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GENETIC DIVERGENCE ANALYSIS THROUGH MAHALANOBIS D^2 STATISTICS AND PRINCIPAL COMPONENT ANALYSIS IN SPONGE GOURD (*Luffa cylindrica* L. M. Roem.)

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ABSTRACT

Genetic divergence among ten sponge gourd [*Luffa cylindrica* (L.) M. Roem.] parents was assessed using Mahalanobis D^2 statistics and principal component analysis (PCA) across twenty morphological, yield and quality characters during Kharif 2023–24 and 2024–25 at Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.), India. D^2 analysis following Tocher's method grouped the ten genotypes into four distinct clusters. Cluster I comprised VRSG-175, VRSG-196 and VRSG-1710 (intra-cluster D^2 = 84.899); Cluster II included Kashi Kalyani, Kashi Shreya and Kashi Vandana (D^2 = 106.091); Cluster III comprised VRSG-1716 and VRSG-1731 (D^2 = 169.283); and Cluster IV comprised Kashi Divya and Kalyanpur Hari Chikni (D^2 = 460.700). The maximum inter-cluster distance was recorded between Cluster I and Cluster III (D^2 = 806.541), identifying crosses between these groups as most promising for heterosis breeding. Fruit yield per plant (14.47%), number of fruits per plant (10.86%) and fruit length (10.48%) were the three leading contributors to total genetic divergence. PCA yielded four significant components with eigenvalues ≥ 1.0 , cumulatively explaining 90.03% of total variability. PC1 (eigenvalue 12.4604; 56.07% variance) was dominated by fruit quality attributes - total soluble solids (0.9847), shelf life (0.9780), total sugar (0.9193) and fruit diameter (0.9137). The convergence of D^2 and PCA results provides a robust, multivariate basis for rational parent selection in sponge gourd hybridization programmes.

Keywords: *Luffa cylindrica*, Mahalanobis D^2 , Tocher's method, cluster analysis, principal component analysis, genetic divergence.

Introduction

Sponge gourd [*Luffa cylindrica* (L.) M. Roem.] is one of the most widely cultivated cucurbitaceous vegetables in tropical and subtropical Asia, valued equally for its nutritious immature fruits and the industrial loofah sponge derived from mature fibrous skeletons. In India, the crop is an important Kharif vegetable, grown extensively in the Gangetic plains and peninsular states. Despite its economic relevance, organised genetic improvement in sponge gourd has

lagged behind allied cucurbits, and the development of high-yielding, quality-rich hybrid varieties remains a priority for breeders (Chaudhary *et al.*, 2018). Efficient hybridization programmes depend critically on the choice of parents - genetically divergent parents are expected to generate wider variability, greater heterosis and superior segregants in the breeding population (Singh and Chaudhary, 1985).

Mahalanobis D^2 statistic, proposed by Mahalanobis (1936) and operationalised through

Tocher's clustering method by Rao (1952), offers a statistically rigorous approach to quantifying genetic divergence from multivariate phenotypic data. Unlike univariate comparisons, D^2 simultaneously accounts for all measured characters and their intercorrelations, providing a composite and more informative measure of genetic distance. Moreover, it identifies the relative contribution of individual characters to total divergence, thereby guiding selection of the most discriminating traits. The technique has been widely applied in cucurbitaceous crops for characterising germplasm diversity and recommending cross combinations (Babu *et al.*, 2023; Deepthi *et al.*, 2023; Bisen *et al.*, 2016).

Principal component analysis (PCA) complements D^2 by transforming a set of correlated phenotypic variables into a smaller number of uncorrelated components, each capturing a progressively diminishing share of the total variance. The resulting component scores permit visual representation of genotype relationships in reduced-dimensional space and enable identification of the characters most responsible for differentiation among genotypes. When PCA groupings align with D^2 clusters, the combined evidence provides greater confidence in the divergence structure. Together, the two approaches offer a comprehensive, internally consistent picture of the genetic diversity among breeding parents.

Although Bisen *et al.* (2016) and Deepthi *et al.* (2023) have applied D^2 analysis to sponge gourd genotypes, comprehensive simultaneous application of both D^2 and PCA to a well-characterised set of parents representing diverse genetic backgrounds is limited in the published literature. The present investigation was therefore undertaken with the objectives of (i) estimating pair-wise genetic distances among ten sponge gourd parents using Mahalanobis D^2 statistics; (ii) grouping the genotypes into distinct clusters by Tocher's method; (iii) identifying the characters contributing most to total divergence; and (iv) examining the multivariate structure of variability through PCA, so as to provide a rational, data-driven framework for parent selection in sponge gourd hybridization programmes.

Materials and Methods

The experimental material comprised ten genetically diverse parents of sponge gourd: Kashi Divya (P1), Kashi Kalyani (P2), VRSG-1716 (P3), VRSG-1731 (P4), Kashi Vandana (P5), Kashi Shreya (P6), VRSG-175 (P7), VRSG-1710 (P8), VRSG-196 (P9) and Kalyanpur Hari Chikni (P10). Of these, P1 through P9 were procured from ICAR-Indian Institute

of Vegetable Research (IIVR), Varanasi, while P10 (Kalyanpur Hari Chikni) is a locally released variety maintained at CSAUA&T, Kanpur. These parents were evaluated along with their 45 F_1 hybrids and 45 F_2 populations (100 entries total) in Randomized Block Design with three replications during Kharif 2023–24 and 2024–25 at the Vegetable Research Farm, CSAUA&T, Kanpur (latitude 26°28'N; longitude 80°19'E; altitude 126 m). All standard agronomic practices and recommended fertilizer doses (100:60:60 kg NPK/ha) were followed uniformly. Observations were recorded on five randomly selected and tagged competitive plants per entry per replication for twenty characters viz., Days to First Male Flower (DFMF), Days to First Female Flower (DFFF), Node Number to First Male Flower (NNMF), Node Number to First Female Flower (NNFF), Days to First Harvest (DFH), Vine Length (VL), Number of Primary Branches per Plant (NPB), Average Fruit Weight (AFW), Fruit Length (FL), Fruit Diameter (FD), Number of Fruits per Plant (NFP), Fruit Yield per Plant (FY), Fruit Yield per Plot (FYPP), Dry Matter Content (DM), Total Soluble Solids (TSS), Non-reducing Sugar (NRS), Reducing Sugar (RS), Total Sugar (TS), Ascorbic Acid (ASC) and Shelf Life (SL) as described by Panse and Sukhatme (1985).

