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PRINCIPAL COMPONENT ANALYSIS OF YIELD RELATED TRAITS IN F_2 SEGREGANTS OF YARD LONG BEAN (*VIGNA UNGUICULATA* SUBSP. *SESQUIPEDALIS* L. VERDCOURT)

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ABSTRACT

Yard long bean is an important legume vegetable crop globally valued for its tender pods, high protein content, and adaptability to diverse agroclimatic zones, playing a crucial role in food and nutritional security. The present investigation aimed to assess the genetic variability and identify key yield-contributing traits among 200 F_2 segregants of yard long bean derived from the cross Kattampally Local × Vellayani Jyothika. Descriptive statistics indicated substantial variation in key traits such as yield per plant, pods per plant, and pod weight, suggesting broad genetic diversity and selection potential. Principal Component Analysis (PCA) revealed that the first three principal components accounted for 70.49% of the total variation. PC1, explaining 42.59%, was strongly associated with yield per plant, pods per plant, and harvest index, serving as the general yield component. PC2 and PC3 reflected variation in pod biomass and morphology, respectively. The study highlights the effectiveness of PCA in simplifying complex trait interactions and identifies promising segregants for yield improvement in yard long bean breeding programs.

Keywords **:** Yard long bean, F_2 population, Genetic variability, Principal Component Analysis, Yield traits.

Introduction

Yard long bean (*Vigna unguiculata* subsp. *sesquipedalis*), a vegetable cowpea variant, is valued for its long, tender pods, nutritional benefits, and adaptability to diverse agroclimatic zones (Suma *et al.,* 2021). Enhancing yield potential while maintaining resilience to biotic and abiotic stresses is central to ongoing breeding efforts. The F_2 generation, being genetically diverse due to segregation, provides an ideal population for identifying superior recombinants and enhancing genetic gain through early selection (Xu *et al.,* 2017).

Yield in yard long bean is a complex trait influenced by multiple components such as pod length, pod weight, number of pods per plant, and harvest index (Edematie *et al.,* 2021). A comprehensive assessment of these traits in early generations is essential to dissect their variability and contribution to yield (Yadesa *et al.,* 2022; Azam *et al.,* 2023).

Principal Component Analysis (PCA) is a valuable tool for breeders and physiologists to streamline genotype evaluation and pinpoint key traits for selecting superior lines (Beena *et al*., 2021). It is also widely applied to study genetic divergence among genotypes (Neelima *et al*., 2021). As reported by Gerrano *et al.* (2015), eigenvalues are useful in determining the principal components that contribute most to the overall variability.

The present study aims to evaluate F_2 segregants evaluated in the field to identify key yield-contributing traits and potential superior segregants using Principal Component Analysis (PCA) for use in future yard long bean improvement programs.

Materials and Methods

Plant Material

The experimental material comprised 200 F_2 segregants from the best-performing cross Kattampally local ×Vellayani Jyothika identified from a previous study at the Department of Genetics and Plant Breeding, College of Agriculture, Vellayani. The lines were selected based on preliminary yield performance and drought tolerance.

Experimental Site and Layout

The field trial was conducted at the Instructional Farm, College of Agriculture, Vellayani, Kerala (8.42917° N, 76.98778° E), during the post-monsoon season (September–December 2023). The soil was sandy clay loam under a tropical humid climate. A single row plot layout was adopted, with each F_2 plant spaced at 1.5 m × 0.45 m and treated as an individual observation unit. Agronomic practices were done as per the prescribed recommendations (KAU, 2016). Data on yield and related traits were recorded for all plants.

Statistical Analysis

Descriptive statistics such as mean, range, coefficient of variation were computed and Principal Component Analysis (PCA) was carried out using GRAPES (General R-based Analysis Platform Empowered by Statistics, (www.kaugrapes.com) software V:1.10 (Gopinath *et al*., 2020) to determine the contribution of each trait to overall variability and to identify trait associations for selection efficiency. Eigenvalues and loading scores were used to interpret principal components, and biplots were generated to visualize genotype and trait clustering patterns.

