



RESEARCH ARTICLE

Genetic diversity and performance evaluation of long-fruited snake gourd genotypes (*Trichosanthes anguina* L.) under sodic soil conditions in Tamil Nadu, India

J Marimuthu¹, K R Vijayalatha^{2*}, V Jegadeeswari³, S Nithila⁴, A Sabir Ahamed², N Malini⁴, T Uma Maheswari⁵, R Rajeswari², S Kumar⁵, K Yamunarani⁶ & A Sangeetha⁴

¹Department of Vegetable Science, Horticultural College and Research Institute, Tamil Nadu Agricultural University (TNAU), Coimbatore 641 003, Tamil Nadu, India

²Department of Vegetable Science, Horticultural College and Research Institute for Women, Tamil Nadu Agricultural University (TNAU), Tiruchirappalli 620 027, Tamil Nadu, India

³Grapes Research Station, Tamil Nadu Agricultural University (TNAU), Theni 625 526, Tamil Nadu, India

⁴Department of Basic Science, Horticultural College and Research Institute for Women, Tamil Nadu Agricultural University (TNAU), Tiruchirappalli 620 027, Tamil Nadu, India

⁵Department of Fruit Science, Horticultural College and Research Institute for Women, Tamil Nadu Agricultural University (TNAU), Tiruchirappalli 620 027, Tamil Nadu, India

⁶Department of Plant Protection, Horticultural College and Research Institute for Women, Tamil Nadu Agricultural University (TNAU), Tiruchirappalli 620 027, Tamil Nadu, India

*Correspondence email - vijayalatha.kr@tnau.ac.in

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Abstract

Snake gourd (*Trichosanthes anguina* L.) is a cucurbitaceous vegetable of economic and nutritional significance, widely cultivated in tropical and subtropical regions. This study evaluated 30 genotypes under sodic soil conditions at Horticultural College and Research Institute for Women, Tiruchirappalli, over 2 seasons (kharif and rabi, 2024–2025) to assess variability for growth, yield, physiological and quality traits. Analysis of variance revealed significant differences among genotypes for all seventeen traits at $p \leq 0.01$, indicating the presence of considerable genetic variability. Phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for most traits, suggesting that environmental factors contributed to the observed phenotypic expression. However, the relatively small differences between PCV and GCV for several traits indicate that environmental influence was present but moderate and that a considerable proportion of the variability was genetically controlled. High heritability coupled with high genetic advance was observed for fruit yield per plant, single fruit weight, fruit length and number of seeds per fruit, reflecting predominant additive gene action and the potential for improvement through selection. Genotypic correlation analysis showed that fruit yield was positively associated with vine length, number of fruits per plant, single fruit weight, proline content and vitamin C, whereas days to flowering and Na^+/K^+ ratio were negatively correlated. Principal component analysis (PCA) identified 3 principal components with eigenvalues >1 . The 17 traits to 3 major components explaining 83.6 % of the total variability, with PC1 alone contributing 70.7 %, highlighting yield and quality traits as major discriminators among genotypes. Mahalanobis D^2 cluster analysis grouped genotypes into four clusters, each exhibiting superiority for specific traits. The highest inter-cluster distances were observed between Cluster I & IV and Cluster I & III, indicating substantial genetic divergence, suggesting these clusters as potential parents for heterotic breeding. Genotypes S06, S21, S27, S12, S09, S18 and S16 were identified as superior performers and represent promising parental lines valuable genetic resources for breeding high-yielding, quality-enhanced and sodicity-tolerant snake gourd cultivars.

Keywords: cluster analysis; genetic variability; principal component analysis; snake gourd; sodic soil; yield traits

Introduction

Snake gourd (*Trichosanthes anguina* L.) is considered to have originated in India, where wild progenitors were identified prior to domestication (1). Wild forms are still distributed in parts of South and Southeast Asia, Australia, West Africa, Latin America and the Caribbean (1). Belonging to the family Cucurbitaceae, which comprises about 70 genera and over 700 species, snake gourd represents one of the economically significant long-fruited

cucurbits. It is known by different vernacular names across regions for instance, snake tomato in Nigeria, pathakaya in India, pakupis in the Philippines, baup ngu in Thailand, pudalankaai in Tamil, paduvalakaayi in Kannada and padavalanga in Malayalam.

India is regarded as a major centre of diversity for snake gourd, with extensive cultivation in states such as Tamil Nadu, Kerala, Andhra Pradesh, Odisha, Karnataka and West Bengal (2). The crop is also widely grown in other tropical and subtropical

countries where it contributes to dietary nutrition and local health traditions. The fruits are rich in dietary fibre, vitamin C (VC) and essential minerals, while being low in calories and various plant parts such as roots, leaves and seeds are traditionally used to manage ailments including fever, bronchitis, skin diseases and diabetes (3, 4). Apart from its nutritional and medicinal values, snake gourd holds economic importance for smallholder farmers as a source of income and food security.

Genetic variability is critical for snake gourd improvement, with significant diversity reported for traits including vine length, fruit length, fruit girth and number of fruits per plant (5). Its monoecious nature and relatively high cross-pollination rate further enhance variability, facilitating effective selection and hybridisation (6). However, soil sodicity remains a major constraint to production in several regions, affecting nearly 3.1 million ha in India (7). Sodic soils are characterised by high pH, excessive exchangeable sodium, poor soil structure and reduced permeability, which collectively impair nutrient availability and root growth (8, 9).

Snake gourd is particularly vulnerable to sodic conditions because it is a shallow-rooted, fast-growing cucurbit with high nutrient and water demand during its vegetative and reproductive phases. Elevated sodium levels disrupt ion homeostasis, especially the Na^+/K^+ balance, interfere with the uptake of essential nutrients such as calcium and potassium and induce osmotic and oxidative stress. These effects lead to reduced vine elongation, delayed flowering, poor pollen viability, impaired fruit set and ultimately lower yield and quality. As sodic soil continues to expand due to irrigation mismanagement and climate-related factors, developing sodicity-tolerant genotypes has become increasingly urgent. Breeding for improved Na^+ exclusion, better ion regulation and sustained yield under high pH conditions is therefore essential to ensure stable production, enhance farmer resilience and safeguard vegetable-based nutritional security in affected regions.

Screening for sodicity tolerance using physiological traits such as Na^+/K^+ ratio (NKR), proline content (Pro), SPAD chlorophyll index and relative water content, along with genetic parameters including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance, is essential for effective selection (10). The NKR serves as a key indicator of ionic homeostasis, as tolerant genotypes maintain lower sodium accumulation and higher potassium retention, thereby protecting metabolic processes and enzyme activity under sodic stress. Proline accumulation functions as an osmoprotectant, stabilising cellular structures, scavenging reactive oxygen species and maintaining osmotic balance. The SPAD chlorophyll index reflects photosynthetic capacity and chlorophyll stability, which are often reduced under sodium-induced stress. Relative water content (RWC) indicates the plant's ability to maintain cellular hydration and turgor under osmotic stress conditions. Together, these physiological parameters provide insight into the mechanisms underlying stress adaptation. Multivariate approaches, such as principal component analysis (PCA) and Mahalanobis D^2 cluster analysis, are valuable for identifying key traits contributing to variability and grouping genetically divergent genotypes, thereby facilitating parent selection for breeding programs. The PCA condenses complex trait variation into major components, while cluster analysis identifies genetically distant and superior lines suitable for heterosis breeding and stress tolerance improvement.

Despite its potential, few studies have evaluated snake gourd under sodic conditions using integrated morphological, physiological and yield parameters in combination with multivariate approaches such as PCA and cluster analysis. Therefore, the present investigation aimed to evaluate the extent of genetic variability, assess the association among growth, yield, physiological and quality traits and identify genetically divergent and superior genotypes suitable for sodicity tolerance breeding using multivariate statistical techniques.

Materials and Methods

The experiment was conducted at the Department of Vegetable Science, Horticultural College and Research Institute for Women, Tiruchirappalli, during 2024–2025 across 2 seasons (kharif and rabi). Geographically, the experimental site is situated at approximately $10^{\circ}48'$ N latitude and $78^{\circ}41'$ E longitude, at an elevation of 85–90 m above mean sea level. The location experiences a mean annual temperature of about 29.3°C and an average annual rainfall of approximately 1350 mm. Prior to experimentation, soil samples were collected from the 0–30 cm depth at 4 randomly selected locations within the experimental field. These samples were thoroughly mixed to form one composite sample for physico-chemical analysis. Soil pH and electrical conductivity (EC) were determined in a 1:2.5 soil-water suspension using a digital pH meter and conductivity meter, respectively. Exchangeable sodium percentage (ESP) was estimated following standard procedures based on ammonium acetate extraction and subsequent determination of exchangeable sodium using flame photometry. The experimental soil exhibited an alkaline reaction with a pH of 8.75. The EC was 0.03 dS m^{-1} , indicating non-saline conditions. However, the ESP was 18.73 %, exceeding the classical threshold of 15 % for sodic soils. Based on these parameters, the soil was classified as sodic (alkali) in nature. The elevated sodium levels likely contributed to soil structural dispersion, reduced permeability and impaired nutrient availability, thereby creating stress conditions suitable for evaluating sodicity tolerance in snake gourd genotypes.

