



Integrating Multivariate and Econometric Approaches to Assess Yield-contributing Traits in Field Pea Production

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10.18805/LR-5688

ABSTRACT

Background: It is essential to identify the important traits that affect the seed yield and maximize the productivity and guide the breeding programs. Research has shown variations in the factors that determine yield, but the issue of prioritizing traits for breeding in pea cultivation is still unresolved.

Methods: In this study, the relationship between the key morphological and yield-related traits of peas was analysed using multiple linear regression and principal component analysis (PCA). The 94 varieties of peas were evaluated on the basis of seed yield, number of legumes, number of seeds per pod, pod length, plant height and number of branches. The statistical models were reliably validated through diagnostic plots and sampling adequacy measures.

Result: Positive seed yield indicators found significant were pod length, number of pods per plant and number of seeds per pod; whereas negligible effect was found for plant height and number of branches. PCA confirmed the multivariate structure of yield and highlighted breeding traits as its main drivers. These findings provide solid and useful information for improving pea varieties and provide guidance to breeders to focus on optimizing pod and seed traits to increase yields under similar growing conditions.

Key words: Agronomical traits, Econometrics, Multivariate, PCA, Pea, Yield.

INTRODUCTION

India's economy is based on agriculture, which contributes significantly to the nation's GDP (Bondyalu, 2015). About 17.66% of India's GDP comes from the agriculture sector (IBEF, 2025). Among the many crops, pulses are crucial for maintaining food security, boosting agricultural output and making money from exports. The pea (*Pisum sativum*) is one of the main pulse crops farmed in India and contributes significantly to the nation's agricultural landscape (Gurusamy *et al.*, 2022). In India, it is specifically grown during the *Rabi* season, covering over 0.64 million hectares and produces roughly 0.88 million tonnes annually (Honglei *et al.*, 2025). The major states of India where peas are grown Uttar Pradesh, Madhya Pradesh, Bihar, Assam and Odisha. Approximately 1.4 tonnes per acre pea productivity have increased over time (FAOSTAT, 2023). Peas play an important role in foreign exchange and domestic consumption. India foreign exchange reserve increase by exporting large quantity of peas to other countries (Divya *et al.*, 2024). India exported more than 1.52 million kg of peas and earn about Rs 121.36 million rupees in the financial year 2023-2024. Maximum exported nations are Bangladesh, Bhutan, Nepal, France and the United Arab Emirates (Ahlawat *et al.*, 2016). A significant global concern is ensuring food security, particularly in India, where a sizable portion of the population is malnourished. Pea is a rich source of micronutrient which reduce micronutrient deficiencies and improve food security (Sahoo *et al.*, 2025). Additionally, it is reported to be able to fix nitrogen, which increases soil fertility and reduces the need for synthetic fertilizers. This makes peas a

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How to cite this article: Jawa, S.K., Gohain, N., Yadav, B., Joliya, P., Laxmi, S., Tomer, G., Khwairakpam, R. and Kumar, A. (2026). Integrating Multivariate and Econometric Approaches to Assess Yield-contributing Traits in Field Pea Production. *Legume Research*. 49(8): 1365-1373. doi: 10.18805/LR-5688.

Submitted: 11-06-2026 **Accepted:** 10-07-2026 **Online:** 03-08-2026

sustainable crop that can contribute to environmentally friendly agricultural practices (Bawa and Seidler, 2023). It is necessary to focus on research and development to further advance the cultivation and utilization of pea

(Lake *et al.*, 2021 and Amarakoon *et al.*, 2012). For example, studies on improving phosphorus use efficiency (PUE) in pea crop can increase its productivity and nutritional value (Wu *et al.*, 2023). Additionally, breeding strategies aimed at increasing the bioavailability of nutrients in pea cultivation may be helpful in overcoming micronutrient deficiencies in plants (Semaskiene *et al.*, 2022). Research efforts focused on improving its productivity, nutritional value and sustainability can be helpful in ensuring safe and nutritious food supply for the growing population (Sharma *et al.*, 2023).

