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Genetic diversity analysis of Ridge Gourd [*Luffa acutangula* (L.) Roxb.] Genotypes using principal component analysis and cluster analysis for yield and quality traits

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Abstract

Genetic diversity assessment of 56 genotypes of ridge gourd (*Luffa acutangula* (L.) Roxb.), comprising 45 F₁ hybrids derived from a half-diallel cross among 10 parental lines along with one standard check variety (Pusa Nasdar), was conducted during the Summer (*Zaid*) Season 2024–2026 at C.S. Azad University of Agriculture and Technology, Kanpur, Uttar Pradesh, India. Twenty-four yield and quality traits were evaluated in a Randomized Complete Block Design (RCBD) with three replications. Multivariate statistical techniques including Principal Component Analysis (PCA) and cluster analysis (D² statistics) were employed to delineate genetic relationships among genotypes. PCA revealed that the first principal component (PC1) alone accounted for 51.21% of the total phenotypic variance, while the first four PCs cumulatively explained 69.74% of variation, indicating substantial trait diversity. Cluster analysis using Mahalanobis D² distances grouped all 56 genotypes into seven distinct clusters. Cluster 2 was the largest comprising 34 genotypes, while Clusters 5, 6 and 7 were singletons or pairs, suggesting the presence of unique genotypes. The maximum inter-cluster distance was observed between Clusters 1 and 4 (D² = 3456.79), indicating high genetic divergence and potential for heterotic exploitation. Cluster 1 exhibited the highest mean values for vine length, fruit length (23.17 cm), fruit weight (120.75 g), number of fruits per vine (14.63), fruit yield (1.85 kg/vine), ascorbic acid content (5.31 mg/100g), and flesh thickness (11.28 cm). These results suggest that crosses between genotypes from widely divergent clusters, particularly Clusters 1 and 4, may yield superior segregants for yield improvement in ridge gourd breeding programs.

Keywords: Ridge gourd, *Luffa acutangula*, principal component analysis, cluster analysis, genetic diversity, Diallel crosses, yield traits

1. Introduction

Ridge gourd [*Luffa acutangula* (L.) Roxb.] Is a commercially important vegetable crop belonging to the family Cucurbitaceae, with a chromosome number of 2n = 26. It is widely cultivated across India and South-East Asia, and is popularly known as 'Kalitori', angled gourd, angled loofah, Chinese okra, silky gourd, or ribbed gourd. The genus name 'Luffa' is derived from the product 'loofah', referring to the fibrous sponge obtained from matured fruits. Tender fruits are green, used in soups, curries, and cooked vegetables, and are notable for their easy digestibility and appetizing quality. Ridge gourd fruits are demulcent, diuretic and nutritive, while seeds possess purgative and emetic properties.

cucurbitaceous vegetables, including ridge gourd (*Luffa acutangula*), are important warm-season vegetable crops cultivated widely in tropical and subtropical regions. The authors highlighted the crop's nutritional importance, flowering behaviour, pollination mechanism, variability in fruit characters, and adaptability under diverse agro-climatic conditions. They also emphasized the significance of genetic variability and selection in the improvement of yield and quality traits in cucurbits. Seshadri (2002) ^[13].

The total area under vegetable cultivation in India is approximately 11 million hectares. Total production stands at around 205–210 million tonnes annually. The average productivity of