The experimental field was prepared following standard agronomic practices. The land was ploughed 3 to 4 times to obtain a fine tilth and well-decomposed farmyard manure (FYM) at 25 t ha^{-1} was incorporated during the final ploughing. Pits of $45 \times 45 \times 45\text{ cm}$ were dug at the recommended spacing and exposed to sunlight for a few days before planting. Each pit was filled with a mixture of topsoil and FYM.

The crop was grown under a pandal (bower) system to facilitate proper vine growth and fruit development. Vertical supports were erected and a wire or rope network was established at approximately 2.0–2.5 m height to train the vines uniformly across treatments.

A basal fertiliser dose of 50:50:50 kg $\text{N:P}_2\text{O}_5:\text{K}_2\text{O}$ per hectare was applied as per recommended practices. The full dose of phosphorus and potassium and half of nitrogen were applied at planting, while the remaining nitrogen was applied in split doses at vine elongation and flowering stages. Irrigation, weeding, training and plant protection measures were carried out uniformly for all genotypes.

A total of 30 snake gourd genotypes collected from different agro-climatic regions of Tamil Nadu and other parts of

India were evaluated. The genotypes were selected based on variability in fruit morphology (length, girth and shape), yield performance, adaptation potential and availability of diverse genetic backgrounds to ensure broad representation for diversity analysis. The list of genotypes along with their sources is presented in Table 1.

The experiment was laid out in a randomized block design (RBD) with 2 replications and conducted across 2 seasons such as kharif (June to September 2024) and rabi (October 2024 to January 2025). Sowing was carried out on 10th June 2024 for the kharif season and 07th October 2024 for the rabi season. Although 2 replications represent the minimum requirement for field experimentation, this design was adopted due to uniform field conditions and logistical considerations and pooled analysis across 2 seasons was performed to enhance the reliability of results. Thirty snake gourd genotypes were evaluated under sodic soil conditions using a pandal (bower) system at a spacing of 2 × 2 m. Three seeds were sown per pit and thinning was carried out 10–12 days after germination to retain one healthy and uniform seedling per pit. Each replication consisted of 5 plants per genotype and observations were recorded on all 5 plants and averaged for statistical analysis.

The genotypes were selected based on variability in fruit morphology (length, girth and shape), yield potential, adaptation to diverse agro-climatic regions and representation of distinct genetic backgrounds to ensure broad genetic variability for diversity analysis. Irrigation was provided immediately after sowing and subsequently at 5–7-day intervals depending on crop stage and soil moisture status. Standard agronomic practices, including nutrient management, vine training under the pandal system, intercultural operations and plant protection measures, were followed uniformly for all treatments. The recorded data on quantitative, physiological and quality traits were subjected to statistical analysis using AGRES statistical software (version 7.01). Analysis of variance was

performed as per Panse and Sukhatme (1985). The GCV and PCV were calculated following Burton (1952), while broad-sense heritability and genetic advance were estimated according to Johnson et al. (1955). Mean values were utilised for correlation analysis, PCA and Mahalanobis D² cluster analysis to assess genetic divergence and identify superior genotypes.

The following traits were recorded: Vine length (VL), leaf area index (LAI), days to first male flower appearance (DFMA), days to first female flower appearance (DFFA), number of male flowers per vine (NMFV), number of female flowers per vine (NFFV), number of fruits per plant (NFPP), days to first harvest (DFH), single fruit weight (SFW), number of seeds per fruit (NSF), fruit length (FL), fruit girth (FG), Na⁺/K⁺ ratio (NKR), Pro, total soluble solids (TSS), VC and fruit yield per plant (FYPP).

Vine length was measured from the base of the plant to the terminal growing point using a measuring tape at the final harvest stage. The LAI was estimated to use a leaf area meter and the values were computed based on total leaf area per plant relative to ground area occupied. Days to first male and female flower appearance were recorded as the number of days from sowing to the opening of the first respective flower. The NMFV and NFPP were counted manually.

Days to first harvest were recorded as the number of days from sowing to the first marketable harvest. Single fruit weight was measured using a digital weighing balance and expressed in grams. Fruit length was measured using a measuring scale, while fruit girth was measured at the central portion of the fruit using a digital vernier caliper for greater precision. The NSF was counted manually after cutting fully matured fruits. The FYPP was calculated by summing the weight of all harvested fruits per plant across picking stages.

Estimation of proline content (µg g⁻¹)

Proline content was estimated using the acid ninhydrin method as

Table 1. Details of genotype and their source

Sl. No	Genotypes	Genotype details	Source of collection
01	S01	Mallamoopampatti (White)	Salem
02	S02	Mallamoopampatti (Green)	Salem
03	S03	Musiri	Trichy
04	S04	Veeramangudi	Tanjore
05	S05	Thathanur	Ariyalur
06	S06	Oddanchatrum	Dindigul
07	S07	Kovil Patti	Thoothukudi
08	S08	Nallipalayam	Namakkal
09	S09	Periya patti	Namakkal
10	S10	Purangani	Cuddalore
11	S11	Puliyur	Cuddalore
12	S12	Bandipalya	Mysore
13	S13	Veera pura	Bangalore
14	S14	Kaniyambadi	Vellore
15	S15	Maduramangalam	Kanchipuram
16	S16	Pampatti	Virudhunagar
17	S17	Odaipatti	Virudhunagar
18	S18	Kandamangalam	Villupuram
19	S19	Thingalur	Erode
20	S20	Villarasampatti	Erode
21	S21	Naganam Patty	Dindigul
22	S22	Kalpadi	Perambalur
23	S23	Vettariyarpalyam	Karur
24	S24	Kulathurpatti	Karur
25	S25	Sembarai	Trichy
26	S26	Vadipatti	Madurai
27	S27	Naranpuram	Sivakasi
28	S28	Kattur	Thiruvavur
29	S29	Kallipalayam	Coimbatore
30	S30	Kallupatty	Madurai

described (11). Approximately 0.5 g of fresh leaf tissue was homogenised in 3 % sulfosalicylic acid and centrifuged at 1000 rpm for 10 min at 4 °C. The clear supernatant was mixed with equal volumes of acid ninhydrin reagent and glacial acetic acid and the mixture was incubated in a boiling water bath for 1 hr. The reaction was terminated by placing the tubes in an ice bath followed by the addition of 4 mL of toluene to extract the chromophore. The toluene phase was separated and absorbance was measured at 520 nm using a spectrophotometer. The Pro was calculated using a standard curve and expressed as $\mu\text{g g}^{-1}$ fresh weight (FW) using the following formula.

$$\text{Proline content } (\mu\text{g g}^{-1}) = \frac{\mu\text{g of proline ml}^{-1} \times 4}{115.50} \times 100$$

Na⁺/K⁺ ratio

The sodium-to-potassium ratio was determined to assess the ionic balance in leaf tissues which serves as a reliable indicator of salinity or sodicity stress tolerance. Fresh leaf samples were collected, rinsed thoroughly with distilled water to eliminate surface impurities and then oven-dried at 70 °C to a constant weight. The dried material was ground finely and digested using a mixture of nitric acid (HNO₃) and perchloric acid (HClO₄) following the procedure described. The digested extract was filtered and diluted with distilled water. Sodium (Na⁺) and potassium (K⁺) concentrations were then quantified using an atomic absorption spectrophotometer (AAS). The NKR was computed by dividing the Na⁺ concentration by the K⁺ concentration as suggested (12, 13).

Genetic parameters

Various genetic parameters viz., genotypic variance (GV), phenotypic variance (PV), environmental variance (EV), GCV, PCV, environmental coefficient of variance, genetic advance (GA) as percentage of mean and heritability were computed for all the traits among 30 genotypes. The parameters are estimated with the recorded observations through the agriculture analyser.

Correlation and multivariate analysis

Genotypic and phenotypic correlation coefficients were estimated to determine the association among yield and related traits following the procedure (10). The computations were performed using AGRI-ANALYZER software and the significance of the correlation coefficients was tested at 5 % and 1 % probability levels.

The PCA was conducted to identify major traits contributing to total variability and to reduce dimensional complexity. Prior to analysis, all quantitative variables were standardised (mean = 0 and standard deviation = 1) to remove scale differences among traits. The PCA was performed using the correlation matrix and eigenvalues and eigenvectors were extracted. The number of principal components (PCs) retained was determined according to Kaiser's criterion (eigenvalue >1). The percentage contribution of each principal component to total variance was calculated to interpret the relative importance of traits in genotype differentiation.

Genetic divergence among genotypes was assessed using Mahalanobis D² statistics. Based on the computed D² values, genotypes were grouped into clusters following Tocher's method, which minimises intra-cluster distances and maximises inter-cluster distances. Average intra- and inter-cluster distances were

calculated to quantify the magnitude of genetic divergence and to identify genetically distant genotypes suitable for hybridisation and heterosis breeding.

Statistical analysis

The pooled mean data recorded across seasons were subjected to statistical analysis to assess the variability among genotypes for the traits under evaluation. The analysis was carried out using AGRI-ANALYZER software, which facilitated computation of analysis of variance (ANOVA) and other genetic parameters. The significance of differences among genotypic means was tested at the 5 % probability level following the procedure outlined (14).