MATERIALS AND METHODS

The present study was conducted using augmented block design involving 94 diverse germplasm samples of pea (*Pisum sativum*), (Appendix 1: List of genotypes); obtained from the Department of Genetics and Plant Breeding of NDUAT, Kumarganj, Faizabad and Crop Improvement Division of IIPR, Kanpur. The objective of this experiment was to identify key components contributing to optimal crop production and inform selection strategies. The augmented block design was chosen due to its suitability for evaluating large numbers of genotypes with limited seed availability and resources. This design allows for evaluation of unreplicated test entries along with standard probes repeated within blocks, thereby improving experimental efficiency while controlling for environmental heterogeneity (Federer, 1956). Each test genotype and check was independently randomly allocated to plots within the respective blocks. All germplasm, including checks, was randomly allocated to each block. Observations were recorded on five competing plants per plot for most traits, except days to 50% flowering and days to maturity, which were measured on a plot basis. The recorded traits included primary branches per plant, plant height (cm), days to maturity, number of seeds per pod, pod length (cm), number of pods per plant, days to 50% flowering, 100-seed weight (grams), biological yield per plant (grams), harvest index (%) and seed yield per plant (grams). To reduce dimensionality and extract meaningful trait patterns, Principal Component Analysis (PCA) was used. PCA transforms a set of correlated variables $X_1, X_2, \dots, X_p$ into a smaller number of uncorrelated components, $T_{K1}, T_{K2}, \dots, T_{Kp}$ which are defined as linear combinations:

$$T_{K1} = a_{11}X_1 + a_{12}X_2 + \dots + a_{1p}X_p$$

Where,

a_{ij} = Coefficients (loadings) chosen such that the first principal component.

T_{K1} = The maximum variance in the data.

Subsequent components are orthogonal and show progressively less variance (Jolliffe, 1986). This method is helpful in reducing the number of variables by highlighting the major characteristics that influence variability. Prior to PCA, assumptions were verified through the Kaiser-Meyer-Olkin (KMO) measure, which assesses sampling adequacy, with values close to 1 indicating that the dataset

is suitable for PCA and Bartlett's test of sphericity to test the hypothesis that the correlation matrix is an identity matrix. A significance test ($p < 0.05$) confirms the correlations between variables sufficient for PCA. Statistical calculations including KMO, Bartlett test and PCA were performed using JASP software. The combination of robust experimental design and rigorous multivariate analysis provided a solid framework for identifying important agronomic traits affecting field pea productivity.

RESULTS AND DISCUSSION

Multiple linear regression (Model fitness and prediction viability)

The full regression model (M_1) exhibited a high R^2 value of 0.648, indicating that approximately 65% of the variability in seed yield could be explained by the combination of selected traits in Table 1. This shows a strong predictive capacity of the model, especially in the context of biological and agricultural research where multiple factors interact. The Durbin-Watson statistic of 1.895 suggests that residuals are not autocorrelated, confirming the independence of errors: an essential assumption for reliable regression modelling. In contrast, the null model (M_0), which included no predictors, had an R^2 of 0.000, clearly demonstrating the improvement brought by the inclusion of agronomic variables. This model provides a strong foundation for predicting seed yield based on key morphological traits, essential for yield forecasting and varietal improvement.

Model significance

Table 2 of ANOVA ($F = 32.441$, $p < .001$) confirms that the model is statistically significant. This means that the set of predictor variables collectively has a strong effect on seed yield and the observed result is unlikely to be due to chance. This is a crucial validation step showing that the model is not only fitting well but is also meaningful in terms of its statistical inference.

Contribution of individual predictors

From the regression coefficients in Table 3, it was found that the Number of pods per plant emerged as the most influential predictor ($\beta = 0.698$, $p < 0.001$). This suggests that increasing the number of pods has a substantial positive impact on seed yield. This is intuitive and aligns with earlier agronomic studies, which identify pod number as a direct determinant of reproductive success in legumes. Number of seeds per pod also had a strong, statistically significant influence ($\beta = 0.314$, $p < .001$), reinforcing the role of reproductive efficiency.

Similarly, a significant but moderate contribution was shown by pod length, which indicated that longer pods with more seeds probably ($\beta = 0.176$, $p = 0.025$). A negligible and non-significant effects of plant height and number of primary branches was found ($p = 0.459$ and 0.978 , respectively). The findings states that these traits do not influence seed yield directly (Sree *et al.*, 2025), in this

Appendix 1: List of genotypes.

