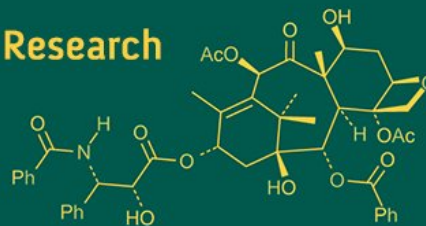


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Multi-variate analysis in grass pea (*Lathyrus sativus* L.)

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Abstract

Grass pea (*Lathyrus sativus* L.) is an important pulse crop known for its drought tolerance, adaptability to low-input environments, and nutritional value. The present study was undertaken to assess genetic variability and identify important traits contributing to divergence among 21 grass pea genotypes. The experiment was conducted during Rabi 2016–17 and 2017–18 at the Agricultural Farm of Palli Siksha Bhavana, Visva-Bharati, Sriniketan, using a randomized block design with three replications. Data were recorded for quantitative traits related to flowering, pod development, plant architecture, root length and yield. Principal component analysis (PCA) was employed to determine the major sources of variation. Six principal components with eigenvalues greater than one accounted for 78.52% of the total phenotypic variation. PC1 contributed 21.36% of the variation and was predominantly associated with flowering and reproductive phenology, whereas PC2 contributed 16.96% and was mainly influenced by pod length, yield and other yield-related traits. The PCA biplot indicated considerable divergence among genotypes, with NIRMAL, WBK-15-1 and WBK-5 showing distinct trait associations. These genotypes, along with MAHATEWRA and PRATEEK, may serve as useful parental materials for future breeding programmes aimed at improving yield and adaptation.

Keywords: Grass pea, *Lathyrus sativus* L., Genetic variability, Genotypic divergence, Principal component analysis, Phenotypic variation, Yield-related traits, Genotype characterization, Plant breeding, Drought tolerance

Introduction

Lathyrus sativus, commonly known as grass pea, belongs to the family Fabaceae and possesses a chromosome number of $2n = 14$. The crop is highly drought tolerant and is well suited for rainfed and low-input farming systems (Palmer et al., 1989) ^[9]. It is widely cultivated in countries such as India, Bangladesh, Ethiopia, Nepal, Pakistan, and China due to its adaptability to adverse environmental conditions. Although grass pea is associated with neurolathyrism caused by the neurotoxin ODAP, breeding advancements have helped reduce ODAP content to safer levels below 0.2%, making it safer for human consumption (Abdel Moneim and Abd-Alla, 1999). The crop is nutritionally rich, providing about 351 calories per 100 g seed with high carbohydrate (58%) and protein content (28–32%) along with essential minerals and vitamins (Aykroyd and Doughty, 1964) ^[2]. It also contains calcium, iron, phosphorus, vitamin B complex, tryptophan, and nicotinic acid, contributing to its nutritional importance (Sharma and Padmanaban, 1969). Due to its resilience and nutritional value, grass pea is considered an important crop for food security in stress-prone regions. Genetic relationships estimated through morphological traits offer a quick and economical approach for evaluating diversity among genotypes, allowing researchers to screen a large number of lines efficiently. Knowledge of genetic relationships among different lines is highly valuable for planning hybridization programs, classifying genotypes into heterotic groups, and accurately identifying varieties for plant varietal protection purposes (Hallauer, Carena, et al., 2010) ^[4]. Multivariate analysis, particularly principal component analysis (PCA) and cluster analysis, has been widely utilized for evaluating genotypes based on multiple traits (Marola, KBNT, et al., 1979) ^[7]. PCA is mainly used to identify relationships among traits and to group genotypes according to their similarities, whereas cluster analysis focuses on categorizing previously ungrouped genotypes (Kaufman and Rousseeuw, 2009) ^[5]. Principal component analysis helps simplify complex datasets by reducing them into fewer dimensions while retaining most of the original variation. It generates a smaller set of new variables,