vegetables is about 19 tonnes per hectare. Vegetables account for nearly 60% of India's total horticultural output. (National Horticulture Board (NHB) and Ministry of Agriculture) 2023–24. Ridge gourd cultivation in India covers an area of 9920 ha generating a substantial production of about 3.17 lakh t with a productivity of 31.95 t ha⁻¹. India ranks second globally in vegetable production, occupying 11.35 million hectares with a total annual output of 219.67 million tonnes India ranks second globally in vegetable production, after China, contributing approximately 15–16% of global output (Anonymous, 2024-25) [1]. The cultivated cucurbits, including ridge gourd (*Luffa acutangula*), possess considerable nutritional and medicinal importance. The authors highlighted that ridge gourd fruits are rich in vitamins, minerals, and dietary components beneficial for human health. They also stated that ridge gourd fruits are demulcent, diuretic, and nutritive in nature, while different plant parts are traditionally used in folk medicine for treating various ailments. The study emphasized the importance of cucurbit vegetables as valuable sources of nutrition and health-promoting compounds. Rahman *et al.* (2008) [9]. The fruits are highly nutritious, rich in Vitamin A, C, calcium, phosphorus, ascorbic acid, iron, and carotene. Its consumption is recommended for patients suffering from malaria and seasonal fevers (Gautama *et al.*, 2017) [2]. The pounded leaves are applied locally against haemorrhoids and leprosy, and leaf juice is used ophthalmic ally in children for granular conjunctivitis. India is the second largest producer of vegetables in the world with an annual production of 185 million tonnes from an area of 10.20 million hectares (NHB, 2018–19), with ridge gourd contributing approximately 983 metric tonnes from 90 hectares. The crop improvement programme in ridge gourd depends largely on the extent of genetic diversity present in the germplasm. The authors observed considerable variability among ridge gourd genotypes for growth, flowering, yield, and fruit traits, indicating ample scope for selection and hybridization. The study emphasized that genetically diverse parents could be utilized effectively in breeding programmes to develop superior high-yielding varieties with desirable horticultural characters. Singh *et al.* (2015) [19]. Despite its economic importance and nutritional significance, development of improved varieties and hybrids in ridge gourd has been rather limited. Identification of superior genotypes through genetic diversity analysis from available germplasm is critical for promoting yield and yield-related traits. Cucurbitaceae is the largest vegetable family, consisting of 118 genera and 825 species with two well-defined sub-families and eight tribes. Cucurbits collectively are the largest producers of biological water, easily digestible, and are recommended for patients suffering from weakness or illness (Rai *et al.*, 2008) [10]. Principal Component Analysis (PCA) is a powerful multivariate statistical technique that transforms a large set of correlated variables into a smaller set of uncorrelated components—principal components (PCs)—while retaining maximum variance in the dataset. In crop improvement, PCA serves as a critical tool to identify key traits contributing to maximum variation among genotypes, thereby simplifying the complexity of multi-trait evaluation. Each principal component is a linear combination of original trait variables and the eigenvalue associated with each PC quantifies the proportion of total phenotypic variance it explains. In ridge gourd, evaluating 24 yield and quality traits simultaneously across 56 genotypes generates a high-dimensional dataset where direct interpretation is difficult. PCA condenses this complexity by extracting the most informative axes of variation. PC1 and PC2 together form

the principal biplot space, where genotypes that appear far apart represent maximum phenotypic divergence. Traits with high loadings on PC1 are the primary discriminators of genotypic performance. This information guides breeders to select traits that are most informative for screening diverse germplasm and designing crosses. Several studies in cucurbits have confirmed that PCA-based selection is more efficient than univariate screening, as it simultaneously considers multiple traits and their interrelationships (Singh *et al.*, 2019; Pandey *et al.*, 2020) [16, 7]. Cluster analysis based on Mahalanobis D² statistics groups genotypes into distinct clusters such that intra-cluster variation is minimized while inter-cluster variation is maximized. This technique was introduced by Mahalanobis (1936) [5] and later adapted for plant breeding by Rao (1952) [11], providing a robust framework for quantifying genetic divergence. In practical breeding programs, crossing parents selected from maximally divergent clusters results in higher heterosis in F₁ hybrids and broader genetic variability in segregating populations. For ridge gourd, cluster analysis aids in: (i) grouping related genotypes to avoid redundant crosses, (ii) identifying unique genotypes with exceptional trait means that may serve as superior parents, and (iii) estimating genetic distances between parental lines to predict hybrid performance. The combination of PCA and cluster analysis provides a comprehensive picture of the genetic architecture of a germplasm collection and has been extensively recommended for systematic evaluation of cucurbit diversity (Kumar *et al.*, 2018; Sharma *et al.*, 2021) [3, 15]. The present investigation was therefore undertaken to assess genetic diversity among 56 ridge gourd genotypes using both PCA and D²-based cluster analysis to identify diverse parental combinations for hybrid breeding.

2. Materials and Methods

2.1 Experimental Location and Season

The experiment was conducted at the Vegetable Research Farm, Department of Vegetable Science, C.S. Azad University of Agriculture and Technology, Kalyanpur, Kanpur, Uttar Pradesh, India during the summer (*Zaid*) Season 2024–2026. The experimental site is located in the Indo-Gangetic Plain (latitude 26°28'N, longitude 80°18'E, altitude 126 m above sea level), characterized by a hot semi-arid climate with mean maximum temperatures ranging between 38°C and 42°C during the cropping season, making it ecologically representative for cucurbit cultivation under North Indian conditions.