Genotype code	Variety	Genotype code	Variety
G1	IPF 13-13	G49	VL 61
G2	EC 386742	G50	NDP 14-11
G3	HFP 554	G51	IPF 13-14
G4	PANT P-217	G52	HUP 2
G5	PANT P 222	G53	KPMR 502
G6	PANT P 247	G54	KPF 1024
G7	IPLK 85	G55	LFP 431
G8	IPLK 117	G56	KPF 1023
G9	PANT P 200	G57	KPMR 931
G10	SKUA P-8	G58	HUDP 11
G11	EC 507770	G59	EC 414483
G12	PANT P 266	G60	FP 34
G13	PRAKASH	G61	IDM 83
G14	RFPG 81	G62	PANT P 244
G15	IPLK 109	G63	RFG 79
G16	HUDP 15	G64	NDP 12-102
G17	RACHNA	G65	IPFD 1-10
G18	HFP 4	G66	KPMR 902
G19	HFP 8909	G67	KPF 1024
G20	VL 58	G68	IPF 12-17
G21	IPF 11-13	G69	HFP 529
G22	KPMR 936	G70	EC 548810
G23	NDP 11-101	G71	JPP 3
G24	KPMR 928	G72	IPF 2014-16
G25	EC 281864	G73	HFP 1010
G26	IPLK 112	G74	EC 392177
G27	IP 11-93	G75	EC 588004
G28	EC 384275	G76	VL 55
G29	PANT P 223	G77	ADARSH
G30	RFP 61	G78	RFPG 79
G31	PANT P 195	G79	KPF 1023
G32	PANT P-101	G80	KPMR 916
G33	FP 868	G81	VL 37
G34	P 1089	G82	IPFD 13-4
G35	PANT P-138	G83	HUDP-17
G36	KPF 1036	G84	PLK 108
G37	IPF 11-15	G85	Pant P-137
G38	IPFD 2014-2	G86	KPMR 970
G39	VL 42	G87	KPMR 853
G40	VL 82	G88	EC 5117
G41	DMR 63	G89	IPFD 12-2
G42	HUP 2	G90	RFP 2009-2-1
G43	KPMR 4	G91	KPF 12-04
G45	IPF 2014-13	G92	KFP 2009-2
G46	PANT P 269	G93	FP 2009-4
G47	VL 56	G94	VL 202
G48	AMAN		

Table 1: Model summary for linear regression.

Model	R	R ²	Adjusted R ²	RMSE	Autocorrelation (p)	Durbin-watson
M ₀ (Intercept only)	0.000	0.000	0.000	0.861	0.167	1.658
M ₁ (Full model)	0.805	0.648	0.628	0.525	0.044	1.895

context of genotype environment and can serve more in a structural role (Marzhan *et al.*, 2022). To improve field pea productivity in breeding programs with targeted trait selection, the distinction between yield contributing and non-contributing traits is important (Tiwari, 2020). Further studies should emphasize towards pod-related traits rather than vegetative growth traits.

Descriptive statistics

Basic statistics is required essentially in regression modelling to get foundational insights in the central tendency and variability of agronomical traits in field pea sample population (n=94).

Seed yield per plant

Moderate variability among genotypes was found with average seed yield per plant of 4.93 gms, with standard deviation of 0.86 gms. A precise population mean and adequate sample size was suggested by a small standard error of 0.089 gm. Therefore, it seems a potential in selection of high yielding plants through breeding.

Plant height

A variation in vertical growth habit was suggested with average plant height of 87.33 cm and 17.6 cm of standard deviation. Although, plant height only can relate to biomass as shown in results (Table 3), indicating that taller plants necessarily do not have effect on seed yield.

Number of primary branches per plant

A mean of 2.08 and low variability; 0.475 of standard deviation shows uniformity in this trait under existing environmental condition. It reveals that this trait is less crucial for yield improvement due to its low variability.

Pods per plant

A good diversified range of reproductive output was found with mean of 7.69 per plant and standard deviation of 1.76 in number of pods per plant. This provides a wide range to

breeders with scope for selection and improvement of high pod bearing varieties, suggesting strongest correlation with seed yield in the regression model.