Results and Discussion

Descriptive Statistical Analysis of Yield and Related Traits

The evaluation of eight key yield-related traits among 200 F_2 segregants of yard long bean revealed considerable phenotypic variability, which is crucial for effective selection in a breeding program. Traits such as yield per plant (CV = 20.8%), number of pods per plant (CV = 17.2%), and vine length (CV = 17.0%) exhibited high to moderate coefficients of variation, indicating substantial genetic diversity and scope for selection. Similar results were observed in chickpea (Gond, 2022). Pod weight also showed moderate variability (CV = 9.0%), while pod length had slightly lower variability (CV = 9.8%), suggesting potential for improvement in these traits through targeted selection. similar results were reported in groundnut (Zongo *et al*., 2017). In contrast, pod width (CV = 2.8%) and crop duration (CV = 6.3%) exhibited relatively low variability, possibly due to genetic fixation or reduced environmental influence. The harvest index showed moderate consistency (CV=14.0%), indicating uniform resource partitioning among segregants. Similar results were reported in soybean (Sichilima, 2017). Notably, yield per plant displayed the widest range and highest variance, reflecting its quantitative nature and complex inheritance (Jiang *et al.,* 2017). Overall, the variation observed across traits affirms the genetic richness of the population and highlights its potential for identifying elite segregants to develop improved, high-yielding yard long bean genotypes.

Principal Component Analysis (PCA) of Yield and Related Traits

Principal Component Analysis (PCA) was carried out to determine the contribution of individual traits to the total variability among 200 F_2 segregants of yard long bean. The analysis revealed that the first few components explained a substantial portion of the total variation, allowing for effective dimensionality reduction and trait prioritization.

Principal Component Analysis (PCA) revealed that PC1, accounting for the highest variance, was positively associated with pods per plant (0.519), yield per plant (0.516), harvest index (0.502), and vine length (0.356), representing a general yield component. Genotypes with high PC1 scores are likely high-yielding with efficient assimilate partitioning. PC2 was mainly influenced by pod weight (0.708), pod width (0.260), and crop duration (0.342), reflecting pod biomass and structure. PC3, defined by a strong negative loading for pod width (–0.864) and moderate positive loadings for pod weight and crop duration, captured variation in pod morphology.PC4 was dominated by crop duration (0.816) and pod length (0.381), representing a phenological component distinguishing early and late-maturing genotypes. PC5 showed a negative association with pod length (–0.844) and a positive loading for pod width (0.356), indicating a potential morphological trade-off. PC6, driven by vine length (0.761) and pod weight (0.402), represented vegetative vigour. PC7 showed a negative loading for harvest index (–0.765) and positive loadings for yield and pod number, highlighting variation in partitioning efficiency. PC8, though explaining minimal variance, revealed a compensatory relationship between yield per plant (0.682) and pods per plant (–0.681). Overall, traits such as yield per plant, pod weight, pods per plant, and harvest index contributed most to the observed variation, making them key targets for selection in yard long bean improvement programs.

The principal component analysis revealed that the first three principal components had eigenvalues greater than one and together accounted for 70.49% of the total variation. The eigenvalues, proportion of variance, and cumulative variance associated with each principal component are summarized in Table 1. PC1 alone explained 42.59% of the variability and was primarily associated with yield-related traits. PC2 contributed 14.91% and was mainly influenced by pod weight and crop duration, while PC3 accounted for 12.98% of the variation and was related to pod morphology. These three components were considered significant and sufficient to capture the majority of trait variation among the F_2 segregants. The contribution of individual principal components to overall variation is represented in the scree plot shown in Figure 1.