2.2 Genetic Material and Mating Design

The genetic material comprised 10 diverse parental lines of ridge gourd (*Luffa acutangula*) including Kashi Nanda, Kashi Shivani, VRRG-1, VRRG-4-17, VRRG-6, VRRG-10, VRRG-17-17, VRRG-23, VRRG-25, and VRRG-68. A half-diallel mating design was employed following Griffing (1956) Method II, generating 45 F₁ hybrid combinations [$n(n-1)/2 = 10 \times 9/2 = 45$ crosses]. All 45 F₁ crosses along with one standard commercial check variety, Pusa Nasdar, were evaluated, resulting in a total of 56 experimental genotypes.

2.3 Experimental Design

All 56 genotypes were evaluated in a Randomized Complete Block Design (RCBD) with three replications. Each genotype was grown in plots with a spacing of 3.0 m × 0.60 m (row to row × plant to plant). Standard agronomic practices and plant protection measures were followed uniformly across all replications throughout the crop growth period.

2.4 Observations Recorded

Twenty-four yield and quality traits were recorded for each genotype across replications. Vine growth traits were measured at 30, 45, 60, and 75 days after sowing (DAS). All traits, their full descriptions, units, and abbreviations are summarized in Table 1.

2.5 Statistical Analysis

All 24 traits were subjected to rigorous statistical analyses to assess genetic diversity among the 56 genotypes. The following analytical procedures were adopted:

Analysis of Variance (ANOVA): Mean squares for all traits were computed using standard RCBD ANOVA to establish significant differences among genotypes. The significance of treatment effects was tested at $P \leq 0.05$ and $P \leq 0.01$ probability levels.

Mahalanobis D² Statistic: Genetic divergence among genotypes was quantified using Mahalanobis D² statistics (Mahalanobis, 1936) [5] following Rao (1952) [11]. D² values were computed from the pooled within-group variance-covariance matrix. The D² values represent the squared genetic distance between any two groups and serve as the basis for grouping genotypes into clusters using Tocher's method.

Cluster Analysis: All 56 genotypes were grouped into distinct clusters using Tocher's method (Rao, 1952) [11]. The criterion adopted was that the average intra-cluster D² distance should be smaller than any inter-cluster D² distance. The resulting clusters were characterized by computing cluster means for all 24 traits and the inter-cluster D² distances were presented in a matrix format.

Principal Component Analysis (PCA): PCA was performed on the standardized mean values of all 24 traits to identify the major sources of phenotypic variation. Eigenvalues, proportion of variance explained by each PC, and cumulative proportion of variance were computed. PCs with eigenvalue greater than 1.0 (Kaiser criterion) were considered significant contributors to genetic variation. Trait loadings on significant PCs were used to identify traits that contribute most to genotypic differentiation.

All statistical analyses were performed using R software (version 4.3.1) with packages 'stats', 'FactoMineR', and 'cluster'. Graphical representations including scree plots, biplots, and dendrograms were generated using 'ggplot2' and 'factoextra' packages in R.

3. Results and Discussion

3.1 Principal Component Analysis

Principal Component Analysis was performed on 24 yield and quality traits across 56 ridge gourd genotypes to understand the structure of phenotypic variation and identify major discriminating traits. A total of 24 principal components were extracted. However, only those with eigenvalue > 1 were considered biologically significant. The results of PCA are presented in Table 2 and figure 1. The first principal component (PC1) had the highest standard deviation of 3.5059 and explained 51.21% of the total phenotypic variance. This indicates that more than half of the observed variation among genotypes is attributable to a single major axis of differentiation. The second component (PC2) contributed an additional 8.997% variance, and together PC1 and PC2 accounted for 60.21% of cumulative variance. The first four PCs (PC1–PC4)