Number of seeds per pod

The mean seeds per pod was 3.54 and SD = 0.518 suggests moderate variability. Since this trait reflect a positive, strong and valuable impact on seed yield (Table 3), increasing number of seed per pod could be a direct strategy to increase yield.

Pod length

The averaged length of pod is 3.70 cm, with 1.01cm standard deviation, showing a significant degree of variability. This characteristic may be an indirect selection criterion, potentially affecting the quantity or size of seeds housed within, given its notable yet moderate impact on production. Hence, the descriptive statistics indicate that the characteristics like pods per plant, seeds per pod and pod length do not only exhibit enough variation to enable selection, but also supports the positive predictive power of this characteristic in the regression analysis. Traits like branching and plant height are more durable but influence of yield is very less. As a result, Table 4 attests to the dataset's significant diversity in yield-contributing characteristics, which is necessary for significant regression and PCA analysis. Additionally, plant breeders aiming to optimize reproductive traits might use these statistics as baseline benchmarks.

Diagnostic plots

Residual diagnostics

Residuals versus Predicted diagnostics shows no pattern which supports homoscedasticity [Fig 1A (a-d)]. Standard which we found the Standardized Residuals to be approximately normal and also our Q-Q Plot which reported that the data points fell along a diagonal line which in turn confirmed normality. Also, we saw Random Scatter in Residuals versus Covariate plots which in turn confirmed

Table 2: ANOVA for model M_1 .

Source	SS	df	Mean square	F	p-value
Regression	44.685	5	8.937	32.441	< 0.001
Residual	24.243	88	0.275	-	-
Total	68.928	93	-	-	-

Table 3: Regression coefficients in model M_1 .

Variables	Coeff. (B)	S.E.	β	t-value	p-value	Confidence interval (95 per cent)
Intercept	-0.320	0.548	-	-0.585	0.560	-1.409 to 0.768
Plant height	0.002	0.003	0.051	0.744	0.459	-0.004 to 0.009
Primary branches/plant	0.005	0.195	0.003	0.027	0.978	-0.382 to 0.393
Pods/plant	0.341	0.052	0.698	6.533	< 0.001	0.237 to 0.445
Seeds/pod	0.522	0.117	0.314	4.468	< 0.001	0.290 to 0.754
Pod length	0.150	0.066	0.176	2.277	0.025	0.019 to 0.282

the linear relationship between predictors and seed yield as well as the assumption of homoscedasticity. In terms of the overall Assessment of Model Assumptions; that is residual distribution and normality we had support in our diagnostic plots which in turn validated the model assumptions (Ribeiro *et al.*, 2025). We noted that the standardized residual histogram was normal. Also, in the Q-Q plot we had residual points which fell along the diagonal which in turn confirmed normality. That we saw no out of the ordinary patterns in Residuals versus Predictors plot which in turn supported the assumption of homoscedasticity. These results in turn gave us confidence in the regression estimates and their large-scale use. Similarly, in Residuals versus Individual Covariate diagnostics [Fig 1B (a-e)], the Scatter plots of residuals against each covariate showed random dispersion with no systematic trends, confirming the linearity and independence of predictors. This is particularly important in agricultural datasets where multicollinearity and interaction effects can distort results.

Individual predictor analysis (Partial and marginal effect plots)

The strong, positive linear relationships with seed yield demonstrated by pod per plant and seeds per pod, even after adjusting for other variables. These are the strong indicators of potential yield and should be prioritized in breeding. Pod length showed a moderate relationship, indicating an auxiliary role. Also, plant height and branches per plant had almost flat trends, reinforcing their lack of predictive utility for yield.

Principal component analysis (PCA)

The results from PCA are in Table 5, which shows that; overall, MSA is above 0.5, acceptable for PCA. However, harvest index and biological yield have low values (<0.5). Pods per plant (0.718) and plant height (0.804) show strong sampling adequacy. Biological yield (0.377) and Harvest index (0.330) have low MSA values (<0.5), meaning these variables may not fit well into the component structure.