The experiment was conducted in a RBD with 2 replications across 2 seasons. The statistical model used for analysis was:

$$Y_{ij} = \mu + G_i + R_j + e_{ij}$$

where Y_{ij} is the observation of the *i*th genotype in the *j*th replication,

μ is the overall mean,

G_i is the effect of the *i*th genotype,

R_j is the effect of the *j*th replication and

e_{ij} is the experimental error

Season-wise analysis of variance (ANOVA) was first performed to test homogeneity of error variances. Since error variances were homogeneous, pooled analysis over seasons was carried out using season means to improve precision and reliability of estimates. The pooled mean data were subjected to ANOVA to assess variability among genotypes. The analysis was performed using AGRI-ANALYZER software and significance of genotypic differences was tested at the 5 % probability level.

Estimation of variance components

Genotypic variance

$$\sigma_g^2 = \frac{MS_G - MS_E}{r}$$

Where

MS_G - Mean square due to genotypes

MS_E - Mean square due to error

r - Number of replications

Environmental variance

Environmental variance refers to the portion of the total phenotypic variance that is attributed to non-genetic factors, such as environmental conditions. It reflects the influence of the environment on trait expression and is typically estimated using the mean square of error from the ANOVA table.

Phenotypic variance

Phenotypic variance encompasses the total observable variability in a trait among individuals within a population. It includes both genetic and environmental components. The phenotypic variance (σ_p^2) was calculated by summing the genotypic variance and the environmental variance:

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

σ_p^2 - Phenotypic variance

σ_g^2 - Genotypic variance

σ_e^2 - Environmental variance

Genotypic coefficient of variation (%)

The GCV provides a relative measure of the extent of genetic variability expressed as a percentage of the mean. It is calculated using the following formula as provided below

$$GCV (\%) = \frac{\sqrt{\text{Genotypic variance}}}{\text{Mean}} \times 100$$

Phenotypic coefficient of variation (%)

The PCV measures the total variability in a trait, including both genetic and environmental components, expressed as a percentage of the mean.

$$PCV (\%) = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Mean}} \times 100$$

Environmental coefficient of variation (%)

The environmental coefficient of variation (ECV) indicates the proportion of variation caused by environmental factors, expressed relative to the trait mean. It is calculated using the formula as provided below

$$ECV (\%) = \frac{\sqrt{\text{Environmental variance}}}{\text{Mean}} \times 100$$

Genetic advance (%)

The GA refers to the expected improvement in the performance of

GAM (%)	Category
0-10	Low
10-20	Moderate
>20	High

a trait in the next generation as a result of selection. It was estimated using the following formula:

$$GA = h^2 \times \sigma_p \times k$$

Where

h^2 = Heritability (in broad sense)

σ_p = Phenotypic standard deviation

$k=2.06$ = Selection differential constant at 5 % selection intensity

Genetic advance as percentage of mean (%)

$$GAM (\%) = \frac{\text{Genetic advance}}{\text{Mean}} \times 100$$

Heritability (%)

GAM (%)	Category
0-10	Low
10-20	Moderate
>20	High

Heritability in the broad sense indicates the proportion of total phenotypic variation in a trait that is due to genetic causes. It reflects the potential for the trait to be passed from one generation to the next and was calculated as

$$\text{Heritability (\%)} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

Heritability (%)	Category
0 %– 30 %	Low
31 %– 60 %	Moderate
>60 %	High

Genotypic correlation coefficient

$$r_g(xy) = \frac{\text{cov. g}(xy)}{\sqrt{\sigma^2 g_x \times \sigma^2 g_y}}$$

Where,

$r_g(xy)$ = Genotypic correlation coefficient between traits x and y

$\text{Cov.g}(xy)$ = Genotypic covariance between traits x and y

$\sigma^2 g_x$ = Genotypic variance of trait x

$\sigma^2 g_y$ = Genotypic variance of trait y

Phenotypic correlation coefficient

$$r_p(xy) = \frac{\text{cov. p}(xy)}{\sqrt{\sigma^2 p_x \times \sigma^2 p_y}}$$

Where,

$r_p(xy)$ = Phenotypic correlation coefficient between traits x and y

$\text{Cov}_p(xy)$ = Phenotypic covariance between traits x and y

σ^2_{px} = Phenotypic variance of trait x

σ^2_{py} = Phenotypic variance of trait y

Results

Growth, high yield and quality trait

Pooled analysis of thirty long-fruited snake gourd genotypes under sodic soil conditions revealed significant ($p \leq 0.05$) differences for all growth, yield and quality traits (Table 2). Vine length ranged from 371.55 cm in S07 to 696.45 cm in S12, with genotypes S06 and S21 also recording superior growth. The LAI varied between 2.03 in S29 and 3.74 in S06, indicating that genotypes with higher LAI contributed to better canopy development. Earliness was observed in S03 and S21 with the earliest days to first male (32.50) and female flower appearance (52.00), while delayed flowering was recorded in S22 and S14. Flowering traits showed wide variation among genotypes. The NMFV was highest in S06 (555.50), while the lowest was observed in S15 (240.50). Similarly, the NFFV ranged from 21.50 in S02 to 42.50 in S06. The fruiting potential was greater in S06 with 33.00 fruits per plant, followed by S21 (31.50) and S27 (28.00). The earliest harvest was recorded in S06 (70.50 days), whereas S24 took the longest duration of 94.50 days to first harvest.

Marked variation was also recorded in fruit traits. Single fruit weight ranged from 130.02 g in S15 to 742.31 g in S06. Fruit yield per plant was maximum in S06 (18.91 kg), followed by S21 (16.12 kg), S27 (14.50 kg) and S09 (13.36 kg), while the lowest was observed in S02 (2.44 kg). Fruit length extended up to 127.00 cm in S21, followed by 86.90 cm in S27, whereas the shortest fruits were noted in S10 (26.60 cm).

Physiological and quality traits also exhibited significant differences among genotypes. The Na^+/K^+ ratio was minimum in S06 (0.79), followed by S21 (1.00) and S18 (1.13), indicating better ionic balance in these genotypes under sodic conditions, whereas the highest value was recorded in S20 (2.37). Proline content was highest in S06 ($3.94 \mu\text{g g}^{-1}$ FW), followed closely by S21 ($3.84 \mu\text{g g}^{-1}$ FW), suggesting improved osmotic adjustment capacity under sodium stress.

Total soluble solids (TSS) ranged from 2.15 °Brix in S15 to 4.70 °Brix in S21. Vitamin C content was highest in S21 ($4.83 \text{ mg } 100 \text{ g}^{-1}$), followed by S06 ($4.81 \text{ mg } 100 \text{ g}^{-1}$), while the lowest value was observed

Table 2. Pooled data on the evaluation of thirty snake gourd (long) genotypes for growth, yield and quality traits under sodic soil

