	0.315	-3.270	-0.298
38.	Gol Batra Tenduna	<b>3.271</b>	<b>1.008</b>	<b>1.203</b>	-1.497	-1.260	-1.396	0.052
39.	IPF 99-25	<b>3.951</b>	<b>2.600</b>	<b>1.381</b>	-1.110	-1.142	1.649	<b>1.154</b>
40.	Tall White(Hybrid)	-2.828	<b>3.177</b>	<b>1.179</b>	-0.158	0.733	-0.261	-0.595
41.	Tall Green(Hybrid)	-2.770	<b>3.048</b>	<b>2.560</b>	0.379	0.512	0.257	-0.016
42.	JP 885	<b>1.841</b>	0.724	-1.301	-0.501	0.393	0.534	-1.018
43.	Kalasona	-0.571	-1.567	<b>2.225</b>	<b>1.404</b>	<b>1.202</b>	0.913	<b>1.358</b>

**Table 5: Genotypes selected on the basis of PC scores in each component showed positive values and shares in other different components.**

PC1	PC2	PC3	PC4	PC5	PC7
Jayanti (1.608)	HUP 2 (1.124)	KPMR 485 (1.070)	HUP 2 (2.908)	HFP 94-12 (1.276)	DDR 52 (2.110)
PP 14 (3.143)	Safed Batri Gudda (1.128)	PP 86 (1.411)	Batana Moolchand (2.555)	Batana Moolchad (2.631)	Kalasona (2.225)
HUP 2 (3.170)	Batana Moolchad (2.645)	HFP 94-12 (1.806)	RP 3 (2.161)	Kashi Samriddhi (1.576)	KPMR 302 (1.554)
KPMR 485 (3.238)	Gol Batra Tenduna (1.008)	Gol Batra Tenduna (1.203)	Kalasona (2.225)	Rachna (1.441)	KPF 151 (2.398)
PP 86 (1.346)	IPF 99-25 (2.600)	IPF 99-25 (1.381)	VL 1 (1.890)	Kalasona (2.225)	KPMR 503 (1.539)
HFP 94-12 (4.268)	VL 3 (1.036)	Tall White (Hybrid) (1.179)	DDR 39 (2.297)	KPMR 327 (1.680)	IPF 99-25 (1.154)
KPMR 402 (1.120)	Kalamatar (4.582)	Tall Green (Hybrid) (2.560)	IPFD 12-2(1.123)	IPFD 11-5 (1.027)	
Safed Batri Gudda (1.769)	KPMR 502 (1.735)	Shikha (2.161)	KPMR 327(1.407)	Aman (1.686)	
Batana Moolchad (1.923)	HFP 94-13 (1.706)	Rachna (1.556)	IPFD 11-5 (1.582)	DDR 94-14 (1.491)	
Gol Batra Tenduna (3.271)	Kashi Samriddhi (1.506)	DDR 52(1.510)		HUVP 12(2.242)	
IPF 99-25 (3.951)	Tall White (Hybrid) (3.177)	RP 3(1.051)			
JP 885(1.841)	Tall Green(Hybrid) (3.048)	KPMR 486(1.065)			
		Kalasona (2.225)			

The genotype IPFD 99-25 showed their presence in PC1, PC2, PC3 and PC7. Genotype Kalasona showed their presence in PC3, PC4, PC5, and PC7. Genotype Batana Moolchand showed their presence in PC1, PC2, PC4 and PC5. Genotype Gol Batra Tenduna showed their presence in PC1, PC2 and PC3 while, other genotypes share their presence in two or three principal components. Their presence in more than one PC and these genotypes might be considered as donor for the transfer of concern traits in the genotypes deficient for these traits and also be utilized for the development of new improved pea dominated with higher yield attributing traits.

## CONCLUSIONS

Genotypes possess high PC scores in the pooled environments will have great potential for the selection of desired genotypes dominated with particular traits. The finding revealed that the genotypes viz. HFP 94-12, Kalamatar, IPFD 99-25, KPMR 485, Tall Green (Hybrid), Tall White (Hybrid), HUP 2, Batana Moolchand and Gol Batra Tenduna reported highest positive PC values and also IPFD 99-25, Kalasona, Batana Moolchand and Gol Batra Tenduna genotypes showed their presence in two or more than two principal components. These genotypes with high PC values are crucial for transferring traits to recipients, and those genotypes present in multiple principal components will be utilized as breeding lines for hybridization programs to identify transgressive segregation in the population. The genotypes found to be more promising as per the standard checks will be utilized in breeding programme to transfer the desired traits after hybridization. The lines showed good performance will be tested under AICRP-MULLaRP for the release as a variety.

## FUTURE SCOPE

PCA expedites the improvement of crops by identifying and prioritizing essential components and their impact on variability. This facilitates the selection of genotypes, i.e., HFP 94-12, Kalamatar, IPFD 99-25, KPMR 485, Tall Green (Hybrid) and Tall White (Hybrid), that exhibit a significant contribution to yield, enabling their use as potential parents in forthcoming breeding programmes.

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**Conflict of Interest.** None.

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