Table 6 results show that, Bartlett's test is significant, supporting factorability of the correlation matrix. The observations in Bartlett's test ($\chi^2 = 859.547$, $p < 0.001$) confirms the dataset is suitable for PCA and the model $\chi^2 = 347.024$, $p < 0.001$, supports factor model validity.

Table 7 show that the Seed yield loads moderately on two components (RC1 and RC2), showing it is influenced

by both yield structure and physiological maturity traits. PCA was used to explore the multivariate structure of yield-related traits and reduce dimensionality.

The Kaiser-Meyer-Olkin (KMO) measure of 0.513 and significant Bartlett's test ($p < 0.001$) confirmed that the data were suitable for PCA. However, the biological yield (0.377) and harvest index (0.330) exhibited inadequate sample adequacy and should be taken cautiously.

Component loadings and trait clustering

Promax-rotated loadings in Table 8, revealed the following: Vegetative growth dimension showed by RC1 by loading strongly on biological yield and plant height. The traits like pods per plant, seed yield and harvest index, aligning with yield structure is showed by RC2. In RC3 and RC4 includes reproductive precision traits like seeds per pod and pod length. Interestingly in both RC1 and RC2 we see seed yield which tells us of a complex relationship between growth and reproductive elements. This puts forth that it is a function of both size of the biomass and also separate yield related traits.

Many different factors play into the determination of seed yield which in turn indicates that it isn't a product of a single group of variables. What we see in the diverse grouping of traits like biological yield, plant height and pods per plant is a reflection of the very many aspects that go into the formation of yield (Patel *et al.*, 2023).

The first three components explain over 56% of total variance, supporting dimensional reduction and helping focus on dominant traits. In the figure, *i.e.*, the Scree Plot shows a sharp drop after 3 components. It justifies retaining 3-4 principal components (above Kaiser's rule of eigen value >1), which confirms retention of 3 components as ideal. In the figure, *i.e.*, the path diagram shows the causal paths between the latent variable (PC) and the observed variable, confirming the multi-trait effect on seed yield, showing how yield is influenced by multiple underlying factors rather than a single dominant trait.

Parallel analysis

Components to retain (Parallel analysis and scree plot)

The scree plot showed a clear bend after the third component and parallel analysis confirmed the persistence of three components based on actual versus simulated eigenvalues (Fig 2). These components together explained 56.9% of the total variance, which suggests that a significant

Table 4: Descriptive statistics.

Variable (N = 94)	Mean	SD	SE
Seed yield/plant (g)	4.929	0.861	0.089
Plant height (cm)	87.330	17.600	1.815
Primary branches/plant	2.077	0.475	0.049
Pods/plant	7.685	1.762	0.182
Seeds/pod	3.537	0.518	0.053
Pod length (cm)	3.699	1.007	0.104