The percentage contribution analysis revealed that PC1 was primarily influenced by pods per plant (26.90%), yield per plant (26.61%), and harvest index (25.22%), confirming its role as the general yield component. According to Neelima *et al*. (2021), seed yield per plant, number of pods per plant, and days to flowering were the major contributors to variability in horse gram. Walle *et al*. (2019) reported that variables with absolute loadings greater than 0.300 are important for genetic divergence, with yield per plant being the most influential trait in PC I.PC2 was dominated by pod weight (50.15%) and vine length (21.96%), representing a biomass and growth axis. PC3 was strongly defined by pod width (74.62%) and to a lesser extent by pod length (5.45%), highlighting a pod morphology axis.PC4 showed major contributions from crop duration (66.52%) and pod length (14.53%), indicating a phenological component. PC5 was mostly influenced by pod length (71.16%) and pod width (12.71%), reflecting pod size variability. PC6 was largely governed by vine length (57.96%) and pod weight (16.16%), pointing to vegetative vigour. PC7 had the highest contributions from harvest index (58.58%) and yield per plant (20.45%), indicating partitioning efficiency. Finally, PC8 was jointly influenced by pods per plant (46.38%) and yield per plant (46.50%), suggesting a yield compensation pattern. Per cent contribution of the eight traits to the first three principal components is shown in Table 2.

The biplot generated from the first two principal components (Fig. 2) displayed the distribution of 200 F_2 segregants of yard long bean across all four quadrants, reflecting the genetic diversity among them. Segregants positioned closer to each other and near the origin are considered more genetically related. Notably, F_3-2, F_3-79, F_3-106, F_3-130, and F_3-184 clustered closely, indicating a high degree of similarity. The selection of these genotypes for further breeding could be instrumental in developing drought-tolerant lines, as they share desirable traits contributing to stress resilience.

The loadings plot for eight traits based on PCA is shown in Figure 3. Traits near the origin have less influence, while those farther away contribute more to variation. Factor loadings of eight traits across principal components are represented in Table 3. According to Molosiwa *et al*. (2016), traits in the same quadrant are positively related, while those in opposite quadrants show a negative association. This helps identify key trait relationships for effective selection in breeding.

Conclusion

The present study revealed substantial genetic variability among 200 F_2 segregants of yard long bean for key yield and related traits, indicating ample scope for selection and crop improvement. Descriptive statistics showed wide variation in traits such as yield per plant, pod weight, and number of pods per plant, highlighting the genetic diversity within the population. Principal Component Analysis (PCA) effectively grouped correlated traits and reduced data dimensionality, with the first three principal components accounting for over 70% of the total variation. PC1, strongly associated with pods per plant, yield per plant, and harvest index, emerged as the major axis of yield expression, while PC2 and PC3 captured variation in pod biomass and morphology, respectively. The findings underscore the utility of multivariate analysis in identifying promising segregants and key traits for selection, thus providing valuable direction for the advancement of high-yielding yard long bean lines in future breeding programs.