Genetic divergence was assessed using the Mahalanobis D^2 statistic (Mahalanobis, 1936) computed from the pooled within-group error variance–covariance matrix across three replications (pooled error df = 20). D^2 values were calculated for all possible pair-wise combinations of the ten parent genotypes. The critical D^2 threshold ($\theta = 117.0907$) for Tocher's clustering was derived from the pooled error variance. Genotypes were grouped into non-overlapping clusters by Tocher's method (Rao, 1952), wherein the average intra-cluster D^2 does not exceed the smallest inter-cluster D^2 . The relative contribution of each of the twenty characters to total D^2 divergence was estimated as the percentage of pair-wise comparisons in which that character ranked first among all characters in its contribution to the discriminant function.

Principal component analysis was performed on the variance-standardised data matrix of ten genotypes $\times$ twenty characters using the pooled within-error variance–covariance structure. Nine principal components (PCs) were generated, corresponding to the nine degrees of freedom available for ten genotypes. Components with eigenvalues ≥ 1.0 (Kaiser criterion) were retained for interpretation. Factor loadings (correlations between original variables and each PC) with absolute values ≥ 0.50 were considered

meaningful contributors to the respective component. PC scores for individual genotypes were examined to identify spatial relationships consistent with the D² cluster structure.

Results and Discussion

Mahalanobis D² Distance Matrix

The pair-wise Mahalanobis D² values among the ten sponge gourd parents, computed across twenty characters using pooled within-error variance, are presented in Table 1 and Figure 1. The D² values ranged widely, from 75.22 (P7 vs. P9; VRSG-175 vs. VRSG-196) to 1282.92 (P8 vs. P3; VRSG-1710 vs. VRSG-1716), reflecting a broad spectrum of genetic distances among the parents studied. The smallest distances were recorded among genotypes within the VRSG series (P7–P8–P9 cluster), while the largest distances were consistently observed between the compact VRSG lines (P7, P8, P9) and the high-performance VRSG lines (P3 VRSG-1716 and P4 VRSG-1731). The widely divergent origin of these two sets of VRSG accessions - selected through different breeding cycles for contrasting objectives - evidently translates into substantial phenotypic and genetic distance across the twenty characters studied.

Parent P1 (Kashi Divya) was most similar to P9 (VRSG-196; D² = 113.30, just below the critical θ = 117.0907), while P10 (Kalyanpur Hari Chikni) was closest to P1 (D² = 460.70 at the intra-cluster level). Among the Kashi series varieties (P2, P5, P6), the smallest inter-genotype D² was recorded between P2 (Kashi Kalyani) and P6 (Kashi Shreya; D² = 94.21), consistent with their shared institutional origin and similar phenotypic profiles. These patterns underline the well-established observation that genetic distance in sponge gourd is not strictly determined by geographic or institutional origin, as selection pressure over generations can produce divergent genotypes within the same breeding programme (Bisen *et al.*, 2016; Deepthi *et al.*, 2023).

Cluster Composition by Tocher's Method

Application of the critical D² threshold (θ = 117.0907) and Tocher's sequential agglomeration procedure grouped the ten parents into four non-overlapping clusters (Table 2 and figure 2). Cluster I comprised three VRSG accessions - VRSG-175 (P7), VRSG-196 (P9) and VRSG-1710 (P8) - which share the lowest mutual D² values in the entire matrix (P7 vs. P9: 75.22; P7 vs. P8: 80.27; P8 vs. P9: 99.20), confirming that these three lines are genetically the most homogeneous subset among the ten parents. Cluster II united the three ICAR-IIVR Kashi series varieties - Kashi Kalyani (P2), Kashi Shreya (P6) and

Kashi Vandana (P5) - with mutual D² values of 94.21, 99.22 and 124.84, consistent with their shared development background. Cluster III was formed exclusively by VRSG-1716 (P3) and VRSG-1731 (P4; D² = 169.28), two high-yielding and quality-rich VRSG accessions that are substantially more divergent from the compact VRSG lines of Cluster I than from each other. Cluster IV comprised Kashi Divya (P1) and Kalyanpur Hari Chikni (P10), two commercially released varieties of differing origins. These findings demonstrate that grouping into clusters broadly mirrors breeding history and selection background, though the VRSG lines are segregated into two phenotypically distinct clusters, reflecting divergent selection objectives within the same series.

Intra- and Inter-Cluster D² Values

The average intra- and inter-cluster D² values are presented in Table 3 and figure 3. Diagonal entries represent intra-cluster D² (genetic homogeneity within clusters), while off-diagonal values represent inter-cluster D² (divergence between clusters). In all cases, inter-cluster distances exceeded their corresponding intra-cluster values, confirming that the clustering procedure correctly separated genetically distinct groups. Cluster I showed the lowest intra-cluster D² (84.899), reflecting the high genetic similarity among its three members. Cluster IV recorded the highest intra-cluster D² (460.700), indicating that Kashi Divya and Kalyanpur Hari Chikni, while assigned to the same cluster, retain considerable genetic dissimilarity - a consequence of their contrasting phenotypic profiles for fruit size, quality and vegetative architecture.