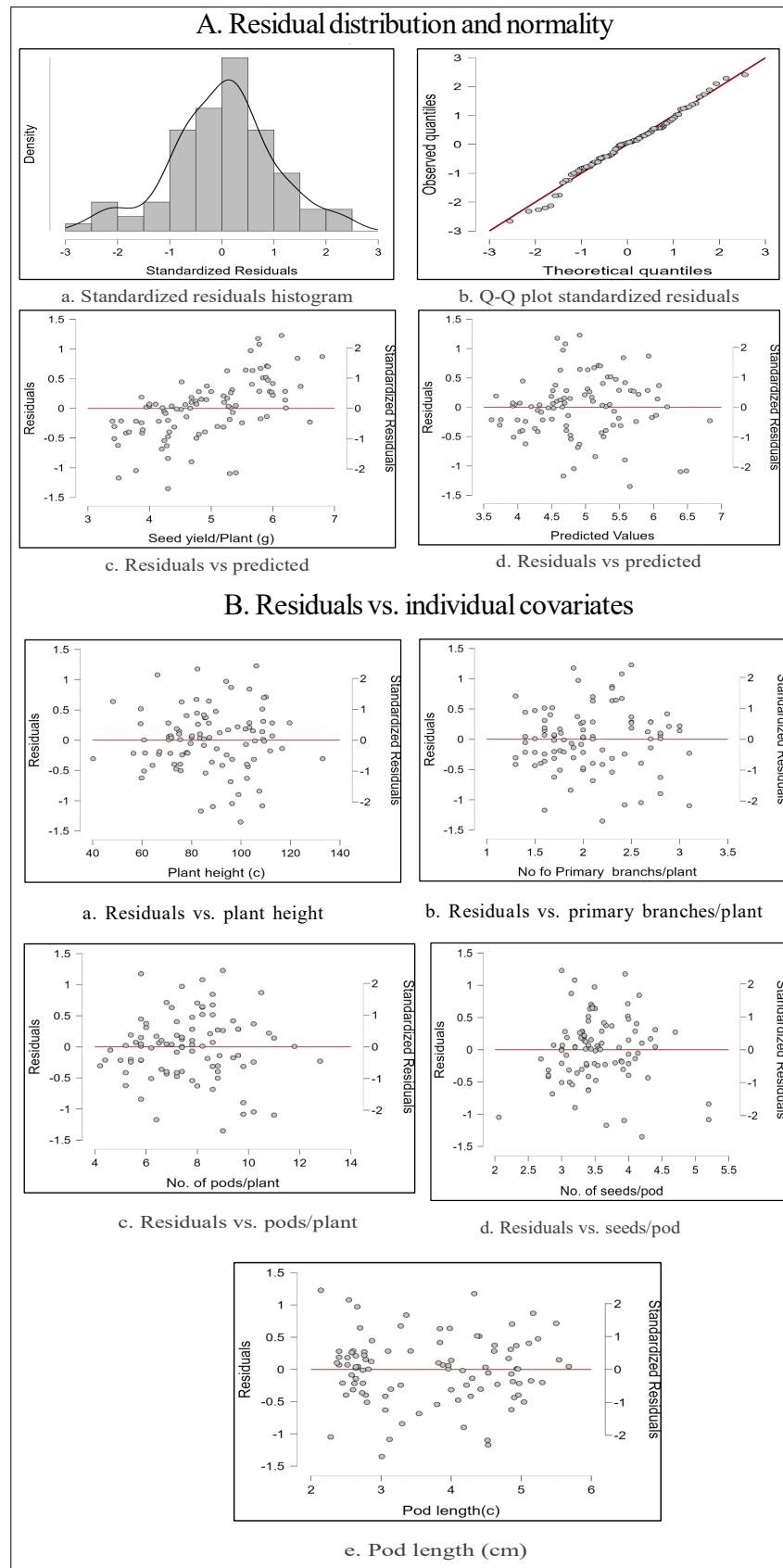


Fig 1: (A and B) Diagnostic plots.

Table 5: Sampling adequacy (MSA).

Trait	MSA value
Overall	0.513
Plant height	0.804
Pods per plant	0.718
Seeds per pod	0.645
Pod length	0.618
Seed yield	0.508
Biological yield	0.377
Harvest index	0.330

Table 6: Bartlett's test of sphericity and chi-squared test of model.

χ^2	df	p-value
Sphericity		
859.547	55	< .001
Chi-squared test of model		
Model χ^2	df	p-value
347.024	17	<.001

portion of trait variability can be explained through the three major axes (Table 9). This dimensionality reduction simplifies future modelling and trait-targeting efforts by highlighting the core structures underlying traits (Angel *et al.*, 2021).

Path diagram

The path diagram depicted (Fig 3) how the latent components (PCs) influence the observed traits. This diagram presents that many traits which are integrated determine seed yield which in turn presents the multi-dimensional aspect of plant productivity (Ranjani and Jayamani, 2024; Jain *et al.*, 2023). In the development of selection indices in crop improvement programs which require at the same time the improvement of related traits this is a useful tool (Kumar *et al.*, 2024).

In our study we identified number of pods per plant, number of seeds per pod and pod length as the main determinants of seed yield in pea crop. The model we present is very statistical in nature and we did test its

Table 7: Component loadings (Promax rotation).

Variable	RC1	RC2	RC3	RC4	Uniqueness
Biological yield	0.934				0.180
Plant height	0.667				0.573
Seed yield	0.578	0.535			0.074
Harvest index		1.009			0.124
Pods/plant		0.540			0.127
Seeds/pod			0.820		0.342
Pod length			0.761		0.385

Table 8: Component characteristics.