G	VL	LAI	DFMA	DFFA	NMFV	NFFV	NFPP	DFH	SFW	FYPP	NSF	FL	FG	NKR	Pro	TSS	VC
S01	412.50	2.54	44.50	66.00	362.50	27.50	16.50	79.00	272.48	4.031	41.50	48.95	12.95	1.37	2.55	2.80	3.20
S02	432.05	2.73	46.50	66.50	346.00	21.50	16.00	82.00	187.31	2.441	37.00	35.15	13.70	1.65	2.62	2.20	3.11
S03	555.20	3.03	32.50	56.00	447.00	27.50	23.50	76.00	413.25	9.647	49.00	62.50	14.80	1.27	3.58	3.40	4.18
S04	406.20	2.06	47.50	63.00	321.00	25.50	17.00	83.00	155.27	2.127	26.50	41.10	11.35	1.45	2.14	3.05	3.45
S05	433.65	2.79	43.50	69.00	409.00	29.00	12.00	85.00	279.09	2.467	44.00	61.00	17.70	1.44	2.43	3.60	3.72
S06	693.90	3.74	35.00	46.50	555.50	42.50	33.00	70.50	742.31	18.905	87.00	114.10	18.20	0.79	3.94	4.40	4.81
S07	371.55	2.85	40.50	63.50	403.50	32.00	13.50	80.50	180.39	2.283	43.00	36.05	13.15	1.30	2.49	3.55	3.56
S08	386.95	2.82	51.00	75.00	382.00	28.00	11.50	94.00	267.20	2.274	23.50	40.45	12.40	1.39	2.68	3.60	3.37
S09	568.60	3.66	37.50	50.50	484.50	32.00	28.50	74.00	478.15	13.358	64.50	79.25	11.85	1.25	3.66	4.35	4.53
S10	463.10	2.94	46.00	64.00	305.50	25.00	18.00	81.50	165.51	2.437	39.50	26.60	12.75	1.76	2.09	2.75	3.51
S11	514.00	3.11	38.50	57.00	429.00	24.00	20.00	75.50	322.05	6.399	55.50	43.45	15.90	1.23	3.54	2.70	4.39
S12	696.45	3.29	39.50	54.00	474.50	30.50	23.5	71.50	500.34	11.205	74.00	103.00	13.95	1.17	3.83	3.90	4.20
S13	420.30	2.50	42.00	61.50	302.50	28.50	12.50	85.50	230.59	2.165	17.50	36.75	13.65	1.48	2.13	3.20	3.78
S14	414.80	2.07	43.00	76.00	360.00	27.00	13.50	89.00	232.34	2.318	24.00	34.75	13.25	1.83	2.18	3.15	3.82
S15	440.00	2.67	42.00	64.00	240.50	25.50	16.00	83.00	130.02	2.281	20.50	35.75	10.60	1.34	2.75	2.15	3.66
S16	527.65	3.07	36.50	56.00	429.00	27.00	25.50	76.00	405.35	10.01	61.50	47.15	14.45	1.26	3.51	2.35	4.43
S17	401.90	2.69	44.00	68.50	369.50	24.50	14.00	83.50	176.95	5.743	31.50	37.85	12.80	1.34	2.31	3.65	3.73
S18	586.60	3.30	35.50	47.50	491.50	30.00	29.00	73.50	369.07	11.081	73.50	101.85	12.15	1.13	3.62	4.10	4.38
S19	410.70	2.96	46.50	69.00	350.00	29.00	14.00	85.50	193.86	2.220	34.50	36.50	13.30	1.31	2.73	3.25	3.65
S20	451.45	2.56	41.50	65.50	329.00	27.00	18.50	81.00	153.65	2.715	26.50	66.40	10.85	2.37	2.23	3.45	3.55
S21	682.45	3.69	32.50	52.00	520.50	34.50	31.50	71.50	532.90	16.117	76.50	127.00	9.40	1.00	3.84	4.70	4.83
S22	416.20	2.40	45.50	77.50	337.50	27.50	16.00	88.50	196.77	3.686	38.00	43.35	12.40	1.64	2.48	2.85	3.38
S23	476.00	2.30	43.50	65.50	413.50	30.00	17.00	85.00	150.76	4.329	27.00	35.65	12.15	1.29	2.32	3.50	3.64
S24	438.95	2.14	39.50	74.00	357.50	23.50	17.00	94.50	260.54	5.374	31.00	39.40	14.75	1.76	2.16	3.70	3.74
S25	407.25	2.44	41.50	70.00	342.00	24.00	13.00	92.00	265.03	3.186	33.00	36.65	14.40	1.34	2.35	3.35	3.70
S26	532.15	3.07	40.00	52.50	440.50	30.50	23.00	74.00	467.29	9.376	57.50	48.45	18.40	1.27	3.56	2.95	4.53
S27	594.45	3.25	37.00	53.00	480.00	32.50	28.00	72.00	519.61	14.502	60.00	86.90	22.30	1.22	3.72	3.85	4.06
S28	397.35	2.54	39.50	74.50	374.00	26.00	12.00	90.00	355.28	2.739	41.50	44.15	16.10	1.28	2.48	3.00	3.86
S29	401.60	2.03	44.00	75.00	399.00	30.00	18.50	93.50	171.64	3.287	28.50	37.00	12.85	1.38	2.43	2.85	3.72
S30	410.65	2.56	41.50	61.50	383.50	29.00	19.50	86.00	190.62	3.627	16.50	28.90	13.35	1.80	2.26	2.50	3.45
S.Ed	9.71	0.05	2.89	1.77	41.06	28.36	1.65	1.86	7.83	0.37	2.30	1.46	0.43	0.11	0.03	0.18	0.04
CD (0.05)	19.87	0.11	5.91	3.63	83.99	4.64	3.37	3.80	16.03	0.76	4.72	2.99	0.88	0.23	0.06	0.37	0.10

VL: Vine length; LAI: Leaf area index; DFMA: Days to first male flower appearance; DFFA: Days to first female flower appearance; NMFV: Number of male flowers per vine; NFFV: Number of female flowers per vine; NFPP: Number of fruits per plant; DFH: Days to first harvest; SFW: Single fruit weight; FYPP: Fruit yield per plant; NSF: Number of seeds per fruit; FL: Fruit length; FG: Fruit girth; NK: Na⁺/K⁺ ratio; Pro: Proline content; TSS: Total soluble solids; VC: Vitamin C; S.Ed: Standard error; CD: Critical difference.

in S13 (3.20 mg 100 g⁻¹). Based on pooled mean performance across growth, yield and physiological traits, genotypes S06, S21, S27, S12, S09, S18 and S16 recorded comparatively superior values for key parameters and may be considered promising lines for further evaluation under sodic soil conditions.

Genetic parameters

Pooled variance component analysis revealed substantial

variability among thirty long-fruited snake gourd genotypes under sodic soil conditions (Table 3). The GV was consistently higher than EV for all characters, indicating predominance of genetic control. The magnitude of GCV and PCV was high for single fruit weight (50.01 and 50.80 %), fruit length (50.11 and 50.19 %), number of seeds per fruit (44.46 and 44.79 %) and fruit yield per plant (79.59 and 79.63 %), suggesting the existence of broad genetic variability. High GCV and PCV were observed for number of fruits per plant

Table 3. Pooled estimate of genetic parameters in thirty snake gourd (long) genotypes for growth, yield and quality under sodic soil

Characters	Mean	EV	GV	PV	ECV (%)	GCV (%)	PCV (%)	h ² (%)	GA	GAM (%)
VL	478.15	94.39	9012.80	9107.19	2.03	19.85	19.95	98.96	194.55	40.68
LAI	2.79	0.002	0.221	0.224	1.92	16.82	16.93	98.71	0.96	34.43
DFMA	41.26	8.37	15.42	23.80	7.01	9.51	11.82	64.81	6.51	15.78
DFFA	63.15	3.16	78.64	81.80	2.81	14.04	14.32	96.14	17.91	28.36
NMFV	394.66	1686.44	4190.48	5876.93	10.40	16.40	19.42	71.30	112.60	28.53
NFFV	28.36	5.14	13.44	18.59	7.99	12.92	15.19	72.30	6.42	22.63
NFPP	19.05	2.72	37.0207	39.75	8.67	31.93	33.09	93.13	12.09	63.49
DFH	81.88	3.46	51.02	54.48	2.27	8.72	9.01	93.65	14.23	17.39
SFW	298.85	61.46	22339.76	22401.22	2.62	50.01	50.8	99.73	307.47	102.88
FYPP	6.07	0.13	23.40	23.54	6.12	79.59	79.63	99.41	9.93	163.48
NSPF	42.80	5.33	362.23	367.57	5.39	44.46	44.79	98.55	38.92	90.93
FL	53.86	2.13	728.84	730.98	2.71	50.11	50.19	99.71	55.53	103.08
FG	13.86	0.18	6.89	7.08	3.12	18.94	19.19	97.36	5.33	38.50
NKR	1.40	0.01	0.08	0.093	8.13	20.16	21.74	85.99	0.54	38.51
PRO	2.82	0.001	0.417	0.418	1.15	22.87	22.90	99.75	1.32	47.06
TSS	3.29	0.03	0.39	0.42	5.59	19.01	19.82	92.02	1.23	37.57
VC	3.86	0.002	0.213	0.216	1.27	11.95	12.02	98.87	0.94	24.49

VL: Vine length; LAI: Leaf area index; DFMA: Days to first male flower appearance; DFFA: Days to first female flower appearance; NMFV: Number of male flowers per vine; NFFV: Number of female flowers per vine; NFPP: Number of fruits per plant; DFH: Days to first harvest; SFW: Single fruit weight; YPP: Fruit yield per plant; NSPF: Number of seeds per fruit; FL: Fruit length; FG: Fruit girth; NK: Na/K ratio; Pro: Proline content; TSS: Total soluble solids; VC: Vitamin C; EV: Environmental variance; GV: Genotypic variance; PV: Phenotypic variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; h²: Heritability; GA: Genetic advance; GAM: Genetic advance as percent of mean.

(31.93 % and 33.09 %), Pro (22.87 % and 22.90 %) and Na^+/K^+ ratio (20.16 % and 21.74 %), indicating substantial variability for these traits and greater scope for selection. The relatively close values of GCV and PCV suggest limited environmental influence on their expression.

Heritability estimates were high (>90 %) for most traits, with maximum values recorded for Pro (99.75 %), SFW (99.73 %), FL (99.71 %) and FYPP (99.41 %), indicating that a major proportion of the observed variation was genetically controlled. High heritability coupled with high genetic advance as percent of mean (GAM) was observed for FYPP (163.48 %), FL (103.08 %), SFW (102.88 %) and NSF (90.93 %), suggesting the predominance of additive gene action and good prospects for improvement through direct selection. In contrast, traits such as days to first male flower appearance, NFFV and VC content exhibited comparatively moderate heritability along with lower genetic advance as percent of mean, indicating possible involvement of non-additive gene effects and environmental influence. Overall, the results reveal substantial genetic variability, high heritability and considerable genetic advance for yield and related traits, highlighting the potential for genetic improvement of snake gourd under sodic soil conditions.

Correlation coefficient analysis

The correlation coefficients among growth, yield and quality traits of snake gourd (long) genotypes under sodic soil conditions are presented in Table 4. Fruit yield per plant exhibited highly significant and positive associations with VL (0.918), LAI (0.812), NMFV (0.956), NFFV (0.760), NFPP (0.946), SFW (0.919), NSF (0.887) and FL (0.860). With respect to quality parameters, Pro (0.887), TSS (0.647) and VC content (0.858) also showed positive correlations with yield. In contrast, DFMA (−0.784), DFFA (−0.794) and Na^+/K^+ ratio (−0.659) were significantly and negatively correlated with fruit yield per plant. The observed associations suggest that improvement in yield under sodic soil conditions may be achieved through selection of genotypes possessing enhanced vegetative growth, reproductive efficiency and favourable physiological traits that are positively associated with yield, while reducing traits linked with delayed flowering and ionic imbalance.