cumulatively explained 69.74% of total variation, while the first seven PCs explained 80.12% of variation. A total of four PCs had eigenvalues greater than 1.0 (Kaiser criterion), indicating that they represent statistically meaningful dimensions of trait diversity. The PCA biplot constructed between PC1 (51.214%) and PC2 (8.997%), together explaining (Figure 1) 60.21% of the total phenotypic variation, revealed substantial genetic diversity among the 56 ridge gourd genotypes. Genotypes such as VRRG-68, Kashi Shivani, VRRG-17-17, and VRRG-1 × Kashi Shivani were positioned at the extreme positive end of PC1, indicating their superiority for fruit yield-related traits, as evidenced by trait vectors of fruit length (FL), fruit weight (FW), fruit yield (FY), flesh thickness (FT), and number of secondary branches (NSB) pointing strongly in the same direction. In contrast, parental lines VRRG-1, VRRG-4-17, VRRG-25, VRRG-10, and Kashi Nanda were located at the extreme negative end of PC1 with low PC2 scores, associated with early flowering traits (FIFTY, DFH, DFFFI) and higher TSS and DRM values. Vine growth traits (VLT, VLS, VLSF, VLF) and ascorbic acid content (ASC) projected toward the upper-right quadrant, indicating their positive mutual association and contribution to PC2 variation. The wide scatter of genotypes across all four quadrants confirmed broad genetic diversity, with F₁ hybrids distributed broadly around the centre while parental lines were positioned toward the periphery, highlighting the potential for heterosis and transgressive segregation in crosses involving genotypes from divergent quadrants. The dominance of PC1 in explaining variance suggests the presence of one overriding trait complex likely vine growth and reproductive traits that differentiates genotypes most strongly. The large proportion of variance in PC1 reflects the strong interrelationship among vegetative vigour traits (vine length at 30, 45, 60, 75 DAS; primary and secondary branches; leaf number) and their collective influence on yield potential. PC2 likely represents fruit quality traits such as fruit weight, fruit length, and ascorbic acid content, which are less correlated with vine vigour. These findings are consistent with Saxena *et al.* (2021) [12], who reported that vine-related traits dominated PC1 in cucurbit germplasm evaluation. The scree plot depicting the proportion of variance explained by each PC is illustrated in Figure 1. The scree plot illustrated a sharp decline in the percentage of explained (Figure 2) variance from PC1 (51.2%) to PC2 (9%), followed by a gradual and progressive decrease across the remaining components, with PC3 contributing 5%, PC4 contributing 4.5%, and subsequent PCs each explaining less than 4% of the total variation, confirming that the first two principal components collectively captured the major share of phenotypic diversity among the evaluated ridge gourd genotypes.

3.2 Cluster Analysis

All 56 genotypes were grouped into seven distinct clusters using Tocher's method based on Mahalanobis D² statistics. The composition of clusters in terms of total number of genotypes and the genetic material included in each cluster is presented in Table 3 and figure 2.

The 56 genotypes were distributed among seven clusters with considerable variation in cluster size. Cluster 2 was the largest, comprising 34 genotypes including several F₁ crosses and parental lines such as VRRG-23, VRRG-25, VRRG-4-17, VRRG-6, VRRG-68, and the standard check Pusa Nasdar. Cluster 3 contained 10 genotypes, while Cluster 1 had 7 genotypes. Clusters 5, 6 and 7 were unique with one genotype each (VRRG-23 × VRRG-10; VRRG-1 × Kashi Shivani; and VRRG-68 × VRRG-25, respectively), and Cluster 4 comprised 2

genotypes (VRRG-23 × VRRG-6 and VRRG-4-17 × VRRG-25).

The unequal distribution of genotypes among clusters with the occurrence of singleton clusters (Clusters 5, 6 and 7) and small clusters (Cluster 4) indicates the presence of genetically distinct materials at the extremes of diversity. These singleton genotypes are especially valuable as parental lines because they carry unique trait combinations not represented elsewhere in the germplasm. Similar unequal cluster distribution has been reported in ridge gourd (Kumari *et al.*, 2020) [4] and bitter gourd (Verma *et al.*, 2019) [17], corroborating that diversity in cucurbit germplasm collections tends to be asymmetrically distributed.

3.3 Cluster Mean Values for Yield and Quality Traits

The mean values of all 24 traits for each cluster were computed to characterize clusters and identify those with superior trait combinations for use in hybridization programs. Cluster means are presented in (Table 4. And figure 3.) Cluster 1, comprising 7 genotypes, recorded the highest mean values for vine length at 30 DAS (104.75 cm), vine length at 45 DAS (237.25 cm), vine length at 60 DAS (315.75 cm), vine length at 75 DAS (402.31 cm), number of primary branches (1.30), number of secondary branches (2.06), intermodal length (21.21 cm), sex ratio (34.30), fruit length (23.17 cm), fruit diameter (3.22 cm), fruit weight (120.75 g), number of fruits per vine (14.63), fruit yield (1.85 kg/vine), ascorbic acid content (5.31 mg/100g), shelf life (6.66 days), and flesh thickness (11.28 cm). This cluster also recorded the earliest male flower initiation (33.50 days) and earliest days to 50% flowering (42.65 days), further indicating its superior agricultural performance. Cluster 4, with 2 genotypes (VRRG-23 × VRRG-6 and VRRG-4-17 × VRRG-25), recorded the highest TSS (4.99 °Brix) and dry matter content (9.87%), along with the lowest fruit yield traits, indicating its value as a quality-specific resource. Cluster 6 (singleton: VRRG-1 × Kashi Shivani) had the lowest values across most vegetative and yield traits, positioning it as the most divergent cluster from Cluster 1. This extreme divergence from the high-yielding Cluster 1 makes Cluster 6 genotypes potential donors for novel trait combinations when crossed with Cluster 1 genotypes.

