



Multivariate analysis for yield, yield attributes and physiological traits in groundnut genotypes suitable for southern zone of Andhra Pradesh

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Abstract

Groundnut yield improvement depends on the availability of genetically diverse genotypes possessing desirable yield and quality traits. Evaluating genetic variability, trait associations and multivariate diversity among genotypes helps breeders identify superior parents for developing high-yielding and quality cultivars. This study evaluated genetic variability, trait associations and selection efficiency in twenty-three groundnut genotypes. Kernel traits varied widely, with 100-kernel weight (25-38 g), sound mature kernel (SMK) weight (23-35 g) and SMK percentage (86-95%). Pod yield (3314-4970 kg ha⁻¹) and kernel yield (2156-2967 kg ha⁻¹) also showed considerable variability. Kernel yield exhibited a strong positive association and high direct effect on pod yield, indicating its usefulness as a selection criterion, although negative correlations with quality traits suggested a trade-off between yield and quality traits. Principal component analysis showed that the first three components explained 66.04% of total variation with PC1 alone contributing 30.29%. The genotypes K-9, K 2658, K 2660 and K 2659 with moderate yield and yield attributes, desirable oil content & protein content can be proposed as parents for developing high-quality and high-yielding groundnut cultivars.

Keywords: Clustering, diversity, association studies, selection index, yield

Introduction

Groundnut (*Arachis hypogaea* L.) is an essential oilseed and food legume crop that is widely grown in tropic and subtropical areas around the globe. It serves as a major source of edible oil, protein and vital nutrients, thus plays a crucial role in nutritional security and supports the livelihood of small and marginal farmers (Parmar *et al.*, 2022) [15]. In India, groundnut is a leading oilseed crop, however its productivity remains relatively low and inconsistent due to various biotic and abiotic challenges, as well as the intricate genetic structure of yield. Yield is a quantitative character controlled by many genes and is significantly affected by environmental factors, making direct selection least significant. The success of any crop improvement program largely depends on the level of genetic variability present in the germplasm. Numerous studies have reported significant variability for yield and its component traits in groundnut, indicating ample potential for improvement through selection (Attia *et al.*, 2022; Yadav *et al.*, 2023; Rupa *et al.*, 2025) [1, 16, 23]. However, yield improvement cannot rely solely on variability estimates, as it is a complex trait influenced by numerous interacting genetic factors. Association studies, such as correlation and path coefficient analysis, helps in understanding the relationship among the traits. Correlation measures the degree and direction of association, while path analysis breaks down these correlations into direct and indirect effects, thereby identifying traits with true causal influence on yield (Kannappan *et al.*, 2022) [10]. Multivariate techniques such as principal component analysis (PCA) and

cluster analysis group genotypes into distinct categories based on multiple traits and provides the best way to choose parents in order to achieve high heterosis and support the hybrid breeding program. Hence, the present study was conducted with an objective to assess genetic variability, trait associations and genetic diversity among groundnut genotypes to select superior genotypes which can be used as valuable parents for yield and quality improvement.

Material and Methods

In this experiment, twenty-five genotypes, along with the check variety, Vishitha and K-6 were evaluated during Kharif 2025 at the Agricultural Research Station, Kadiri, using a Randomized Block Design with three replications. The crop was sown at a spacing of 30 cm x 10 cm. Standard agronomic practices recommended for groundnut cultivation were followed to ensure optimal crop growth and development. Observations were recorded on five randomly selected plants per replication for each genotype (plot basis for days to 50% flowering and days to maturity) for sixteen physiological, yield attributing and quality characters, viz., days to 50% flowering, days to maturity, SPAD chlorophyll meter reading (SCMR) at 60 DAS, specific leaf area (SLA) at 60 DAS, plant height, number of primary branches per plant, number of mature pods per plant, hundred pod weight, hundred kernel weight, shelling percentage, dry haulms yield per plant, harvest index, kernel yield per plant, oil content, protein content and pod yield per plant by following the standard procedure. PCA was assessed using

the procedure outlined by Banfield (1978). Statistical analysis was done using R studio version 2024.12.1+563.