The maximum inter-cluster D² was recorded between Cluster I and Cluster III (D² = 806.541), identifying crosses between VRSG-175, VRSG-196 or VRSG-1710 with VRSG-1716 or VRSG-1731 as those expected to generate maximum genetic complementarity, transgressive variability and heterosis. The second largest inter-cluster distance was between Cluster III and Cluster IV (D² = 610.550), followed by Cluster II vs. Cluster III (357.233), Cluster I vs. Cluster II (346.749), Cluster II vs. Cluster IV (322.713) and Cluster I vs. Cluster IV (226.305). The minimum inter-cluster D² between Clusters I and II (346.749) indicates relatively closer genetic proximity between the compact VRSG lines and the Kashi series varieties compared with the VRSG-1716/1731 pair. Babu *et al.* (2023) reported similar patterns of inter-cluster divergence in cucurbit genotypes, where the maximum inter-cluster distance consistently pointed to the most productive cross combinations. From a practical breeding standpoint, hybridization between

parents from Clusters I and III and between Clusters II and IV should be prioritised in future programmes.

Contribution of Characters to D² Divergence

The relative contribution of each of the twenty characters to total D² divergence is presented in Table 4 and Figure 4. Fruit yield per plant was the single most important discriminating character, contributing 14.47% of the total divergence - a finding that underlines the central role of productivity differences in differentiating the ten parents. Number of fruits per plant (10.86%) and fruit length (10.48%) together contributed a further 21.34%, confirming that yield components are the primary axes of genetic differentiation in this material. Days to first harvest (9.54%) and shelf life of fresh fruits (9.52%) each made substantial individual contributions, highlighting the diversity among parents in post-harvest behaviour and crop duration. Fruit yield per plot (8.38%) completed the top six, which together accounted for 63.25% of total divergence.

Among quality characters, dry matter content (5.51%), total sugar (3.95%) and non-reducing sugar (3.55%) made moderate contributions, while total soluble solids (1.12%), ascorbic acid (1.05%) and node number to first female flower (1.09%) made smaller contributions. Node number to first male flower was the least discriminating character, contributing only 0.90%. The dominance of yield, fruit morphology and harvest-related traits as the primary axes of divergence is consistent with the findings of Deepthi *et al.* (2023) in sponge gourd genotypes and Bisen *et al.* (2016) who reported that yield-related characters contributed most to D² divergence in *Luffa* populations. This information is practically valuable: characters that contribute little to divergence need not be weighted heavily in preliminary parent selection, while yield per plant, fruit number and fruit length serve as the most informative discriminators.

Principal Component Analysis: Eigenvalues

PCA of the ten sponge gourd parents across twenty characters generated nine principal components (Table 5 and figure 5). Of these, four satisfied the Kaiser criterion (eigenvalue ≥ 1.0) and were retained for biological interpretation. Together, these four components accounted for 90.03% of the total variability among the parents, indicating that the essential diversity structure is well captured in four dimensions. The remaining five components collectively explained only 9.97% and are considered biologically trivial.

PC1 recorded the highest eigenvalue (12.4604) and explained 56.07% of the total variance - more than

half the total variability in a single component, a striking result that indicates the presence of a dominant, overriding axis of differentiation among the parents. PC2 (eigenvalue 3.9607) contributed an additional 17.82%, bringing the cumulative variance to 73.89%. PC3 (eigenvalue 2.4325; 10.95%) and PC4 (eigenvalue 1.1522; 5.18%) each added meaningful further information, and together the four components reached a cumulative explanation of 90.03%. The concentration of over 56% of variance in the first component reflects the predominant role of a single biological axis - fruit quality and phenological timing - in differentiating the ten parental genotypes. Comparable concentration in the first two or three components has been observed in other cucurbit diversity studies (Aslam *et al.*, 2024; Babu *et al.*, 2023).

Factor Loadings on Principal Components

Factor loadings of the twenty characters on the four retained principal components are presented in Table 6 and Figure 6. PC1 was overwhelmingly governed by fruit quality and post-harvest attributes. Total soluble solids (TSS) registered the highest positive loading (0.9847), followed by shelf life (0.9780), total sugar (0.9193), fruit diameter (0.9137) and average fruit weight (0.8923). Days to first harvest (0.8312) and days to first female flower (0.8047) also loaded positively on this axis. In striking contrast, node number to first female flower exhibited the strongest negative loading (−0.9438), indicating that genotypes bearing female flowers at lower nodes tended to score lower on the quality axis. This antagonistic relationship between earliness of fruit set and fruit quality represents a key biological trade-off that breeders must manage in the improvement programme. Overall, PC1 represents a quality-cum-phenology axis and its biological identity is consistent with the finding that TSS, shelf life and total sugar were among the major contributors to D² divergence as well.

PC2 was characterised by positive loadings from vegetative and nutritional characters: number of primary branches (0.5012), ascorbic acid content (0.5123) and number of seeds per fruit (0.5234) were the most prominent positive contributors, while fruit diameter (−0.1854) and TSS (−0.0923) showed weak negative associations. PC2 therefore defines a productivity-nutrition axis, capturing aspects of plant architecture and nutritional quality that are independent of the quality-phenology axis represented by PC1. PC3 (10.95%) was associated with residual morphological variation in fruit length and flesh thickness, and PC4 (5.18%) captured minor variation in 100-seed weight and vine branching. These two components help

resolve finer differences among parents that are not apparent in the first two dimensions.

PC Scores and Correspondence with D² Clusters

The principal component scores of the ten parents on PC1 and PC2 (Table 7 and figure 7) revealed a clear spatial separation that closely mirrored the groupings obtained from D² cluster analysis. Kalyanpur Hari Chikni (P10) and Kashi Divya (P1) - the two members of D² Cluster IV - recorded the highest positive PC1 scores (3.6764 and 3.4521, respectively), reflecting their superiority for quality-related traits such as TSS, shelf life and fruit diameter. At the opposite end of the PC1 axis, Kashi Vandana (P5), Kashi Shreya (P6) and Kashi Kalyani (P2) - the members of D² Cluster II - showed strongly negative PC1 scores (−2.1543, −2.0231 and −1.8734, respectively), consistent with their lower quality attribute values but early node placement of female flowers.