known as principal components, which explain the majority of variability present in the observed data. In PCA, eigenvalues are first calculated to determine the extent of variation represented by each principal component axis. The first principal component accounts for the highest proportion of total variability in the dataset, while the second principal component explains the maximum remaining variation independent of the first component, and the process continues similarly for subsequent components (Jolliffe, 1986) ^[5]. Multivariate statistical methods are widely employed to summarize and explain the existing variation among genotypes. Among these methods, Principal Component Analysis (PCA) is an important technique used to identify the plant traits responsible for distinguishing different genotypes (Chakravorty, Ghosh, et al., 2013) ^[3]. PCA also aids in grouping populations into distinct categories based on similarities among one or more traits, thereby assisting breeders in selecting suitable parents for hybridization programs (Omokhame and Alika, 1999). The principal components derived from PCA can further serve as criterion variables for subsequent analyses (Ray, Dutta, et al., 2014) ^[10]. Therefore, the present study aims to identify superior genotypes and key contributing traits through PCA and to classify the genotypes into different clusters using hierarchical grouping methods.

Materials and Methods

The present experiment was conducted during Rabi 2016-17 and Rabi 2017-18 at the Agricultural Farm of Palli Siksha Bhavana (Institute of Agriculture), Visva-Bharati, Sriniketan. The experiment was conducted with 21 genotypes using randomized block design with three replications. The list of genotypes were presented in the table 1. The observations were recorded in all the two seasons on the following different quantitative characters in the field. Data on various characters viz., days to flower initiation, days to 100% flowering, days to 50% pod maturity, plant height, number of primary branches, number of secondary branches, number of pods plant⁻¹, pod length, number of seeds pod⁻¹, days to harvesting, root length and yield were recorded on Five randomly selected competitive plants from the plot. Cluster analysis done based on the hierarchical grouping and clustering of genotypes in to similarity groups using average linkage between groups method (Peeters and Martinelli, 1989) by SPSS (IBM Corp. Released 2013. IBM SPSS Statistics for Windows, Version 22.0. Armonk, NY: IBM Corp.). Principal component analysis was done as suggested (Nadarajan, 2005) using OPSTAT (Sheoran, 1998).

Table 1: List of genotypes used in this experiment

S.no	Genotype	S.no	Genotype	S.no	Genotype
1	Velva local	8	Mahatewra	15	Biol-212
2	Prateek	9	Nowda local	16	WBK-21-2-2
3	Nirmal	10	WBK-9-3	17	B-222
4	Waise	11	B-111	18	Shiruha local
5	WBK-13-1	12	WBK-5	19	WBK-20-5
6	WBK-11-3-1	13	PUSA-24	20	WBK-14-7
7	WBK-11-3	14	WBK-2	21	WBK-15-1

Results & Discussion

PCA is an effective multivariate statistical approach that reduces the dimensionality of complex datasets while retaining maximum variability, thereby facilitating the identification of key traits contributing to genetic divergence (Jolliffe, 1986; Chakravorty et al., 2013) ^[3, 5].

Table 2: Eigen values, percentage of total variation and cumulative percentage for corresponding traits

Principal Component	Eigenvalue	Variance (%)	Cumulative Variance (%)
PC1	3.26	20.36	20.36
PC2	2.90	18.15	38.51
PC3	2.20	13.75	52.26
PC4	1.52	9.48	61.74
PC5	1.21	7.56	69.31
PC6	1.14	7.11	76.41
PC7	0.98	6.11	82.52
PC8	0.87	5.43	87.95
PC9	0.60	3.74	91.69
PC10	0.42	2.60	94.29
PC11	0.39	2.43	96.72
PC12	0.23	1.42	98.13
PC13	0.19	1.19	99.33
PC14	0.07	0.44	99.77
PC15	0.03	0.21	99.97
PC16	0.00	0.03	100.00