Results and Discussion

The principal component analysis (PCA) of ten agronomic traits revealed that the first seven principal components (PC) collectively accounted for over 98% of the total variation. Notably, the first three principal components (PC1 to PC3), with eigenvalues >1, together explained 80.83% of the variability, with PC1 (eigenvalue of 4.64) alone contributed 46.41% (Table 1). PC1 was mainly influenced by days to 1st flowering (0.93), days to 50% flowering (0.81), dry pod yield (0.83) and kernel yield (0.50), with smaller contributions from initial (0.14) and final plant stand (0.22). The genotypes K 2667, K 2662, K 2677, K 2661, K 2673, K 2666 and K 2675 were represented in PC1, with K 2667 and K 2662 identified as significant contributors due to their positioning further from the origin along the yield vectors, suggesting their potential for yield enhancement (Fig. 3). PC1 and PC2 together explained 67.39% of the total variation, with PC2 contributing 20.98%. The main

contributors to PC2 were shelling percentage (0.40), days to 50% flowering (0.26), kernel yield (0.24) and 100 kernel weight (0.02). Genotypes K 2664, K 2657 and K 2656 were located in Quadrant II, which was mainly influenced by genotypes Kadiri 9, K 2658, K 2660 and K 2659, associated with quality traits like 100-kernel weight, SMK weight and SMK%. These results align with the findings of Daudi *et.al.*, 2021 and Sukrutha *et al.* (2023) [4, 19], who emphasized pod and kernel traits as key contributors in groundnut diversity studies, as well as Danalakoti *et al.* (2024) and Mubai *et al.* (2020) [3, 14], who highlighted yield and quality traits as primary contributors. These traits exhibited a negative correlation with yield components, indicating a trade-off between yield and quality (Upadhyaya, 2003) [21]. Quadrant IV (Q-4) comprised genotypes K 2665, K 2670, K 2671, K 2676, K 2668, K 2672, and K 2674, which were linked to initial and final plant stand. These traits were closely related and moderately contributed to overall variability, underscoring their importance in crop establishment and stability.

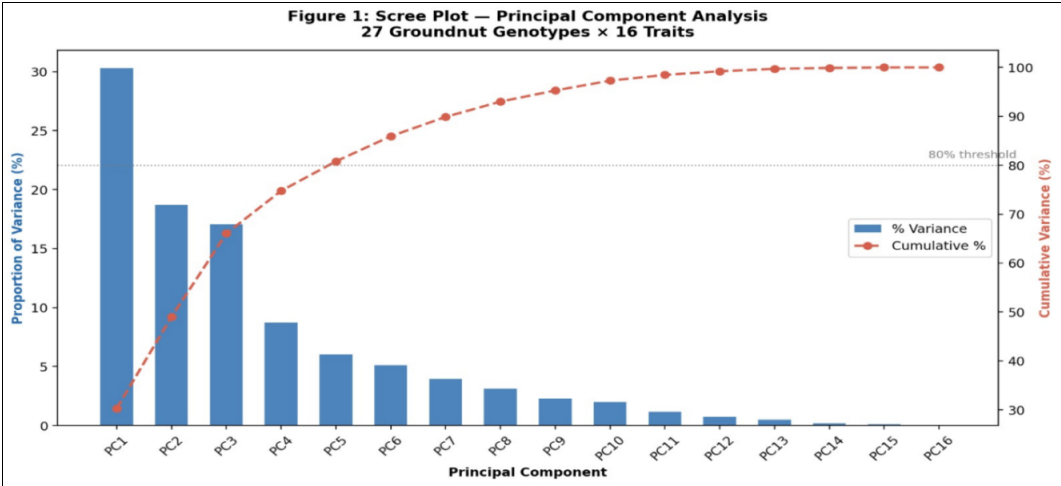


Fig 1: Screen plot with connecting curves

Table 1: Eigenvalues and Variance Explained by Principal Components

PC	Eigenvalue	% Variance	Cumulative %
PC1	5.0333	30.2927	30.2927
PC2	3.1083	18.7073	49.0000
PC3	2.8343	17.0585	66.0585
PC4	1.4470	8.7087	74.7672
PC5	1.0032	6.0380	80.8053