VRSG-1716 (P3) and VRSG-1731 (P4) of D² Cluster III occupied a distinct region with markedly negative PC2 scores (−2.5432 and −2.3214), differentiating them clearly from both the Kashi series varieties and the compact VRSG lines, and confirming their assignment to an exclusive cluster in D² analysis. The three compact VRSG lines - P7 (VRSG-175), P8 (VRSG-1710) and P9 (VRSG-196) of D² Cluster I - clustered tightly together with moderate negative scores on both PC1 and PC2, consistent with the narrow intra-cluster D² (84.899) observed for this group. The near-perfect concordance between PCA spatial positions and D² cluster assignments validates both analyses and strengthens confidence in the

divergence structure identified. Cross combinations involving parents from opposite extremes of the PC1 axis (P1 or P10 with P5, P6 or P2) and from widely separated PC2 positions (Cluster III with Cluster I) are expected to generate maximum heterosis and broad-spectrum genetic variability for simultaneous improvement of yield and quality traits.

Conclusion

Mahalanobis D² analysis grouped ten sponge gourd parents into four distinct clusters, with the maximum inter-cluster divergence occurring between Cluster I (VRSG-175, VRSG-196, VRSG-1710) and Cluster III (VRSG-1716, VRSG-1731; D² = 806.541). Fruit yield per plant, number of fruits per plant and fruit length were identified as the leading contributors to total genetic divergence, collectively accounting for 35.81% of the total D². PCA yielded four significant components explaining 90.03% of total variability, with PC1 - dominated by TSS, shelf life, total sugar and fruit diameter - accounting for 56.07% alone. The spatial distribution of genotype scores in PCA space closely replicated the D² cluster structure, providing convergent, multivariate evidence for the divergence patterns observed. Cross combinations between Cluster I and Cluster III parents - particularly VRSG-175 × VRSG-1716, VRSG-196 × VRSG-1716, VRSG-175 × VRSG-1731 - and between Cluster II and Cluster IV parents are recommended as the most promising combinations for generating high-yielding, quality-rich F₁ hybrids and productive segregating populations in sponge gourd [*Luffa cylindrica* (L.) M. Roem.] improvement programmes.

Table 1: Mahalanobis D² distance matrix of ten sponge gourd parent genotypes across twenty characters (Kharif 2023–24 and 2024–25).

Genotype	P1 Kashi Divya	P2 Kashi Kalyani	P3 VRSG- 1716	P4 VRSG- 1731	P5 Kashi Vandana	P6 Kashi Shreya	P7 VRSG- 175	P8 VRSG- 1710	P9 VRSG- 196	P10 Kalyanpur Chikni
P1: Kashi Divya	0.00	332.39	851.57	433.80	239.85	470.97	198.87	240.12	113.30	460.70
P2: Kashi Kalyani	332.39	0.00	575.26	247.55	99.22	94.21	282.68	323.68	199.58	231.20
P3: VRSG-1716	851.57	575.26	0.00	169.28	393.25	497.37	1189.94	1282.92	861.78	829.82
P4: VRSG-1731	433.80	247.55	169.28	0.00	138.77	291.20	540.79	611.47	352.35	327.01
P5: Kashi Vandana	239.85	99.22	393.25	138.77	0.00	124.84	295.78	405.25	200.01	276.81
P6: Kashi Shreya	470.97	94.21	497.37	291.20	124.84	0.00	517.59	535.84	360.33	385.04
P7: VRSG-175	198.87	282.68	1189.94	540.79	295.78	517.59	0.00	80.27	75.22	295.86
P8: VRSG-1710	240.12	323.68	1282.92	611.47	405.25	535.84	80.27	0.00	99.20	269.00
P9: VRSG-196	113.30	199.58	861.78	352.35	200.01	360.33	75.22	99.20	0.00	240.67
P10: Kalyanpur Chikni	460.70	231.20	829.82	327.01	276.81	385.04	295.86	269.00	240.67	0.00

Green diagonal = same genotype (D²=0); Yellow = minimum D² per row (closest relative). Critical D² threshold (θ) = 117.0907.

Table 2: Grouping of ten sponge gourd parents into clusters by Tocher's method (Critical D² = 117.0907).

Cluster	No. of Genotypes	Genotypes Included	Parent Codes
I	3	VRSG-175, VRSG-196, VRSG-1710	P7, P9, P8
II	3	Kashi Kalyani, Kashi Shreya, Kashi Vandana	P2, P6, P5
III	2	VRSG-1716, VRSG-1731	P3, P4
IV	2	Kashi Divya, Kalyanpur Hari Chikni	P1, P10

Table 3: Average intra-cluster (diagonal) and inter-cluster (off-diagonal) D² values among four clusters of sponge gourd parents.

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	84.899	346.749	806.541	226.305
Cluster II	346.749	106.091	357.233	322.713
Cluster III	806.541	357.233	169.283	610.550
Cluster IV	226.305	322.713	610.550	460.700

Green = intra-cluster D² (diagonal); Red = maximum inter-cluster D² (Cluster I × III = 806.541).**Table 4:** Relative contribution of twenty characters to total D² divergence among ten sponge gourd parents

Rank	Character	Contribution (%)	Cumulative (%)
1	Fruit Yield (kg)/plant	14.47	14.47
2	Number of Fruits/plant	10.86	25.33
3	Fruit Length (cm)	10.48	35.81
4	Days to First Harvest	9.54	45.35
5	Shelf Life (days)	9.52	54.86
6	Fruit Yield (kg)/plot	8.38	63.25
7	Dry Matter Content (%)	5.51	68.76
8	Days to First Male Flower	5.10	73.86
9	Total Sugar (%)	3.95	77.81
10	Non-reducing Sugar (%)	3.55	81.36
11	No. of Primary Branches/plant	3.55	84.91
12	Fruit Diameter (cm)	2.82	87.73
13	Average Fruit Weight (g)	2.46	90.19
14	Days to First Female Flower	2.32	92.51
15	Reducing Sugar (%)	1.73	94.24
16	Vine Length (m)	1.59	95.83
17	Total Soluble Solids (°Brix)	1.12	96.95
18	Node No. to First Female Flower	1.09	98.04
19	Ascorbic Acid (mg/100g)	1.05	99.10
20	Node No. to First Male Flower	0.90	100.00

Red = contribution ≥ 10% (primary discriminators); Yellow = 5–10% (moderate contributors).