Principal component analysis

Pooled data from 2 seasons (kharif and rabi, 2024–2025) for 30 snake gourd genotypes were subjected to principal component analysis using seventeen traits. Seventeen PCs were generated, of which 3 exhibited eigenvalues greater than unity in accordance with Kaiser's criterion (Table 5). The PC1 accounted for 49.97 % of the total variation (eigenvalue 12.02), while PC2 and PC3 contributed 0.43 % and 0.40 %, respectively (Fig. 1). The PC1 recorded an eigenvalue of 12.02 and accounted for 70.7 % of the total variation. The PC2 and PC3 contributed 7.1 % and 5.8 % of the total variance, respectively. Together, the first 3 PCs explained 83.6 % of the total variability, indicating that a major proportion of the trait variation was captured within these components. The PC1 showed strong positive loadings for FYPP, VL, NSF, Pro, SFW, NFPP, NMFV, FL, VC, LAI, NFFV, TSS and FG. Negative loadings were observed for NKR, DFMA, DFH and DFFA. This suggests that PC1 primarily represents a yield–vigour–physiological efficiency axis under sodic conditions. The PC2 exhibited high positive loading for FG and moderate contributions from SFW, Pro, NSF and VC, indicating a fruit size and quality component. The PC3 was mainly influenced by NKR, NFPP, Pro and LAI, suggesting its association

with ionic balance and stress-related traits.

The biplot analysis (Fig. 2 and 3) revealed distinct dispersion of genotypes. Genotypes S06, S21, S27, S03, S11, S16, S26, S18, S12 and S09 were positioned away from the origin, indicating greater contribution to overall genetic variability. The S06 and S21 were strongly associated with yield-contributing traits along PC1, whereas S27 showed favorable association along PC2. Traits such as VL, NFPP, SFW, FL, Pro, VC and YPP exhibited high positive loadings and contributed substantially to genotypic differentiation. Genotypes located near the origin (S01, S02, S04, S08, S10, S14, S15, S19, S22 and S30) showed relatively lower divergence.

Mahalanobis D^2 cluster analysis

The 30 snake gourd genotypes were grouped into 4 distinct clusters based on Mahalanobis D^2 statistics (Table 6) (Fig. 4). Cluster I was the largest, comprising 20 genotypes (S01, S02, S04, S05, S07, S08, S10, S13, S14, S15, S17, S19, S20, S22, S23, S24, S25, S28, S29, S30), indicating high genetic similarity. Cluster II included 4 genotypes (S03, S11, S16, S26), Cluster III contained 2 genotypes (S06, S21) and Cluster IV had 4 genotypes (S09, S12, S18, S27), reflecting considerable genetic divergence and potential for heterosis breeding.

Cluster III exhibited superior performance with longer vines (688.17 cm), higher LAI (3.72), early flowering (33.75 and 49.25 days for male and female flowers), more fruits per plant (32.25), heavier fruits (637.60 g), longer fruits (120.55 cm) and the highest fruit yield (17.51 kg/plant^{−1}). It also had the lowest Na^+/K^+ ratio (0.89) and superior quality traits including proline (3.89 $\mu\text{mol g}^{-1}$ FW), TSS (4.55 °Brix) and VC (4.82 mg 100 g^{−1}) (Table 7). Cluster II showed moderate performance (8.85 kg plant^{−1}), while Cluster I recorded the lowest yield (3.08 kg plant^{−1}) and delayed flowering.

Intra-cluster distances were lower than inter-cluster distances, ranging from 553.41 (Cluster II) to 1670.06 (Cluster IV), indicating high similarity within clusters and substantial divergence between clusters (Table 8). Maximum inter-cluster distance was observed between Cluster I and IV ($D^2 = 19541.14$), followed by I and III (9616.59), suggesting that crosses between distant clusters could effectively generate transgressive segregants with desirable growth, yield and quality traits under sodic soil conditions.

Discussion

The present study was undertaken to evaluate 30 snake gourd genotypes for growth, yield and quality traits under sodic soil conditions. The results revealed substantial variability among the genotypes for most of the characters studied, indicating the presence of considerable genetic variability that can be exploited through selection. Among the genotypes, S06 and S21 were identified as early maturing and high-yielding, suggesting their potential suitability for utilisation in future breeding programmes aimed at developing early and sodicity-tolerant cultivars with improved yield and quality.

The evaluation of 30 snake gourd genotypes under sodic soil conditions revealed considerable genetic variability for growth, yield and quality traits, which is an essential prerequisite for crop improvement. The wide variation in VL, LAI and flowering traits indicated that significant genetic diversity exists, like earlier reports in cucurbitaceous crops in bottle gourd (15) and bitter melon (16). Earliness observed in genotypes S03 and S21 suggests their

Table 4. Genotypic and Phenotypic correlation for growth, yield and quality of snake gourd (long) genotypes under sodic soil

	VL	LAI	DFMA	DFFA	NMFV	NFFV	NFP	DFH	SFW	NSPF	FL	FG	NKR	Pro	TSS	VC	YPP
VL	1	0.803**	-0.824**	-0.834**	0.887**	0.6822 **	0.918**	-0.841**	0.861**	0.884**	0.889**	0.2384	-0.575**	0.883**	0.590**	0.827**	0.928**
LAI	0.799**	1	-0.687**	-0.820**	0.794**	0.6529 **	0.768**	-0.836**	0.784**	0.853**	0.751**	0.230	-0.626**	0.865**	0.536**	0.739**	0.812**
DFMA	-0.671**	-0.546**	1	0.794**	-0.854**	-0.546**	-0.885**	0.742**	-0.813**	-0.790**	-0.766**	-0.287	0.520**	-0.812**	-0.522 **	-0.933**	-0.881**
DFFA	-0.819**	-0.804**	0.643 **	1	-0.772**	-0.626**	-0.886**	0.946**	-0.719**	-0.772**	-0.707**	-0.225	0.574**	-0.820**	-0.410*	-0.762**	-0.820**
NMFV	0.737**	0.682**	-0.577**	-0.624**	1	0.908**	0.879**	-0.760**	0.932**	0.940**	0.869**	0.405*	-0.741**	0.893**	0.765**	0.859**	0.956**
NFFV	0.575**	0.544**	-0.401**	-0.510**	0.600**	1	0.717**	-0.538**	0.753**	0.675**	0.756**	0.264	-0.648**	0.613**	0.695**	0.639**	0.760**
NFP	0.877**	0.736**	-0.660	-0.824**	0.731**	0.571**	1	-0.832**	0.803**	0.846**	0.821**	0.176	-0.505**	0.856**	0.508**	0.812**	0.946**
DFH	-0.805**	-0.804**	0.576**	0.896**	-0.5834 **	-0.494**	-0.779**	1	-0.699**	-0.827**	-0.728**	-0.230	0.512**	-0.834**	-0.356	-0.691**	-0.793**
SFW	0.855**	0.780**	-0.652**	-0.705**	0.7896 **	0.641**	0.775**	-0.675**	1	0.879**	0.810**	0.505**	-0.684**	0.865**	0.596**	0.837**	0.919**
NSPF	0.870**	0.842**	-0.636**	-0.756**	0.7943 **	0.546**	0.806**	-0.794**	0.874**	1	0.843**	0.331	-0.703**	0.894**	0.562**	0.816**	0.887**
FL	0.885**	0.746**	-0.606**	-0.694**	0.7388 **	0.640**	0.796**	-0.703**	0.807**	0.834**	1	0.131	-0.529**	0.775**	0.772**	0.718**	0.860**
FG	0.229	0.219	-0.236	-0.2149	0.3355 **	0.222	0.168	-0.213	0.499**	0.325*	0.128	1	-0.291	0.328	0.058	0.274	0.325
NKR	-0.534**	-0.572**	0.400**	0.506**	-0.5724 **	-0.476**	-0.461**	0.461**	-0.630**	-0.638**	-0.491**	-0.269*	1	-0.721**	-0.443*	-0.652**	-0.659**
PRO	0.876**	0.858**	-0.649**	-0.801**	0.7667 **	0.520**	0.826**	-0.803**	0.864**	0.886**	0.774**	0.326*	-0.667**	1	0.442*	0.835**	0.887**
TSS	0.560**	0.504**	-0.397**	-0.396**	0.6142 **	0.592**	0.464**	-0.339**	0.570**	0.541**	0.740**	0.056	-0.370**	0.421**	1	0.548**	0.647**
VC	0.818**	0.730**	-0.743**	-0.741**	0.7268 **	0.546 **	0.779**	-0.667**	0.831**	0.803**	0.712**	0.270*	-0.604**	0.831**	0.53**	1	0.858**
YPP	0.918**	0.801**	-0.703**	-0.796**	0.8161 **	0.647**	0.924**	-0.762**	0.915**	0.877**	0.857**	0.322*	-0.605**	0.885**	0.622**	0.851**	1**

** Significant at 1% level; * Significant at 5% level. Upper diagonal: Genotypic correlation; Lower diagonal: Phenotypic correlation. VL: Vine length; LAI: Leaf area index; DFMA: Days to first male flower appearance; DFFA: Days to first female flower appearance; NMFV: Number of male flowers per vine; NFFV: Number of female flowers per vine; NFPV: Number of fruits per plant; DFH: Days to first harvest; SFW: Single fruit weight; NSPF: Number of seeds per fruit; FL: Fruit length; FG: Fruit girth; NK: Na/K+ ratio; Pro: Proline content; TSS: Total soluble solids; VC: Vitamin C; YPP: Yield per plant. Proline content; TSS: Total soluble solids; VC-Vitamin C; FY/P-Fruit yield/plant).