The scree plot indicated that the first few principal components captured the majority of the total variation among the 27 groundnut genotypes evaluated for 16 traits. PC1 accounted for approximately 30.3% of the total variance, followed by PC2 (18.7%) and PC3 (17.0%), together explaining about 66% of the variation. PC4 contributed a further 8.7%, bringing the cumulative variation to approximately 75%, while PC5 increased it to about 81%, thereby exceeding the commonly used 80% threshold. Subsequent components contributed progressively smaller proportions of variation, indicating diminishing explanatory power. Thus, the first five principal components adequately summarized the major sources of multivariate variation in the dataset and can be considered the most informative components for interpreting genotype

diversity and trait relationships, while the remaining PCs contributed relatively little additional information. (Table 1& Fig 1)

Kernel yield (KY) exhibited a strong and significant positive correlation with dry pod yield (0.68 at genotypic and 0.82 at phenotypic levels). Path analysis further revealed that dry pod yield (DPY) exerted the highest positive direct effects (1.0986, 1.0197), followed by shelling percentage (0.8074, 0.5970). This pronounced direct effect, along with its significant positive correlation with kernel yield, suggests that selecting for DPY would be highly effective in boosting overall kernel productivity (Kumari and Sasidharan 2020; Shoba *et.al.*, 2023) [12, 17]. Conversely, shelling percentage showed inconsistent association with kernel yield, being significant only at the phenotypic level, suggesting environmental influence on its expression, making it less reliable as a sole selection criterion. A significant and positive correlation of kernel yield with days to 1st flowering (0.51) and days to 50% flowering (0.45) was observed at the genotypic level, indicating that genotypes with relatively longer durations tend to accumulate more assimilates, ultimately leading to higher yields. At the genotypic level, dry pod yield (DPY) showed highly significant and positive correlations with days to first

flowering (0.95), days to 50% flowering (0.75), initial plant stand (0.62) and final plant stand (0.48). A similar trend was observed at the phenotypic level, although the positive correlations for initial and final plant stand were non-significant. Path analysis further clarified these relationships, revealing that DPY contributed substantial positive indirect effects on kernel yield through days to first

flowering (0.3075, 0.4775), days to 50% flowering (0.8340, 0.4578), initial plant stand (0.6858, 0.066) and final plant stand (0.5282, 0.0313). Among these, days to 50% flowering exerted the highest indirect effect and maintained a significant positive correlation with kernel yield at both genotypic and phenotypic levels, highlighting its reliability as a selection criterion. (Fig 2)



Fig 2: Correlation plotted against different traits with respective principal components

The contribution of the studied traits varied considerably across the first seven principal components showed that PC1 was primarily characterized by positive loadings for KYP (0.439), PYP (0.433), HPW (0.402), HI (0.376), and HKW (0.281), indicating that these traits were important contributors to the major source of variation. PC2 showed relatively strong positive contributions from DHY (0.493), PH (0.478), and DFF (-0.121), while SCMR (-0.465) contributed negatively. PC3 was strongly influenced by PC (-0.425), OC (0.423), NMP (0.437), and NPP (0.398), suggesting that these traits were major sources of variation along this axis. PC4 was dominated by DM (0.622) and

DFF (0.532), whereas PC5 showed substantial positive loading for NPP (0.559) and negative loading for OC (-0.494) and SP (-0.443). PC6 was mainly associated with NMP (0.517) and PC (0.466), with SLA showing a negative contribution (-0.399), while PC7 was characterized particularly by NPP (0.512), HKW (0.351), and DM (-0.445). Overall, the loading pattern indicates that different groups of morphological, physiological, and yield-related traits contributed to variation across the principal components, with the strongest loadings identifying traits that may be particularly useful for distinguishing genotypes and guiding selection in breeding programs. (Table 2)

Table 2: Eigen values, variance percentage and factor loadings for physiological, yield component and quality traits in groundnut