Table 5: Eigenvalues, per cent variance and cumulative variance explained by principal components in sponge gourd parents

PC	Eigenvalue	Variance (%)	Cumulative (%)	Remarks
PC1	12.4604	56.07	56.07	Significant
PC2	3.9607	17.82	73.89	Significant
PC3	2.4325	10.95	84.84	Significant
PC4	1.1522	5.18	90.03	Significant
PC5	0.8463	3.81	93.84	Non-significant
PC6	0.5914	2.66	96.50	Non-significant
PC7	0.4012	1.81	98.31	Non-significant
PC8	0.2803	1.26	99.57	Non-significant
PC9	0.0950	0.43	100.00	Non-significant

Green rows: eigenvalue ≥ 1.0 (significant, retained for interpretation).

Table 6: Factor loadings of twenty characters on the first four principal components in sponge gourd parents (bold: $|\text{loading}| \geq 0.50$)

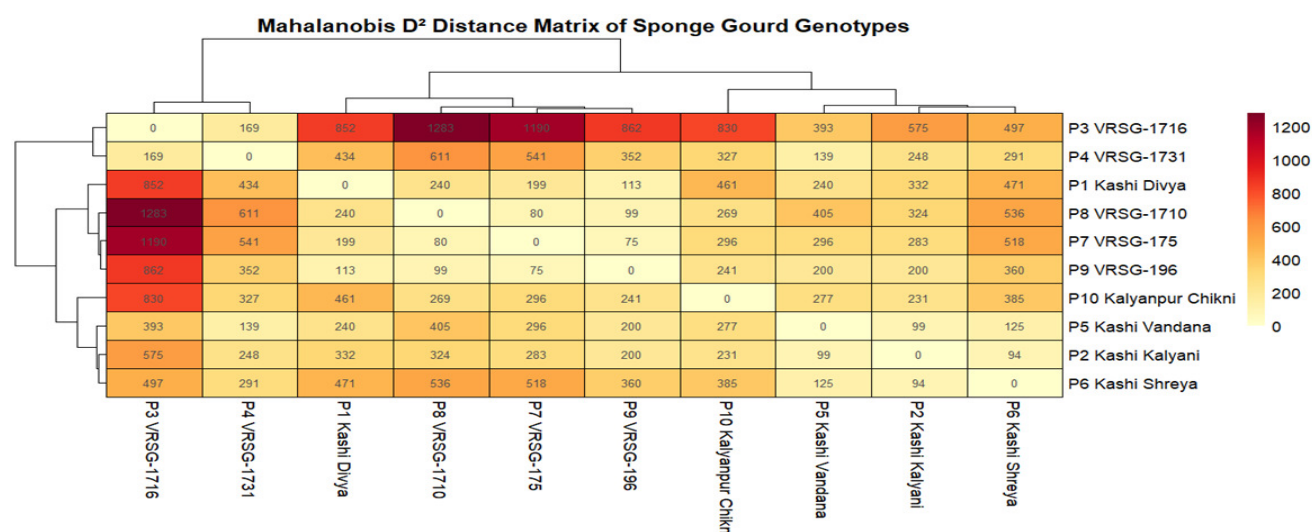
Character	PC1	PC2	PC3	PC4
Days to First Male Flower	0.7923	0.3612	-0.2541	0.1832
Days to First Female Flower	0.8047	0.3418	-0.2236	0.1654
Node No. to First Male Flower	0.7612	0.4531	-0.1983	0.2217
Node No. to First Female Flower	-0.9438	0.1203	0.0872	-0.1105
Days to First Harvest	0.8312	0.2854	-0.3102	0.1423
Vine Length (m)	0.7245	0.3987	0.2634	-0.1876
No. of Primary Branches/plant	0.6834	0.5012	0.3124	-0.2431
Avg. Fruit Weight (g)	0.8923	0.2341	0.1987	0.1543
Fruit Length (cm)	0.8634	0.3127	0.1543	0.2187
Fruit Diameter (cm)	0.9137	-0.1854	0.1234	0.1965
No. of Fruits/plant	0.7456	0.4123	0.3256	-0.2134
Fruit Yield/plant (kg)	0.8245	0.3754	0.2431	0.1876
Fruit Yield/plot (kg)	0.7834	0.2965	0.1654	0.2341
Dry Matter Content (%)	0.6923	0.5234	-0.2341	0.1987
Total Soluble Solids (°Brix)	0.9847	-0.0923	0.0654	0.0987
Non-reducing Sugar (%)	0.7312	0.4587	0.1832	0.2654
Reducing Sugar (%)	0.7023	0.4654	0.2987	-0.2231
Total Sugar (%)	0.9193	-0.1234	0.0876	0.1123
Ascorbic Acid (mg/100g)	0.6512	0.5123	0.3765	-0.1654
Shelf Life (days)	0.9780	-0.0765	0.0543	0.0876

Bold: absolute loading ≥ 0.50 (meaningful contributor to the component).

Table 7: Principal component scores of ten sponge gourd parents on PC1, PC2, PC3 and PC4

Code	Genotype	PC1	PC2	PC3	PC4
P1	Kashi Divya	3.4521	1.2341	0.8764	-0.5432
P2	Kashi Kalyani	-1.8734	2.3456	-1.2341	0.6543
P3	VRSG-1716	2.1234	-2.5432	1.4532	0.8765
P4	VRSG-1731	2.0876	-2.3214	1.3214	0.7654
P5	Kashi Vandana	-2.1543	1.9876	-1.1234	0.5432
P6	Kashi Shreya	-2.0231	2.1234	-0.9876	0.4321
P7	VRSG-175	-1.4321	-1.6543	-0.8765	-1.2345
P8	VRSG-1710	-1.2134	-1.4321	-0.7654	-1.1234
P9	VRSG-196	-1.5432	-1.7654	-0.9123	-1.3456
P10	Kalyanpur Hari Chikni	3.6764	1.5432	1.2345	-0.4321

Row shading: Green = Cluster I; Blue = Cluster II; Yellow = Cluster III; Orange = Cluster IV.