3.4 Inter-Cluster Distances

The Mahalanobis D^2 inter-cluster distances were computed to quantify genetic distances between all pairs of clusters. These values are presented in the matrix format in Table 5 and figure 4. Higher inter-cluster distances indicate greater genetic divergence and greater potential for exploitation of heterosis in crosses between genotypes from those clusters. The maximum inter-cluster distance was observed between Clusters 1 and 4 ($D^2 = 3456.79$), suggesting that these two clusters are the most genetically divergent. This finding has direct implications for hybrid breeding: crosses between high-yielding genotypes of Cluster 1 (e.g., Kashi Nanda, VRRG-68 × VRRG-10) and Cluster 4 genotypes (VRRG-23 × VRRG-6, VRRG-4-17 × VRRG-25) are expected to exhibit maximum heterosis for yield and quality traits. The second largest inter-cluster distance was between Clusters 1 and 6 ($D^2 = 2152.26$), followed by Clusters 1 and 3 ($D^2 = 1920.97$). Minimum inter-cluster distance was observed between Clusters 2 and 5 ($D^2 = 408.91$), indicating close genetic affinity between these groups and suggesting that crosses within them would yield limited genetic variability. These results highlight that breeders should prioritize crosses between Cluster 1 and Clusters 4 or 6, while avoiding crosses between Clusters 2 and 5 for diversity-based selection. Similar patterns of high inter-cluster distances between divergent

clusters have been reported in ridge gourd by Prajapati *et al.* (2019) [8] and in other cucurbits by Sharma *et al.* (2020) [14], reinforcing that D^2 -based cluster analysis reliably identifies genetically distant materials suitable for hybridization programs. The intra-cluster distances (diagonal elements) were zero, conforming to Tocher's clustering criterion where genotypic similarity within clusters is maximized. The genetic diversity assessment of 56 ridge gourd genotypes using PCA and cluster analysis in the present study revealed substantial phenotypic variation that is amenable to exploitation in breeding programs. The dominance of PC1 in explaining 51.21% of total variance underscores the strong contribution of vegetative growth and vigor traits to overall genotypic differentiation. This is ecologically meaningful because vine vigor directly influences light interception, photosynthetic capacity, and ultimately fruit yield in climbing cucurbit crops. The finding aligns with reports in cucumber (Pandey *et al.*, 2020) [7], bottle gourd (Singh *et al.*, 2019) [16], and bitter gourd (Kumar *et al.*, 2018) [3], where vine-related traits consistently emerged as the primary contributors to PCA variation. The identification of seven clusters with highly unequal sizes reflects the genetic structure typical of cultivated cucurbit germplasm, where elite lines tend to cluster together in large groups while unique or exotic materials remain isolated. The large Cluster 2 (34 genotypes), which includes the commercial check Pusa Nasdar, represents the 'core' cultivated gene pool with moderate performance across all traits. In contrast, Cluster 1 (7 genotypes) represents the high-yielding elite group with superior fruit yield (1.85 kg/vine), the highest fruit weight (120.75 g), and earliest harvest dates. These genotypes from Cluster 1 are therefore the most promising candidates for direct selection in yield improvement programs. The maximum inter-cluster D^2 distance between Clusters 1 and 4 ($D^2 = 3456.79$) has significant practical implications. Genotypes from these two divergent clusters differ not only in vegetative traits but also in fruit quality parameters (TSS, DRM, ascorbic acid content), suggesting that crosses between them would generate F_2 populations with broad-spectrum variability for simultaneous selection of yield and quality traits. Such crosses, particularly between Cluster 1 elite genotypes (Kashi Nanda, VRRG-68 × VRRG-10) and Cluster 4 quality-superior genotypes (VRRG-4-17 × VRRG-25), may be explored for developing high-yielding, quality-rich ridge gourd hybrids. The singleton clusters (Clusters 5, 6 and 7) deserve special mention. VRRG-68 × VRRG-25 (Cluster 7), VRRG-23 × VRRG-10 (Cluster 5), and VRRG-1 × Kashi Shivani (Cluster 6) are genetically unique and would introduce novel alleles when used in crosses with mainstream genotypes from Clusters 1 or 2. Their low inter-cluster distances with Clusters 2 and 3 relative to Cluster 1 suggest they represent divergent derivatives from the main cultivated gene pool and may carry favourable recessive alleles for specific traits. Such genotypes are particularly valuable in recurrent selection or back-cross breeding programs aimed at introgressing specific quality traits into high-yielding backgrounds. The present findings corroborate several earlier studies on genetic diversity in Luffa species. Kumari *et al.* (2020) [4] reported seven clusters among ridge gourd genotypes with maximum inter-cluster distance between extreme clusters, recommending crosses between diverse cluster members for yield improvement. Similarly, Prajapati *et al.* (2019) [8] emphasized the use of D^2 statistics for identifying genetically divergent parents in ridge gourd diallel breeding. The use of half-diallel F_1 hybrids in the present study, rather than pure parental lines alone, provides a richer diversity profile by capturing both additive and dominance genetic effects, thereby