Table 5. Seventeen principal components for growth, yield and quality traits among the 30 snake gourd (long) genotypes under sodic soil

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14	PC15	PC16	PC17
VL	0.27	-0.06	0.11	0.10	-0.05	-0.12	-0.23	-0.12	-0.30	-0.20	0.16	0.23	-0.17	0.34	0.65	-0.08	0.05
LAI	0.25	-0.004	0.13	-0.25	-0.21	-0.26	0.30	0.59	0.03	0.08	-0.37	-0.08	-0.16	0.18	0.12	0.23	0.07
DFMA	-0.22	-0.04	-0.13	-0.41	-0.50	-0.22	-0.31	0.08	0.07	-0.47	0.28	-0.004	0.01	-0.02	-0.14	0.08	-0.02
DFFA	-0.24	-0.03	-0.33	0.06	0.19	-0.25	-0.37	0.20	-0.05	0.31	-0.00	-0.03	-0.26	-0.42	0.26	0.19	0.28
NMFV	0.26	-0.008	-0.22	0.03	0.03	-0.004	-0.14	-0.07	0.75	0.15	0.10	0.27	0.21	0.19	0.12	0.28	0.006
NFFV	0.21	-0.17	-0.38	-0.12	-0.34	0.67	-0.07	0.22	-0.15	0.24	0.08	0.03	-0.09	-0.04	0.05	-0.14	-0.07
NFPP	0.26	-0.08	0.20	0.16	-0.05	0.22	-0.36	-0.08	0.20	-0.24	-0.26	-0.28	-0.26	0.01	-0.2	-0.04	0.53
DFH	-0.24	-0.05	-0.38	0.09	0.34	-0.01	-0.24	0.24	-0.01	-0.16	-0.29	-0.009	-0.10	0.54	-0.16	-0.19	-0.23
SFW	0.26	0.15	-0.17	0.08	0.02	-0.10	-0.18	0.20	-0.28	-0.05	-0.06	-0.12	0.77	-0.02	-0.008	-0.07	0.25
YPP	0.27	-0.01	-0.02	0.10	0.02	0.02	-0.19	-0.05	0.01	-0.27	-0.31	-0.23	0.005	-0.38	0.16	0.24	-0.63
NSF	0.27	0.05	0.02	-0.08	-0.004	-0.30	-0.14	-0.01	0.12	0.35	0.346	-0.55	-0.11	0.11	-0.05	-0.38	-0.21
FL	0.25	-0.28	-0.07	0.11	-0.12	-0.24	-0.13	-0.24	-0.37	0.26	0.006	0.17	-0.08	0.15	-0.48	0.40	-0.07
FG	0.09	0.75	-0.36	0.28	-0.26	-0.06	0.15	-0.11	-0.04	-0.07	-0.01	0.017	-0.26	0.03	-0.07	0.04	0.03
NKR	-0.19	-0.16	0.22	0.72	-0.38	-0.07	-0.05	0.36	0.12	0.04	0.11	0.07	0.06	-0.03	-0.03	-0.11	-0.13
PRO	0.26	0.14	0.13	-0.15	0.08	-0.16	-0.19	0.14	0.05	0.02	-0.14	0.59	-0.10	-0.30	-0.2	-0.47	-0.09
TSS	0.18	-0.46	-0.46	0.13	-0.02	-0.26	0.45	-0.13	0.09	-0.27	-0.03	-0.02	-0.05	-0.1	0.02	-0.28	0.14
VC	0.25	0.03	0.02	0.09	0.43	0.12	0.11	0.41	-0.05	-0.30	0.56	0.01	-0.15	-0.07	-0.18	0.23	0.01

VL: Vine length; LAI: Leaf area index; DFMA: Days to first male flower appearance; DFFA: Days to first female flower appearance; NMFV: Number of male flowers per vine; NFFV: Number of female flowers per vine; NFPP: Number of fruits per plant; DFH: Days to first harvest; SFW: Single fruit weight; YPP: Fruit yield per plant; NSF: Number of seeds per fruit; FL: Fruit length; FG: Fruit girth; NK: Na⁺/K⁺ ratio; Pro: Proline content; TSS: Total soluble solids; VC: Vitamin C; PC: Principal component.

Table 6. Cluster formation among thirty snake gourd (long) genotypes evaluated under sodic soil based on Mahalanobis D² analysis

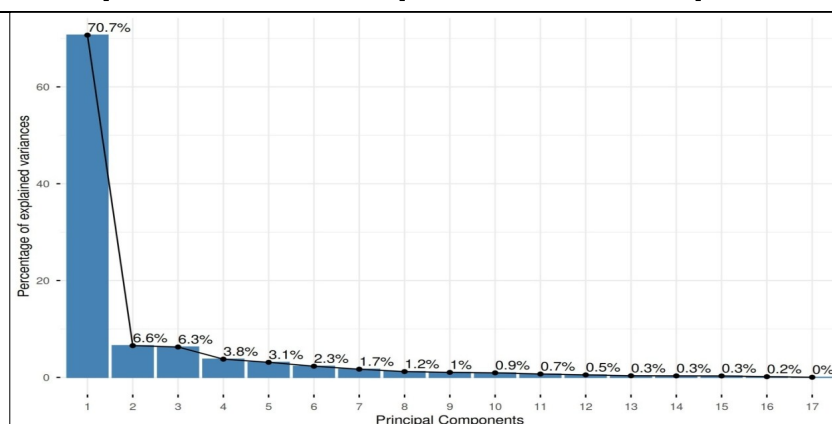
Cluster	Number of genotypes	Name of genotypes
I	20	S01, S02, S04, S05, S07, S08, S10, S13, S14, S15, S17, S19, S20, S22, S23, S24, S25, S28, S29, S30
II	4	S03, S11, S16, S26
III	2	S06, S21
IV	4	S 09, S 12, S 18, S 27

Table 7. Cluster mean obtained through Mahalanobis D² analysis for different growth, yield and quality traits among thirty snake gourd (long) genotypes

Trait	Cluster 1	Cluster 2	Cluster 3
Vine length	419.65	532.25	688.17
Leaf area index	2.53	3.07	3.72
Days to 1 st male flower appearance	43.67	36.87	33.75
Days to 1 st female flower appearance	68.47	55.37	49.25
Number of male flowers per vine	354.40	436.37	538
Number of female flowers per vine	27.00	27.25.00	38.50
Number of fruits per plant	15.30	23.00	32.25
Days to first harvest	86.10	75.37	71.00
Single fruit weight	210.76	401.98	637.60
Number of seeds per fruit	31.25	55.87	81.75
Fruit length	40.12	50.387	120.55
Fruit girth	13.22	15.88	13.80
N ⁺ /K ⁺ ratio	1.52	1.26	0.89
Proline content	2.39	3.55	3.89
Total soluble solids	3.10	2.85	4.55
Vitamin C	3.58	4.38	4.82
Fruit yield per plant	3.08	8.85	17.51

Table 8. Intra cluster and Inter cluster distance obtained through Mahalanobis D² analysis among the five clusters obtained from four snake gourd (long) genotypes for different growth, yield and quality traits

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	1196.23	4475.69	9616.59	19541.14
Cluster II	-	553.41	2747.12	9359.81
Cluster III	-	-	1430.40	3717.39
Cluster IV	-	-	-	1670.06

**Fig. 1.** Screen plot illustrating the variance explained for the first 17 principal components.

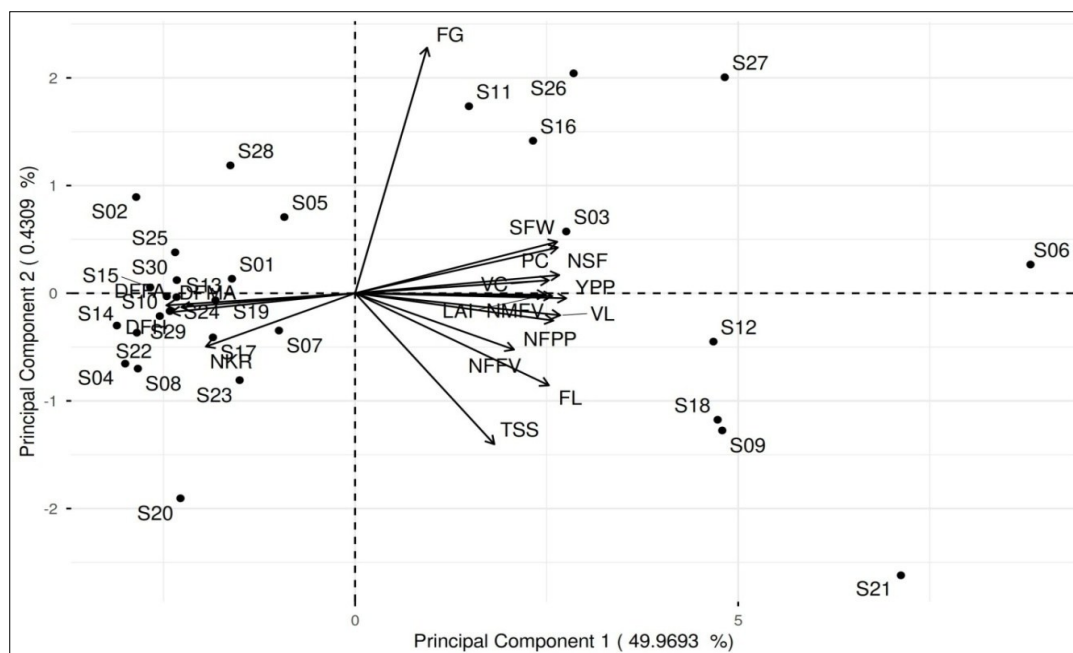


Fig. 2. Principal component analysis (PCA) biplot with groupings for thirty snake gourd (long) genotypes plotted for PC1 and PC2 components.