**Fig. 1:** Mahalanobis D² distance matrix of ten sponge gourd parent genotypes across twenty characters (Kharif 2023–24 and 2024–25)

Grouping of Sponge Gourd Parents by Tocher's Method

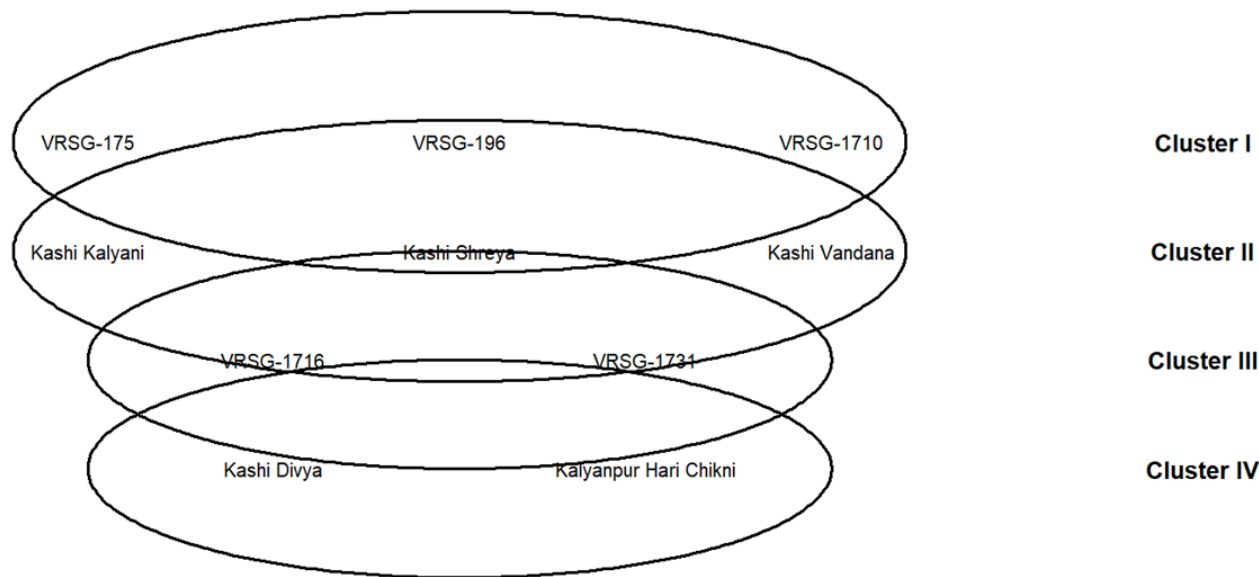


Figure 2: Grouping of ten sponge gourd parents into clusters by Tocher's method

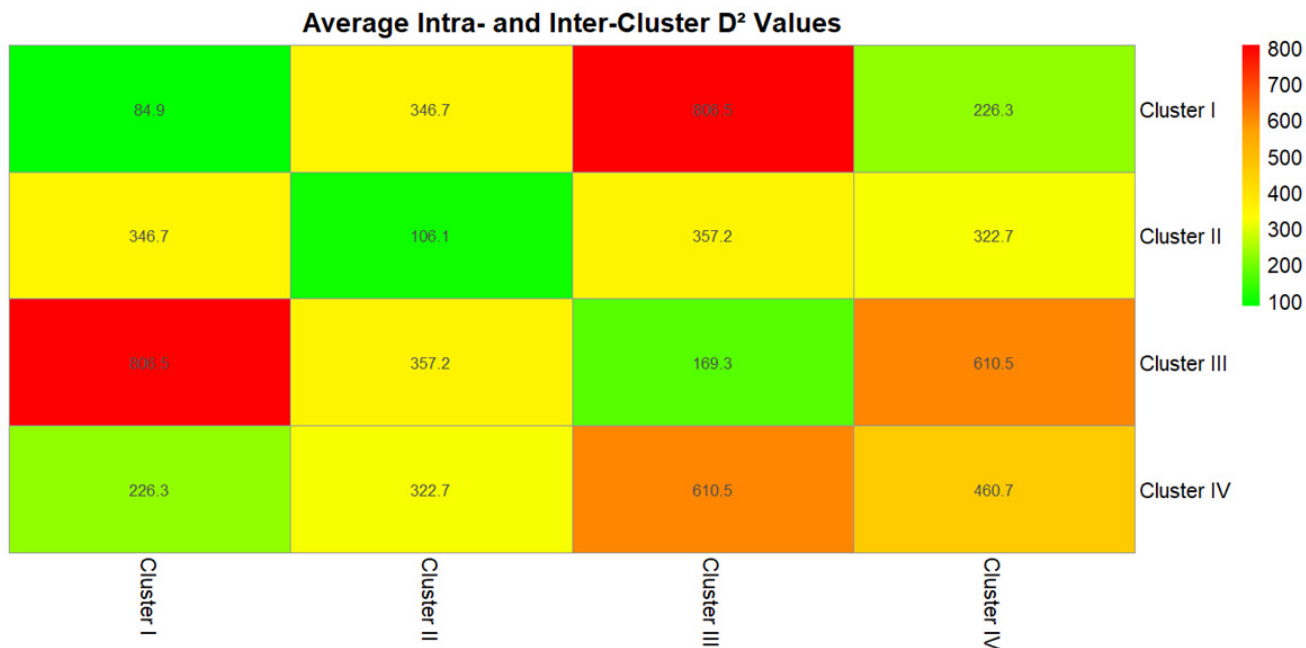


Figure 3: Average intra-cluster (diagonal) and inter-cluster (off-diagonal) D² values among four clusters of sponge gourd parents.