Component	Eigen value	Proportion variance	Cumulative (%)
RC1	2.238	20.3%	20.3%
RC2	2.079	18.9%	39.2%
RC3	1.944	17.7%	56.9%
RC4	1.944	17.7%	74.6%

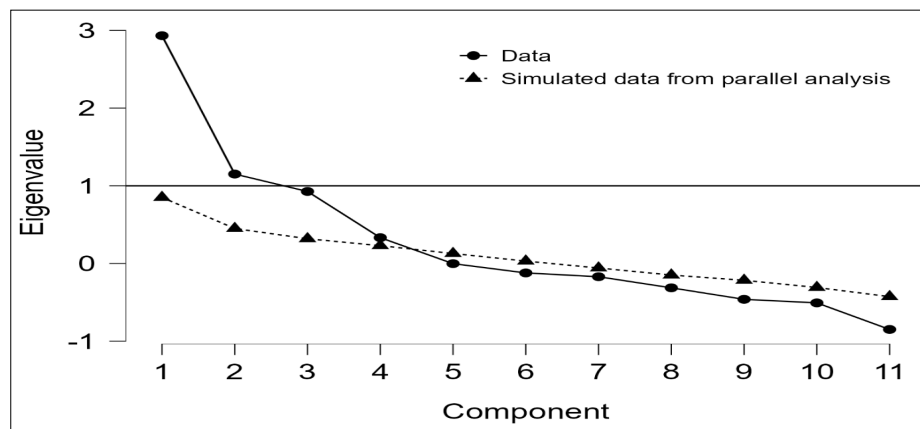
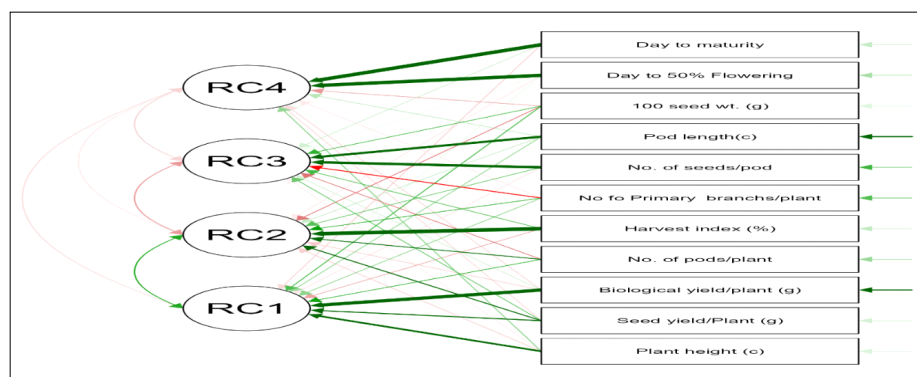
**Fig 2:** Scree plot.

Table 9: Parallel analysis for component retention.

Component	Real eigenvalue	Simulated mean	Retain?
1	3.353	1.570	Yes
2	1.974	1.391	Yes
3	1.873	1.260	Yes
4	1.005	1.170	No

**Fig 3:** Path diagram of traits studied.

assumptions in great detail. PCA, we used to bring out some meaningful trait groups which in turn simplified the complex trait relationships.

CONCLUSION

This study emphasizes the aspects of the pea plant, responsible for seed yield which is mainly a function of reproductive traits number of pods per plant, number of seeds within each pod and pod length. We noted that among the vegetative traits like plant height and primary branching do not play a large role in improving yield. We report from our studies and regression models, which we supported with principal component analysis, that the best way for breeding programs is to put focus on improving key reproductive traits. Also, we note from our multivariate analysis that, which is the very complex nature of yield determination which in turn stresses the point that for crop improvement which you have to go in and target specific traits. These results will find breeders very useful in their work which in turn will help them to increase genetic gain and develop high yielding pea varieties. Therefore, the insights gained not only elucidate the genetic determinants of yield, but also provide statistically sound guidance for strategies in pea breeding programs.

ACKNOWLEDGEMENT

This study is supported by the Department of GPB and AE, ANDUAT, Kumarganj, Ayodhya, Uttar Pradesh.

Disclaimers

The authors accept responsibility for the accuracy and quality of the content in the article.

Conflict of interest

None of the authors has any conflict of interest.

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