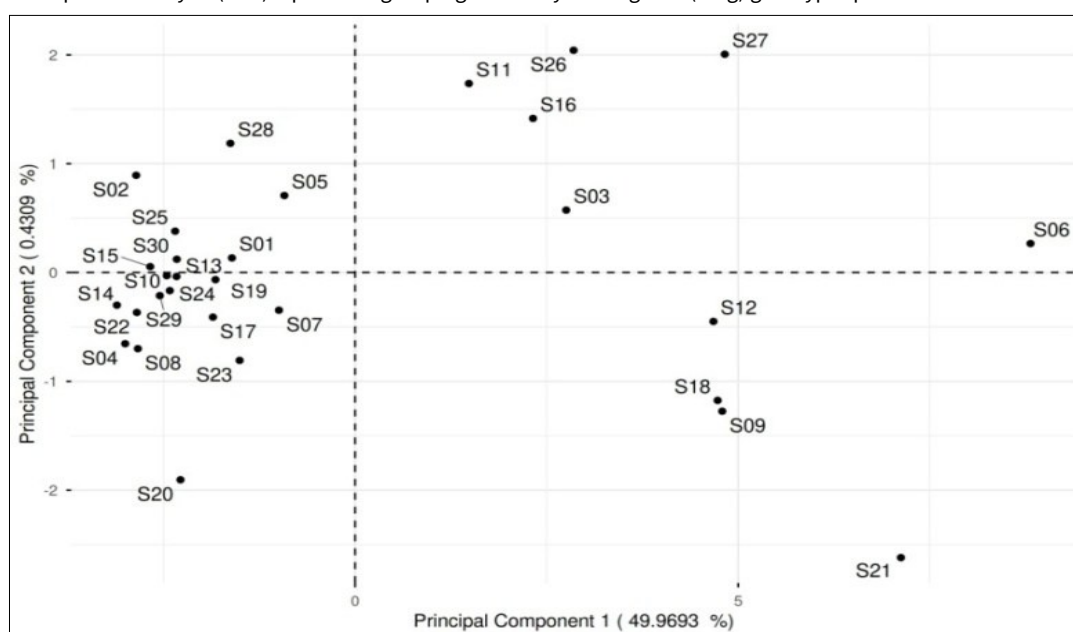


Fig. 3. Association of 30 snake gourd (long) genotypes and various growth, yield, quality related parameters owing to the PC1 and PC2 principal component.

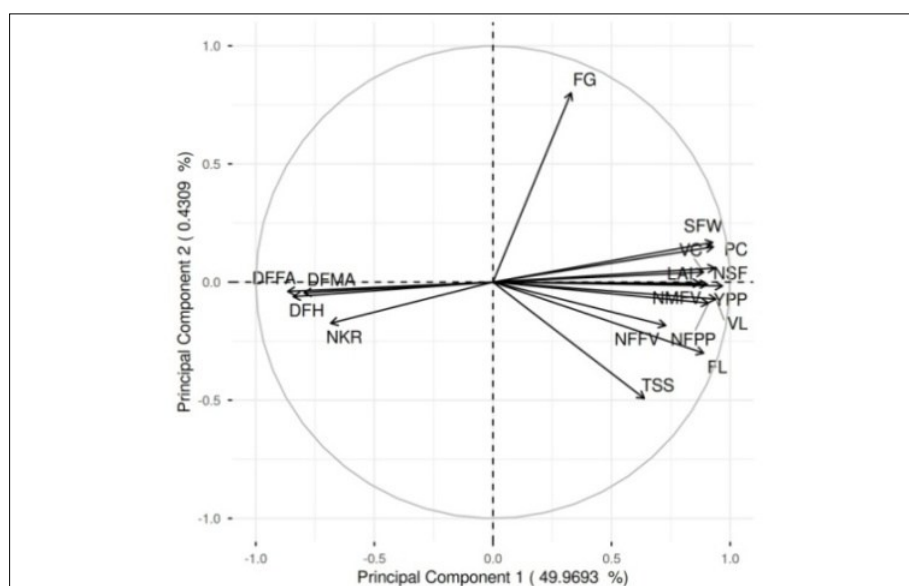


Fig. 4. Cluster diagram of thirty snake gourd (long) genotypes under sodic soil conditions based on Mahalanobis D^2 statistics.

potential use in breeding short-duration cultivars capable of withstanding sodicity stress, in line with findings, who emphasised the importance of earliness in cucurbits under saline conditions (17).

Yield-related parameters such as NFPP, SFW, FL and NSF contributed significantly to overall fruit yield. Superior performance of genotypes S06, S21 and S27 demonstrates the need to improve both fruit size and fruit number simultaneously, which corroborates the observations in round melon (18) and ridge gourd (19). Moreover, the role of physiological traits such as low NKR, higher Pro and improved VC and TSS levels in conferring tolerance under sodic conditions is consistent with reports in bottle gourd (13) and cereals, where ionic balance and osmotic adjustment were emphasised as key tolerance mechanisms (20).

The genetic parameter analysis revealed high heritability coupled with high genetic advance as percent of mean for traits such as FYPP, SFW, FL and NSF, suggesting the predominance of additive gene action. These results agree with the findings in snake gourd (21) and pumpkin, which also reported that simple selection would be effective for improving such traits (22). In contrast, flowering traits and VC content showed moderate heritability with lower GA, indicating possible influence of non-additive effects and environmental factors for which heterosis breeding could be more effective, as suggested by previous researchers in cucumber (23).

Correlation studies indicated that fruit yield per plant had strong and positive associations with VL, LAI, fruit number, SFW, FL and seed number, along with quality parameters such as proline, TSS and VC (Fig. 5 and 6). These findings are consistent with reports bitter gourd (24) and cucumber, who highlighted the importance of fruit number and fruit size in yield determination (25). Conversely, the negative association of fruit yield with days to flowering and NKR reinforces the importance of earliness and ionic regulation in enhancing productivity under sodic soils, supporting the observations (26, 27).

The PCA extracted 3 major components with eigen values greater than one, which together explained 83.6 % of the total phenotypic variability. Among them, PC1 alone contributed 49.97 %, indicating that a single principal axis captured most of the variation for growth, yield and quality traits. The dominance of PC1 in explaining variability was primarily due to its strong positive loadings for yield per plant, VL, NFPP, SFW, FL, pulp content, VC and LAI, suggesting that these traits play a major role in the genetic divergence among snake gourd genotypes under sodic stress. Similar findings, where PC1 contributed the highest proportion of total variance and was largely associated with yield and vegetative characters, have been reported in other cucurbits such as bottle gourd (28), ridge gourd (29) and bitter gourd (30).

The PCA biplot (Fig. 1) distinguished genotypes contributing prominently to variation in yield and physiological traits under sodic soil conditions. High-yielding and relatively sodicity-tolerant genotypes such as S06, S21, S27, S11, S16, S26, S18, S12 and S09 were positioned away from the origin, indicating greater divergence and stronger contribution to overall variability compared to most low- to moderate-performing genotypes. Notably, S06 and S21 were located on the positive side of PC1 and were closely associated with yield-contributing and quality traits, including FYPP, SFW, FL, Pro and VC. Genotype S27 showed favourable association with fruit-related attributes along PC2. The clear spatial differentiation of genotypes in the biplot emphasises the multivariate nature of genetic variability and its utility in identifying divergent parents for

breeding programmes aimed at yield enhancement and sodicity tolerance. Comparable trait-based differentiation through PCA has also been reported in cucurbit crops, where yield and physiological traits were identified as major contributors to genetic divergence.

The Mahalanobis D^2 analysis further confirmed the presence of genetic divergence, grouping the 30 genotypes into 4 distinct clusters. The unequal distribution of genotypes, with Cluster I containing 20 genotypes and other clusters (II, III, IV) being smaller, indicates non-homogeneous genetic composition among the evaluated materials. Similar uneven clustering patterns were reported in cucurbitaceous crops, where large clusters often represent genotypes with similar performance patterns under the evaluated traits (29, 33).