giving more realistic estimates of the diversity spectrum available for selection. In conclusion, the multivariate analysis using PCA and cluster analysis has successfully delineated the genetic architecture of the 56 ridge gourd genotypes under study. Cluster 1 genotypes represent superior parents for yield,

while Clusters 4 and 6 offer contrasting trait profiles for quality improvement. Crosses between Clusters 1 and 4 are most likely to yield productive and genetically diverse segregating populations for development of improved ridge gourd varieties and hybrids.

Table 1: Abbreviations and description of traits recorded

Abbrev.	Full Name	Abbrev.	Full Name
VLT	Vine Length at 30 DAS (cm)	VLF	Vine Length at 45 DAS
VLS	Vine Length at 60 DAS	VLSF	Vine Length at 75 DAS
NPB	No. of Primary Branches	NSB	No. of Secondary Branches
NNPB	Nodes per Branch	NLP	No. of Leaves per Plant
IL	Internodal Length (cm)	DFMFI	Days to 1st Male Flower Init.
DFFFI	Days to 1st Female Flower Init.	FIFTY	Days to 50% Flowering
SR	Sex Ratio	DFH	Days to First Harvest
FL	Fruit Length (cm)	FD	Fruit Diameter (cm)
FW	Fruit Weight (g)	NFPV	No. of Fruits per Vine
FY	Fruit Yield (kg/vine)	ASC	Ascorbic Acid (mg/100g)
TSS	Total Soluble Solids (°Brix)	DRM	Dry Matter Content (%)
SLF	Shelf Life (days)	FT	Flesh Thickness (cm)

Table 2: Principal Component Analysis of 24 Yield and Quality Traits in Ridge Gourd (*Luffa acutangula*) Genotypes

Principal Component	Standard Deviation	Proportion of Variance (%)	Cumulative Proportion (%)
PC1	3.5059	51.214	51.214
PC2	1.4695	8.997	60.211
PC3	1.0977	5.020	65.231
PC4	1.0398	4.505	69.736
PC5	0.9541	3.793	73.529
PC6	0.9314	3.614	77.143
PC7	0.8455	2.979	80.122
PC8	0.7816	2.545	82.667
PC9	0.7734	2.492	85.160
PC10	0.7550	2.375	87.535
PC11	0.6853	1.957	89.492
PC12	0.6596	1.813	91.304
PC13	0.6105	1.553	92.858
PC14	0.5368	1.201	94.058
PC15	0.5050	1.063	95.121
PC16	0.4789	0.956	96.077
PC17	0.4479	0.836	96.913
PC18	0.4308	0.773	97.686
PC19	0.4007	0.669	98.355
PC20	0.3489	0.507	98.862
PC21	0.2929	0.358	99.219
PC22	0.2788	0.324	99.543
PC23	0.2572	0.276	99.819
PC24	0.2086	0.181	100.000

Table 3: Cluster Composition of 56 Ridge Gourd Genotypes Based on Mahalanobis D² Statistics

Cluster	No. of Genotypes	Genetic Material
1	7	Kashi Nanda, Kashi Shivani × Kashi Nanda, Kashi Shivani × VRRG-68, VRRG-23 × VRRG-17-17, VRRG-1 × Kashi Nanda, VRRG-23 × Kashi Nanda, VRRG-68 × VRRG-10
2	34	Kashi Nanda × VRRG-25, Kashi Nanda × VRRG-6, Kashi Nanda × VRRG-68, Kashi Shivani × VRRG-6, Kashi Shivani × VRRG-10, Kashi Shivani × VRRG-17-17, Kashi Shivani × VRRG-25, Pusa Nasdar, VRRG-1 × VRRG-4-17, VRRG-1 × VRRG-10, VRRG-1 × VRRG-17-17, VRRG-23, VRRG-6, VRRG-68 and others (34 total)
3	10	Kashi Nanda × VRRG-10, Kashi Shivani, VRRG-1, VRRG-10, VRRG-17-17 × VRRG-10, VRRG-17-17 × VRRG-6, VRRG-23 × VRRG-68, VRRG-25 × VRRG-10, VRRG-4-17 × Kashi Nanda, VRRG-6 × VRRG-10
4	2	VRRG-23 × VRRG-6, VRRG-4-17 × VRRG-25
5	1	VRRG-23 × VRRG-10
6	1	VRRG-1 × Kashi Shivani
7	1	VRRG-68 × VRRG-25