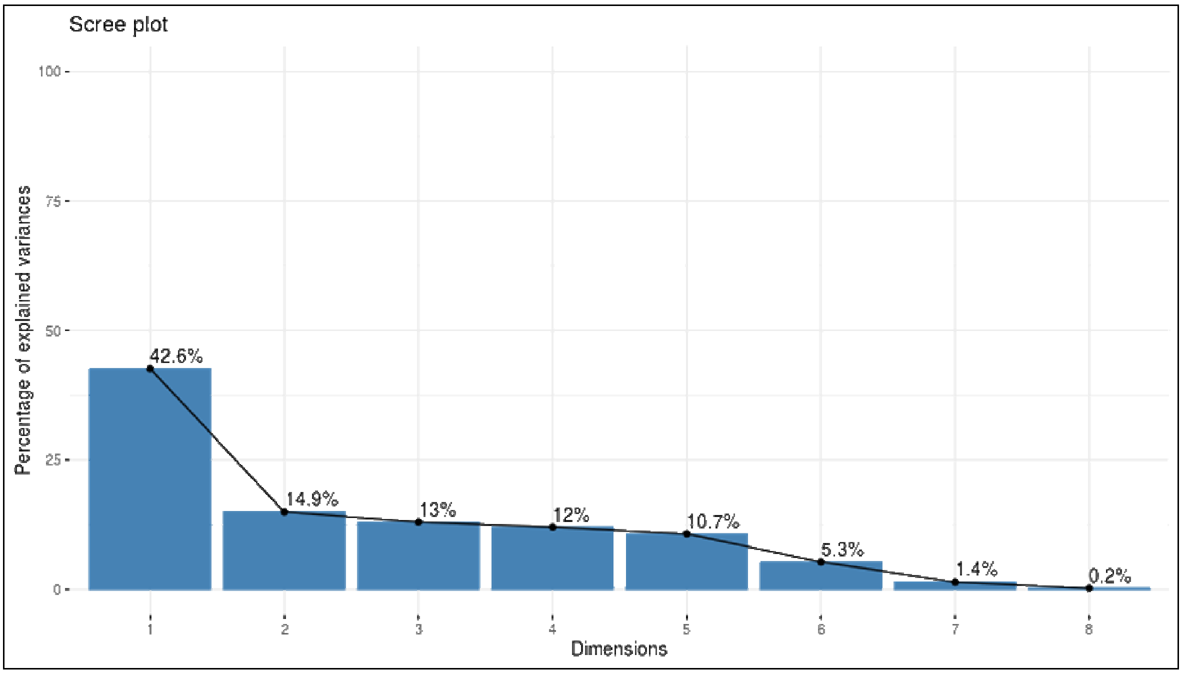

Fig. 1 : Scree plot showing the contribution of each principal component to the total variation.

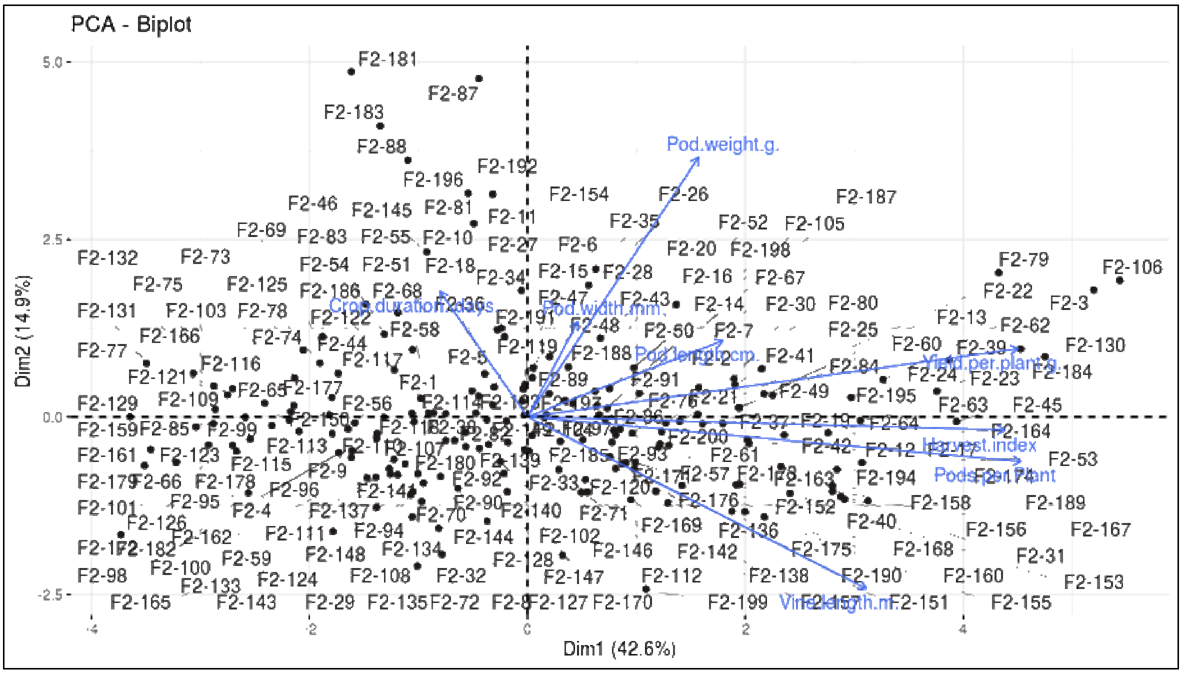

Fig. 2 : Biplot illustrating the genetic variation among 200 yard long bean segregants.