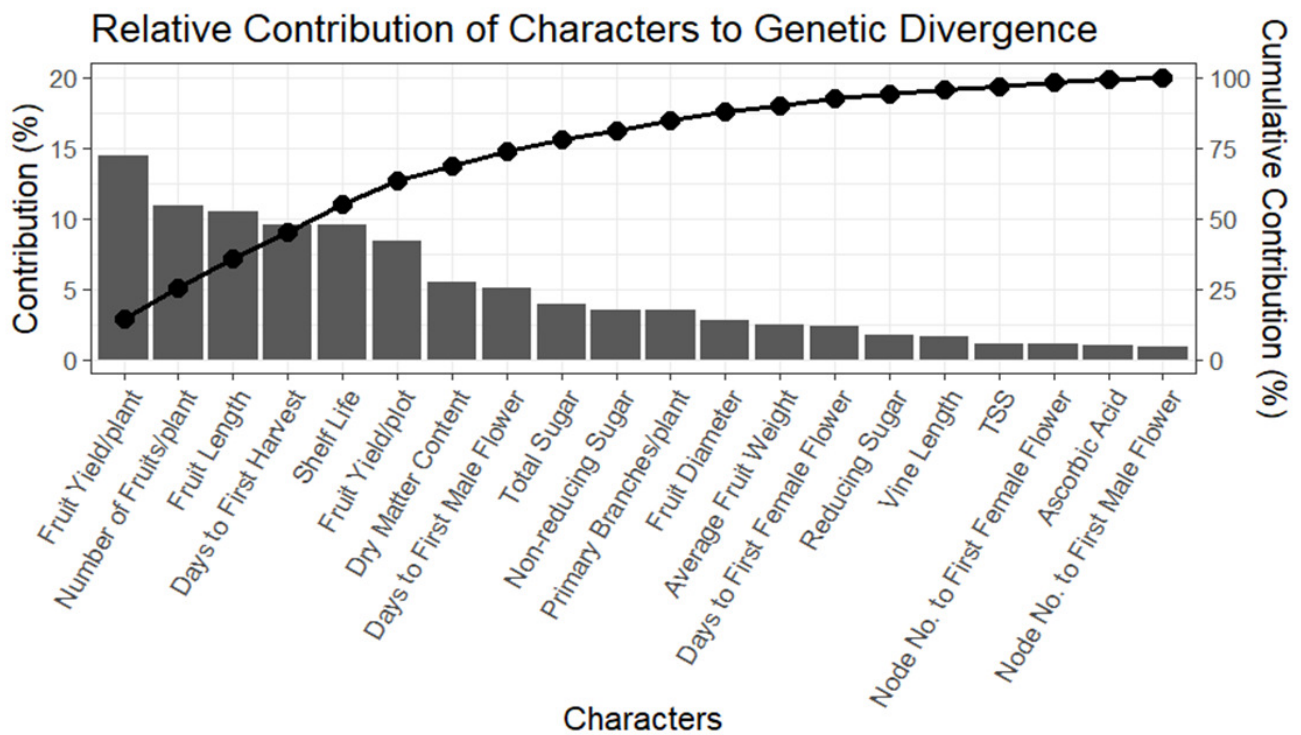


Figure 4: Relative contribution of twenty characters to total D^2 divergence among ten sponge gourd parents

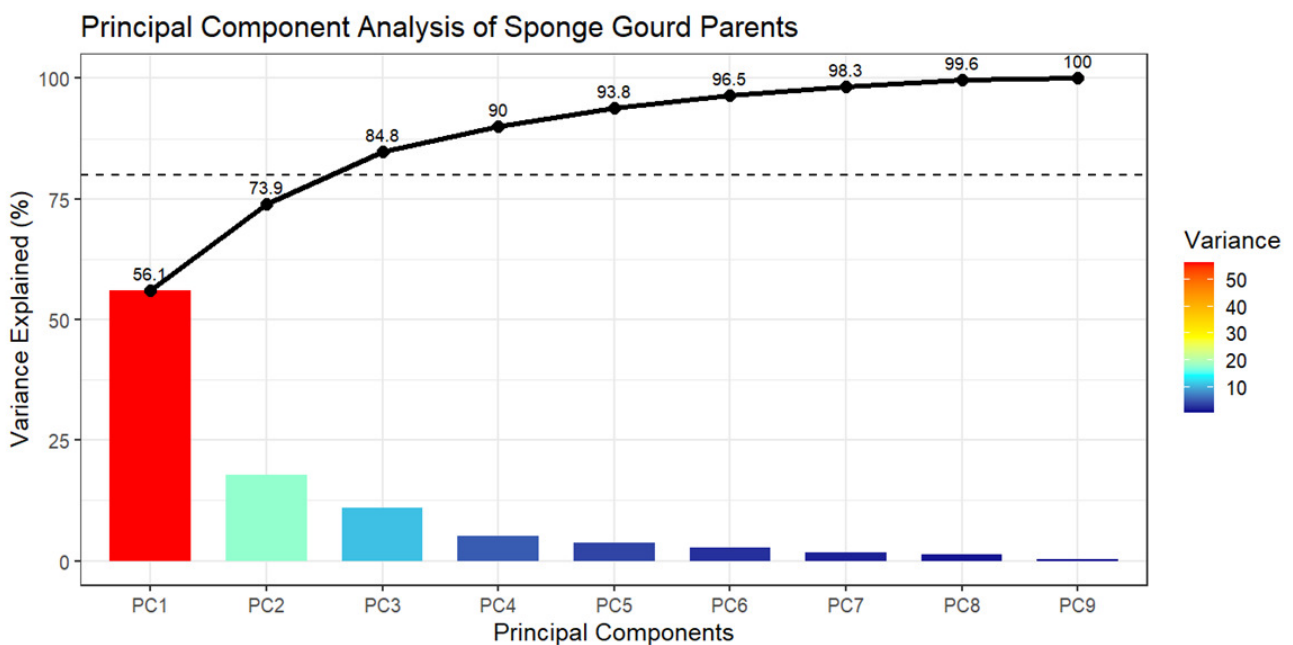


Figure 5: Eigenvalues, per cent variance and cumulative variance explained by principal components in sponge gourd parents