Table 4: Cluster Mean Values for 24 Yield and Quality Traits in Ridge Gourd Genotypes

Trait	C1	C2	C3	C4	C5	C6	C7
VLТ	104.75	93.38	92.44	87.54	92.34	61.74	98.64
VLF	237.25	191.93	167.91	150.24	150.24	93.68	200.13
VLS	315.75	287.33	278.45	261.45	309.12	192.25	289.31
VLSF	402.31	362.43	358.86	331.24	345.67	317.20	371.24
NPB	1.30	0.93	0.95	0.71	0.81	0.47	1.13
NSB	2.06	1.55	1.60	1.40	1.91	1.21	1.77
NNPB	40.24	35.62	37.43	37.41	33.26	32.91	38.81
NLP	47.50	44.35	43.28	40.00	40.50	38.05	41.20
IL	21.21	18.50	18.40	16.00	18.20	15.55	19.17
DFMFI	33.50	37.56	37.25	40.12	39.10	37.25	39.50
DFFFI	38.19	41.34	41.44	44.70	44.30	45.25	38.70
FIFTY	42.65	45.39	46.16	51.24	49.00	49.41	45.70
SR	34.30	31.52	30.43	27.00	28.60	26.60	28.30
DFH	47.89	51.68	52.63	57.45	49.70	55.62	53.10
FL	23.17	18.51	19.35	16.50	22.10	16.89	20.70
FD	3.22	2.92	2.88	2.21	2.70	2.50	2.90
FW	120.75	99.01	101.77	114.70	104.20	90.71	111.20
NFPV	14.63	13.78	13.63	13.00	13.80	11.93	13.70
FY	1.85	1.46	1.47	1.32	1.55	1.26	1.22
ASC	5.31	4.93	4.82	3.89	5.35	3.63	4.75
TSS	3.81	4.58	4.56	4.99	4.37	4.95	4.52
DRM	6.83	8.40	8.08	9.87	7.86	8.76	9.35
SLF	6.66	3.47	5.05	6.20	4.00	3.60	4.90
FT	11.28	7.81	8.65	6.20	9.40	6.85	6.40

Table 5: Mahalanobis D² Inter-Cluster Distance Matrix Among Seven Clusters of Ridge Gourd Genotypes

Cluster	1	2	3	4	5	6	7
1	—	1103.47	1920.97	3456.79	1183.69	2152.26	1449.74
2	1103.47	—	547.12	1098.26	408.91	714.13	424.36
3	1920.97	547.12	—	860.42	423.77	1048.83	443.41
4	3456.79	1098.26	860.42	—	1205.72	800.42	1076.76
5	1183.69	408.91	423.77	1205.72	—	1181.57	521.22
6	2152.26	714.13	1048.83	800.42	1181.57	—	486.63
7	1449.74	424.36	443.41	1076.76	521.22	486.63	—

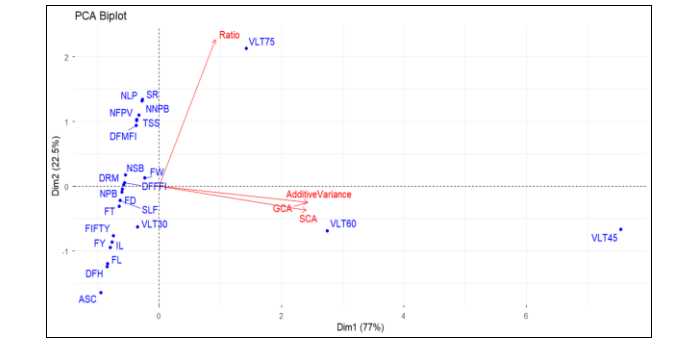


Fig 1: Principal Component Analysis of 24 Yield and Quality Traits in Ridge Gourd (*Luffa acutangula*) Genotypes