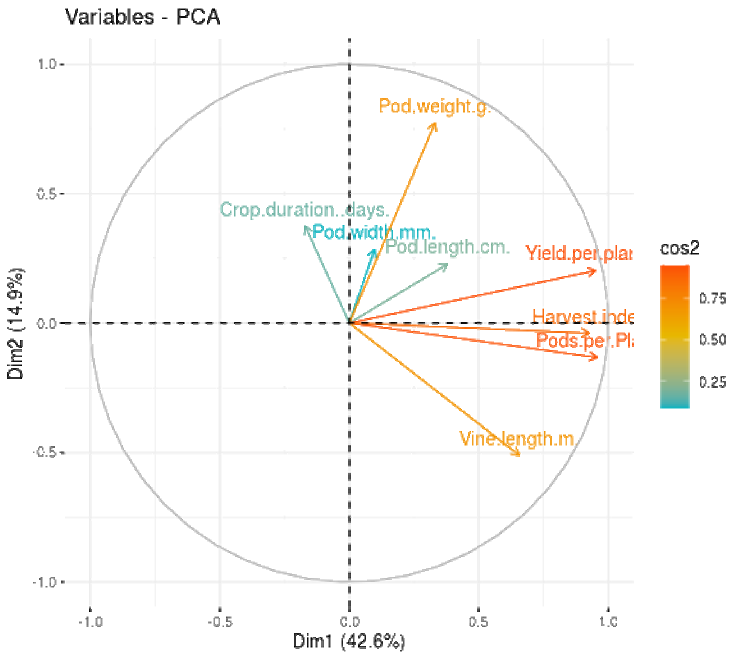

Fig. 3 : Factor loadings plot showing the contribution of different traits based on principal components.

Table 1 : Eigenvalues, percentage of variance, and cumulative variance of principal components.

Principal components	eigenvalue	percentage of variance	cumulative percentage of variance
PC1	3.407	42.591	42.591
PC2	1.193	14.914	57.505
PC3	1.039	12.985	70.49
PC4	0.959	11.992	82.482
PC5	0.854	10.676	93.158
PC6	0.421	5.263	98.421
PC7	0.11	1.374	99.795
PC8	0.016	0.205	100

Table 2 : Per cent contribution of eight traits to the first three principal components.

Trait	PC1	PC2	PC3
Pod length	4.223	4.341	5.448
Pod width	0.279	6.759	74.616
Pod weight	3.231	50.146	9.416
Pods per Plant	26.904	1.483	0
Yield per plant	26.606	3.457	0.369
Vine length	12.69	21.96	1.465
Harvest index	25.219	0.13	0.033
Crop duration days	0.847	11.724	8.654

Table 3 : Factor loadings of eight traits across principal components.

Trait	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Pod length	0.206	0.208	-0.233	0.381	-0.844	0.03	-0.035	-0.029
Pod width	0.053	0.26	-0.864	0.07	0.356	0.226	0	-0.02
Pod weight	0.18	0.708	0.307	-0.357	0.001	0.402	-0.146	-0.248
Pods per Plant	0.519	-0.122	0	0.051	0.117	-0.24	0.422	-0.681
Yield per plant	0.516	0.186	0.061	-0.101	0.063	-0.11	0.452	0.682
Vine length	0.356	-0.469	0.121	0.21	0.062	0.761	-0.092	0.056
Harvest index	0.502	-0.036	-0.018	0.017	0.142	-0.368	-0.765	0.069
Crop duration days	-0.092	0.342	0.294	0.816	0.346	-0.044	0.021	0.018

Competing interests

The authors have no relevant financial or non-financial interests to disclose.

Author contributions

BT contributed to the conception and design of the study. RN conducted the experiments, curated the information, and wrote the first draft. RN and BT have contributed to the draft manuscript revision and have critically reviewed and edited the submitted manuscript.

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