The analysis generated sixteen principal components (PCs), of which the first six components exhibited eigenvalues greater than one and collectively accounted for 78.52% of the total phenotypic variation. The first principal component (PC1) explained 21.36% of the total variation, followed by PC2 (16.96%), PC3 (11.79%), PC4 (11.37%), PC5 (9.33%), and PC6 (7.71%). The cumulative variance explained by the first two principal components was 38.31%, indicating that these components captured a substantial proportion of the total variability present among the genotypes. The scree plot revealed a gradual decline in eigenvalues, with a distinct inflection after the sixth component, suggesting that the first six PCs adequately represented the diversity within the germplasm. The trait loadings indicated that PC1 was predominantly associated with flowering and reproductive phenology traits, including days to pod initiation (-0.677), days to 50% pod initiation (-0.647), days to flower initiation (-0.606), days to 50% flowering (-0.602), days to 100% flowering (-0.598), and number of primary branches (-0.588). Thus, PC1 primarily reflected variation related to crop maturity and flowering behaviour. In contrast, PC2 was mainly influenced by pod length (0.598), yield per plant (0.522), days to 50% pod initiation (0.447), number of seeds per pod (0.396), and days to 50% pod maturity (0.348), indicating the importance of yield-contributing and pod-related traits in differentiating the genotypes.

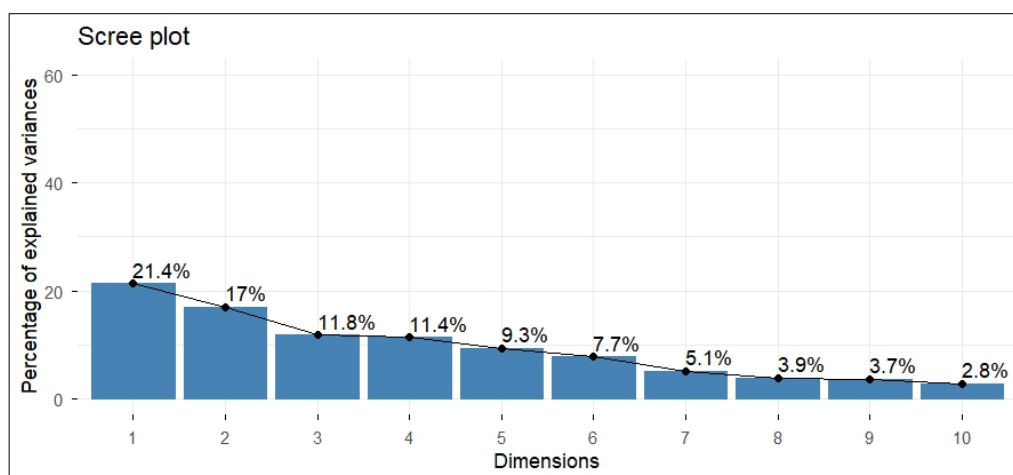


Fig 2: Scree plot of sesame genotypes between Eigen values and principal components

The PCA biplot further illustrated the distribution of genotypes and their associations with specific traits. Genotypes NIRMAL, WBK-15-1, and WBK-5 were located far from the origin, indicating greater genetic divergence and unique trait combinations. The genotype NIRMAL exhibited a strong association with pod length and days to 50% pod maturity, whereas WBK-15-1 was closely associated with yield, suggesting its potential utility as a donor parent in yield improvement programmes. Similarly, genotypes MAHATEWRA, WBK-9-3, WBK-14-7, and PRATEEK were positioned in the direction of the root length vector, indicating superior root development. On the other hand, VELVA LOCAL, SHIRUHA LOCAL, and WBK-11-3-1 were associated with flowering and pod initiation traits, reflecting their distinct phenological characteristics. Overall, the PCA effectively partitioned the genetic variability among grass pea genotypes and identified the major traits responsible for divergence. The genotypes NIRMAL, WBK-15-1, WBK-5, MAHATEWRA, and PRATEEK were found to be highly divergent and may serve as valuable parental materials in breeding programmes aimed at improving yield traits, and adaptation. Similar findings highlighting the usefulness of PCA have been reported in grain legumes by Jolliffe (1986) [5], Mohammadi and Prasanna (2003), Chakravorty et al. (2013), and Ray et al. (2014) [3, 8, 10].

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