Importantly, Cluster III, which included only 2 genotypes (S06 and S21), exhibited superior mean performance for most yield and quality traits, such as longer vines, higher LAI, early flowering, higher fruit number, heavier fruits, longer fruit length, lower NKR and Pro, TSS and VC content. This indicates that genotypes in this cluster possess a combination of high yield potential and better physiological tolerance to sodic soils. Similar reports of identifying elite clusters with high yield and salt tolerance potential through D^2 analysis exist in bottle gourd (5) and sponge gourd (29).

The intra-cluster distances were lowest for Cluster II ($D^2 = 553.41$), suggesting close genetic relationship among its members (S03, S11, S16, S26), while Cluster IV recorded the highest intra-cluster distance ($D^2 = 1670.06$), implying greater heterogeneity within this group. Such differences are valuable for selecting genetically variable parents even within a single cluster, as noted in ridge gourd (34). The maximum inter-cluster divergence was observed between Cluster I and Cluster IV ($D^2 = 19541.14$) followed by Cluster I and Cluster III (9616.59), indicating that genotypes from these clusters are highly diverse and may provide opportunities for generating broader recombination or the development of transgressive segregants with desirable combinations of yield and quality. The importance of selecting parents from genetically distant clusters for enhancing heterosis and genetic gain under stress conditions has been emphasised in cucurbits (31, 32).

From a breeding perspective, the present findings suggest that genotypes S06 and S21 (Cluster III) and S27, S12, S18 (Cluster IV) can serve as promising donors for yield, earliness, fruit quality and sodicity tolerance, while crossing them with Cluster I genotypes could maximise genetic recombination and heterotic potential. The strong association of NKR and Pro with high-yielding clusters also highlights the role of these physiological stress indicators in improving sodicity tolerance in snake gourd, as suggested earlier in cucurbits (30, 35). Overall, the combined use of PCA and D^2 analysis effectively identified genetic divergence and key trait contributors under sodic soil conditions. Such multivariate approaches are widely recommended for strategic parent selection, especially in stress-prone environments, to accelerate the development of climate-resilient and high-yielding cultivars (28, 33).

Conclusion

The evaluation of 30 long fruited snake gourd genotypes under sodic soil conditions revealed substantial genetic variability for growth, yield, physiological and quality traits. High heritability coupled with significant genetic advance for fruit yield, single fruit weight, fruit length and number of seeds per fruit indicates that

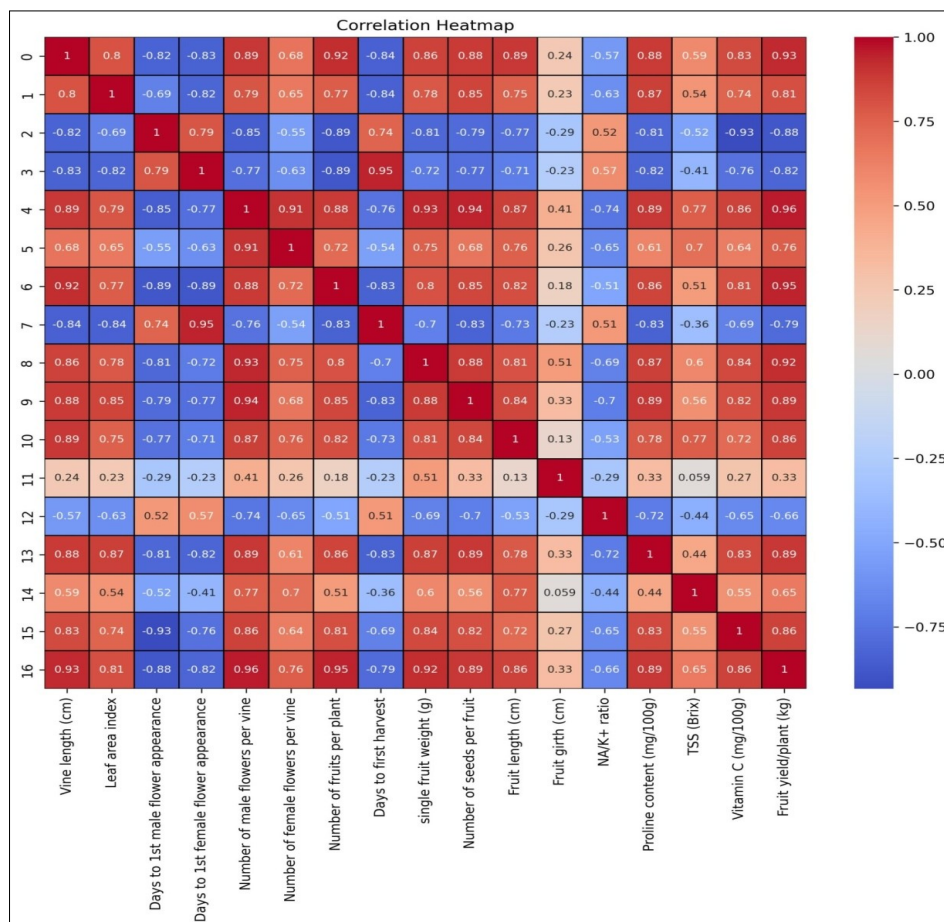


Fig. 5. Genotypic correlation heatmap for growth, yield and quality of snake gourd (long) genotypes under sodic soil.

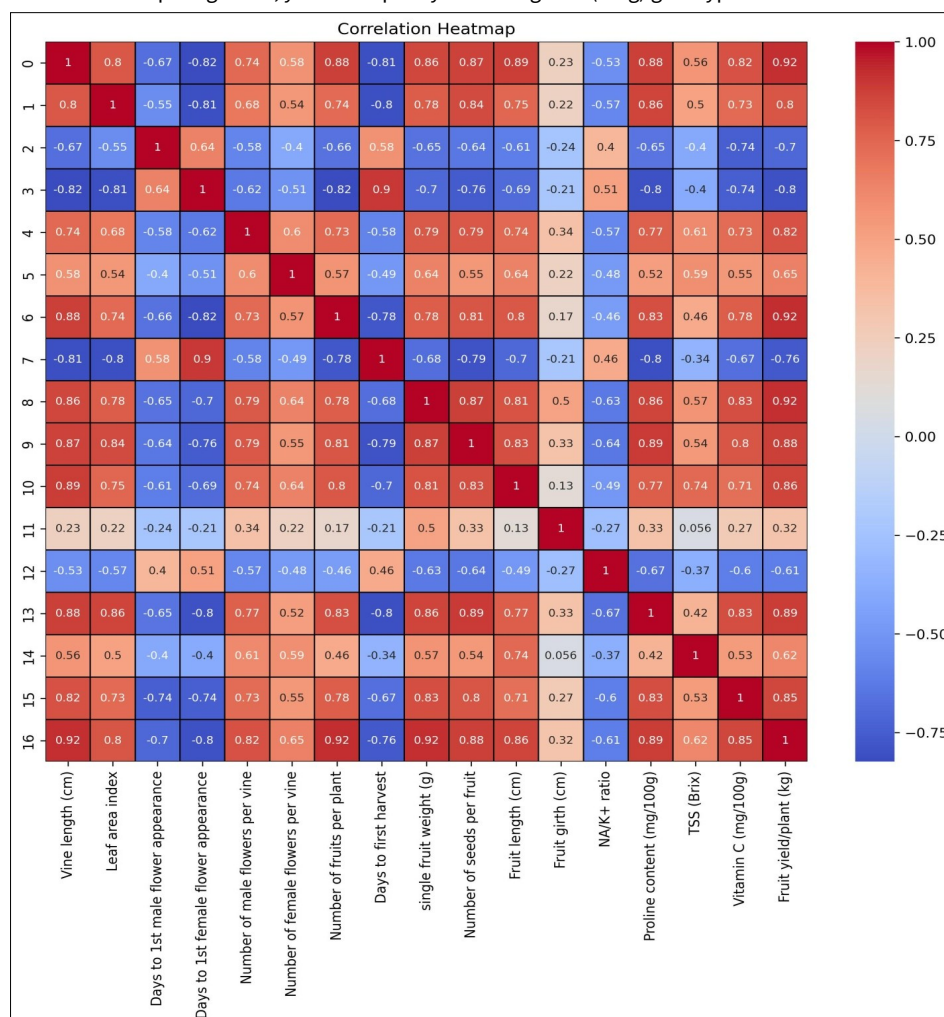


Fig. 6. Phenotypic correlation heatmap for growth, yield and quality of snake gourd (long) genotypes under sodic soil.

these traits suggest substantial additive genetic effects by additive gene action and can be effectively improved through direct selection. The PCA identified key traits contributing to total variability, while Mahalanobis D^2 cluster analysis grouped genotypes into four distinct clusters, highlighting genetically divergent lines that may be considered for hybridisation. Genotypes such as S06, S21, S27, S12, S09, S18 and S16 consistently exhibited superior performance for growth, yield and quality traits, along with better physiological adaptability under sodic stress. These genotypes can serve as promising parental lines for developing high-yielding, quality-enhanced and sodicity-tolerant snake gourd cultivars.

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Authors' contributions

JM, KRV, ASA, AM, KD, KY and VJ carried out the conceptualization. KY, SN, TUM, ASA, AS and KRV performed the formal analysis. KRV, NM, AM, KD, AS, SK, RR and VJ conducted supervision and validation. JM and KRV carried out the language editing. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

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