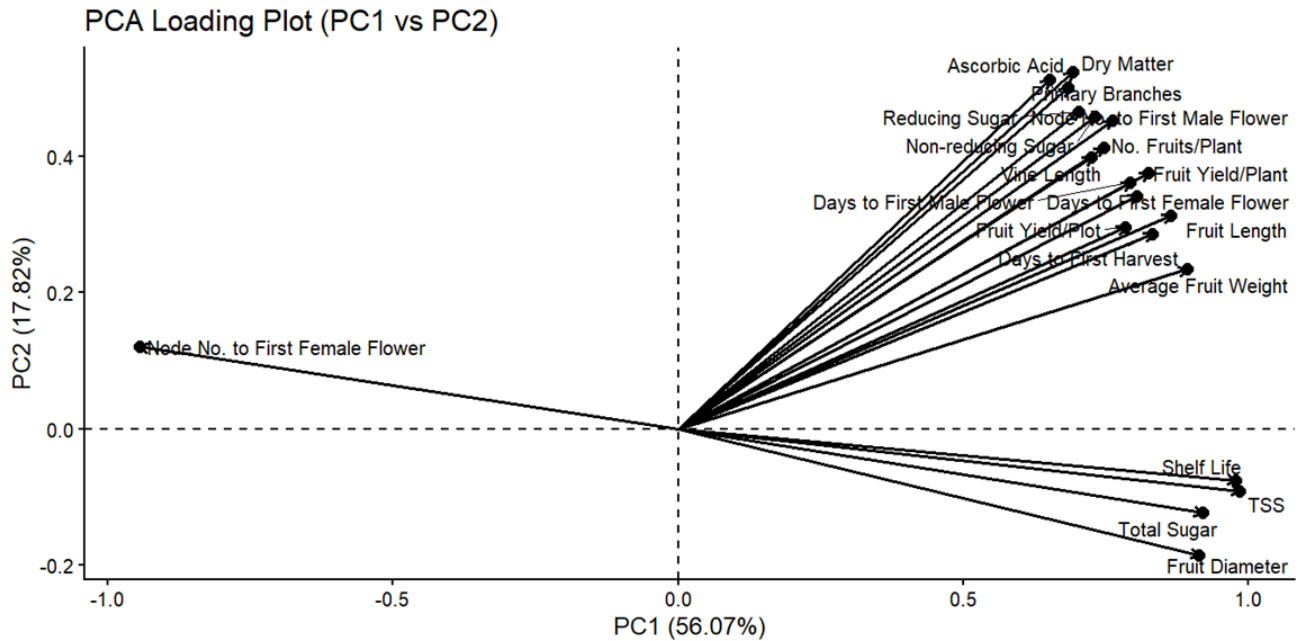


Figure 6: Factor loadings of twenty characters on the first four principal components in sponge gourd parents.

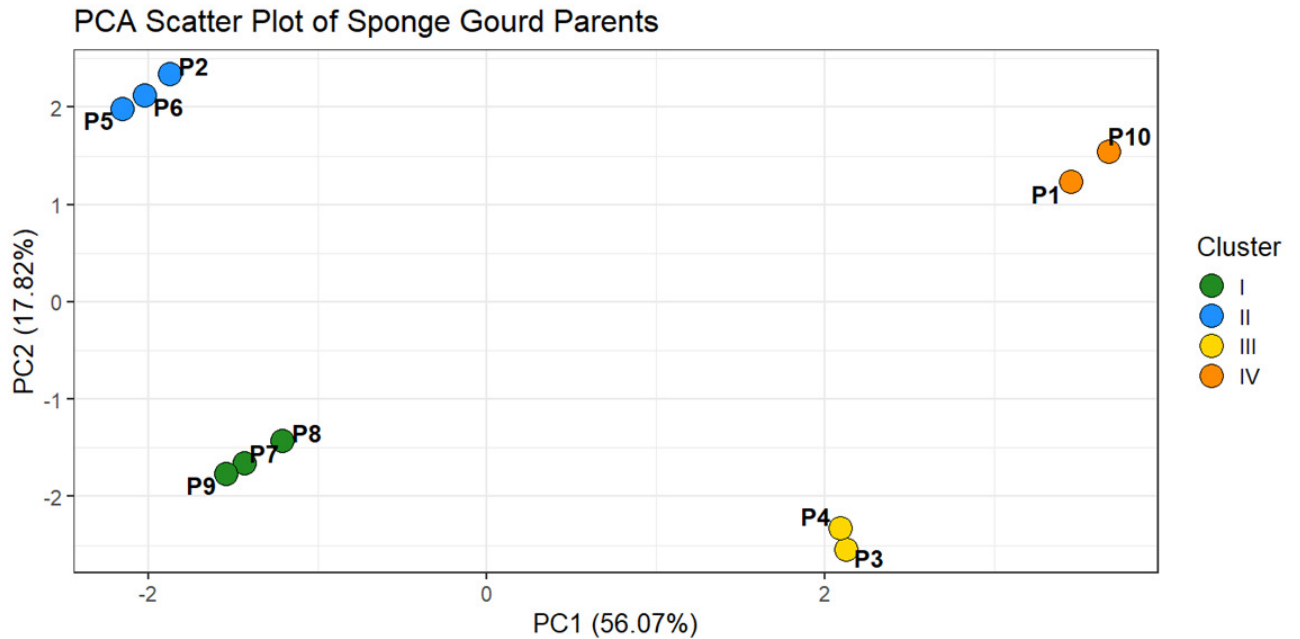


Fig. 7: Principal component scores of ten sponge gourd parents on PC1, PC2, PC3 and PC4

Author's Contribution

Rohit Rawat – Conceptualization, Conducted experiment, Data Analysis and Data Curation

Dr. D.P. Singh– Supervision, Methodology and Review Remaining Authors – Preparation of final draft and Revision

Declaration: The authors declare that they have no conflict of interests.

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