Trait	PC1	PC2	PC3
Days to 50% flowering	-0.1854	-0.1211	-0.2293
Days to Maturity	-0.0311	-0.2243	0.1485
Plant Height	0.1772	0.4780	-0.0943
No. of pods plant -1	-0.0591	-0.0193	0.3978
No. of mature pods	0.0966	0.1137	0.4366
SCMR Readings	0.1295	-0.4651	-0.0609
Specific Leaf Area (cm2/g)	0.2175	0.2461	-0.2239
Dry Haulm Yield (g)	0.1534	0.4928	-0.0778
Kernel Yield per Plant (g)	0.4390	0.0054	0.1056
Shelling Percentage (%)	0.1858	-0.2439	0.1824
Hundred Pod Weight (g)	0.4016	-0.0749	0.0718
Hundred Kernel Weight (g)	0.2809	-0.1855	-0.2461
Harvest Index (%)	0.3755	-0.1909	0.1791
Oil Content (%)	-0.0982	0.1388	0.4229
Protein Content (%)	0.1647	-0.1105	-0.4252
Pod Yield per Plot (kg)	0.4331	0.0774	0.0762
Eigen value	5.03	3.10	2.83
Variance percent	30.29	18.70	17.05
Cumulative variance percent	30.29	49	66.05

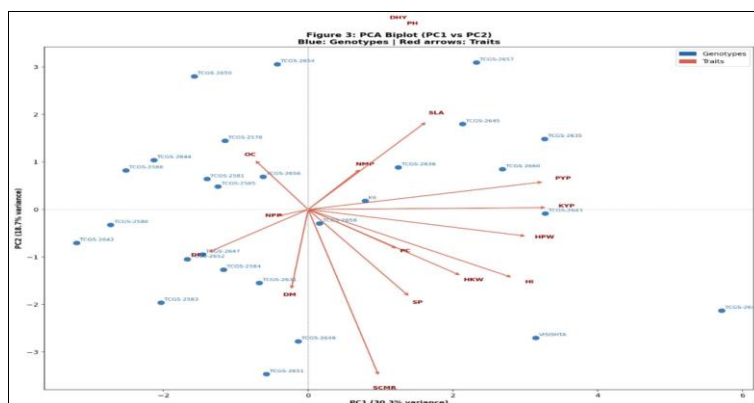


Fig 3: Biplot against PC1 and PC2 for physiological, yield & quality traits in groundnut

The PCA biplot revealed clear patterns of multivariate variation among the genotypes and their associations with the measured traits. The first two principal components (PC1 and PC2) accounted for 49.1% of the total variation, with PC1 explaining 30.3% and PC2 explaining 18.7%. Traits such as PYP and KYP showed strong positive associations with PC1, whereas SLA and NMP were positively associated with both PC1 and PC2. In contrast, DM, NPP, and OC were negatively associated with PC1, while SCMR, SP, HI, and HKW contributed mainly to the negative direction of PC2 and positive direction of PC1. Genotypes positioned in the direction of particular trait vectors exhibited stronger associations with those traits, whereas genotypes located near the origin showed comparatively average performance across the traits. (Table 4 & Fig 3)

Conclusion

Significant variation among 27 groundnut genotypes was observed for most of the traits, indicating substantial genetic variability. Kernel-related traits, including 100-kernel weight, sound mature kernel (SMK) weight and SMK

percentage, exhibited wide variability. Similarly, dry pod yield and kernel yield also showed considerable differences, reflecting variation in yield potential. Principal component analysis indicated that the first three components, with eigenvalues greater than one, accounted for 80.83% of the total variation, with the first principal component alone contributing 46.41%. The genotypes K 2672, K 2667, K 2662, K 2661 and K 2675 were identified as superior for dry pod yield. The genotypes belonging to PC1, PC2, PC3, PC4 and PC5 involving characters of major economic importance viz., no. of pods can be employed in peanut improvement programme to generate potential hybrids based on genetic distances. However, the genotype x environment interactions can be further studied through multi-location trials before releasing the selected genotypes for commercial cultivation. The biplot demonstrates substantial genetic diversity and differential trait associations among the evaluated genotypes, providing useful information for identifying genotypes with desirable combinations of agronomic, physiological & quality traits for groundnut improvement. (Table3)