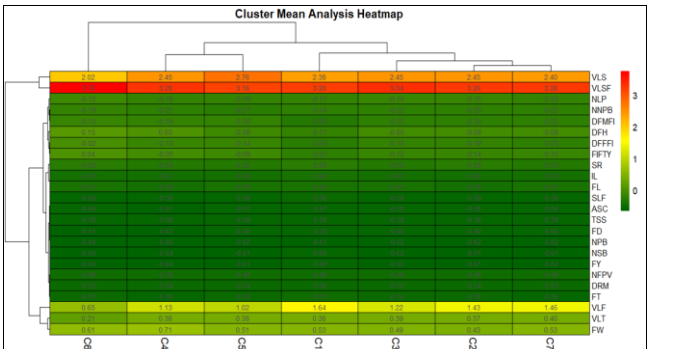


Fig 3: Cluster Mean Values for 24 Yield and Quality Traits in Ridge Gourd Genotypes

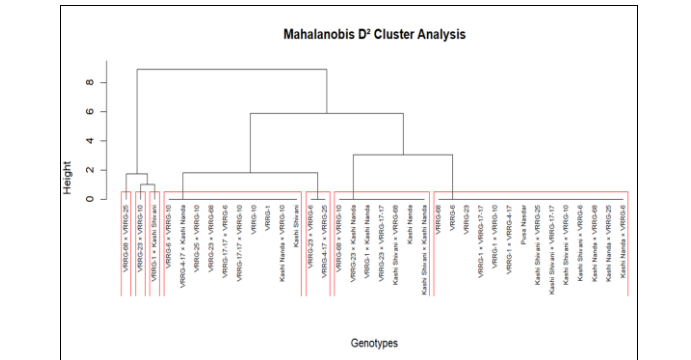


Fig 2: Cluster Composition of 56 Ridge Gourd Genotypes Based on Mahalanobis D² Statistics

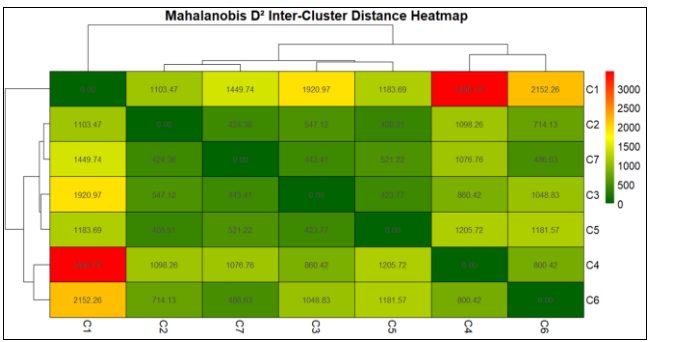


Fig 4: Mahalanobis D² Inter-Cluster Distance Matrix Among Seven Clusters of Ridge Gourd Genotypes

Conclusion

The genetic diversity among 56 ridge gourd genotypes using Principal Component Analysis (PCA) and Mahalanobis D² cluster analysis revealed substantial phenotypic variability for yield and quality traits. PCA identified four major principal components with eigenvalues greater than one, collectively accounting for a major proportion of total variation. The first principal component alone explained 51.21% of the total variance, indicating that vegetative growth and yield-contributing traits were the primary determinants of genotypic differentiation. The PCA biplot further demonstrated wide dispersion of genotypes, confirming the presence of broad genetic diversity within the experimental material. Cluster analysis grouped the genotypes into seven distinct clusters with unequal distribution, indicating varying degrees of genetic divergence among the genotypes. Cluster 1 was identified as the most superior cluster for yield and related traits, recording higher mean values for vine growth, branching, fruit length, fruit weight, number of fruits per vine, fruit yield, and ascorbic acid content along with early flowering behaviour. In contrast, Cluster 4 exhibited superior quality attributes such as higher TSS and dry matter content, while singleton clusters represented highly divergent and unique genotypes possessing valuable trait combinations. The maximum inter-cluster distance observed between Clusters 1 and 4 indicated a high degree of genetic divergence and suggested strong potential for exploitation of heterosis through hybridization between genotypes belonging to these clusters. Crosses involving elite high-yielding genotypes from Cluster 1 and quality-oriented genotypes from Cluster 4 may therefore generate superior segregants combining high yield with desirable fruit quality traits. Overall, the study demonstrated that multivariate analysis is an effective approach for assessing genetic diversity and identifying promising parental combinations in ridge gourd. The identified divergent and superior genotypes can be effectively utilized in future breeding programmes aimed at developing high-yielding, early, and quality-rich ridge gourd hybrids and varieties.

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