Table 3: Principal component scores of the genotypes

Genotype	PC1	PC2	PC3	PC4	PC5
K6	0.7854	0.1806	-0.0501	-0.4642	-0.8462
TCGS-2578	-1.1488	1.4472	2.3594	-0.2111	1.6429
TCGS-2580	-2.7286	-0.3251	-1.7114	-0.6026	0.1392
TCGS-2581	-1.3974	0.6411	1.0662	0.5600	-0.7812
TCGS-2583	-2.0331	-1.9609	2.5127	-1.9137	0.0203
TCGS-2584	-1.1693	-1.2684	0.4051	-1.2883	0.4080
TCGS-2585	-1.2452	0.4807	3.1423	0.6082	-0.4243
TCGS-2586	-2.5193	0.8209	-1.1875	-0.6888	-1.5302
TCGS-2631	-0.6776	-1.5475	4.2891	1.6622	0.1919
TCGS-2635	3.2637	1.4845	0.8845	-0.3822	-0.1489
TCGS-2636	1.2447	0.8866	-0.5234	-0.2423	-1.1002
TCGS-2642	-3.1997	-0.7041	0.5107	0.9515	-0.3564
TCGS-2643	3.2716	-0.0862	-0.7585	0.7187	0.7727
TCGS-2644	-2.1303	1.0399	-1.0150	-0.2265	-0.6648
TCGS-2645	2.1329	1.7977	0.3629	-1.6389	1.9318
TCGS-2647	-1.4586	-0.9495	-3.0498	1.7944	2.4378
TCGS-2648	5.7115	-2.1289	-0.8617	1.0592	-0.0659
TCGS-2649	-0.1383	-2.7763	-1.8824	-0.3472	0.7874
TCGS-2650	-1.5718	2.8021	-1.3314	2.8204	-0.4416
TCGS-2651	-0.5782	-3.4672	-1.7872	-0.7712	-0.7940
TCGS-2652	-1.6699	-1.0499	0.1330	-0.1791	1.5639
TCGS-2654	-0.4264	3.0565	-1.4023	0.5252	-0.5068
TCGS-2656	-0.6237	0.6879	-0.3720	-1.0006	-0.1390
TCGS-2657	2.3235	3.0922	-0.3782	-2.5054	0.2207
TCGS-2658	0.1552	-0.2959	-1.3080	-0.0407	-0.9230
TCGS-2660	2.6844	0.8462	1.4278	1.6652	0.0765
VISISHTA	3.1435	-2.7045	0.5253	0.1375	-1.4706

Table 4: Percent contribution of traits for each Principal component

Trait	Trait Full Name	PC1	PC2	PC3	PC4	PC5
DFF	Days to First Flowering	3.438	1.466	5.256	28.294	4.016
DM	Days to Maturity	0.097	5.033	2.207	38.730	4.164
PH	Plant Height (cm)	3.141	22.851	0.889	5.431	0.233
NPP	No. of Pods per Plant	0.349	0.037	15.824	0.579	31.296
NMP	No. of Mature Pods	0.932	1.294	19.066	2.729	1.428
SCMR	SPAD Chlorophyll Meter Reading	1.677	21.629	0.371	0.100	3.560
SLA	Specific Leaf Area (cm ² /g)	4.729	6.056	5.012	3.214	0.072
DHY	Dry Haulm Yield (g)	2.353	24.288	0.605	4.895	0.156
KYP	Kernel Yield per Plant (g)	19.270	0.003	1.116	0.038	0.609
SP	Shelling Percentage (%)	3.453	5.949	3.325	9.787	19.584
HPW	Hundred Pod Weight (g)	16.131	0.561	0.516	0.281	0.612
HKW	Hundred Kernel Weight (g)	7.891	3.441	6.058	0.133	5.185
HI	Harvest Index (%)	14.102	3.646	3.209	3.340	0.017
OC	Oil Content (%)	0.964	1.926	17.888	0.998	24.448
PC	Protein Content (%)	2.712	1.222	18.078	0.715	4.476
PYP	Pod Yield per Plot (kg)	18.761	0.598	0.580	0.737	0.143

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Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

Competing Interests

Authors have declared that no competing interests exist

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