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PRINCIPAL COMPONENT AND CLUSTER ANALYSIS FOR GENETIC DIVERSITY ASSESSMENT IN SUMMER SQUASH (*Cucurbita pepo* L.)

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ABSTRACT

Genetic diversity assessment and selection of superior parents serves as a cornerstone for developing efficient breeding strategies for crop improvement. This study was conducted at the Vegetable Experimental Farm, SKUAST-Kashmir, Shalimar Srinagar in Kharif-2023 to examine genetic divergence among 30 phenotypically different summer squash genotypes for various quantitative and qualitative parameters. Mahalanobis D² analysis using Ward's method grouped the genotypes into seven distinct clusters. Cluster II had the highest number of genotypes (9), subsequently clusters III and VI contained (6) genotypes each. Both the clusters I and V consisted of 3 genotypes. Cluster IV included 2 genotypes while cluster VII was represented by a single genotype. Intra-cluster distance was recorded to be maximum in cluster IV (80.26) and minimum in cluster VII (0.00). Clusters VI and VII exhibited maximum inter-cluster distance (706.37) in contrast to the minimum distance observed between clusters III and V (94.04). Crossing genotypes from most genetically distant clusters is necessary to create hybrids with enhanced traits. PCA revealed that six out of ten components with (eigen values > 1.0) explained 75.20% of total variation. PC1 accounted for highest variability i.e. 25% of total genetic variance. The subsequent components (PC2 to PC6) captured 17.25%, 12.02%, 8.57%, 6.34%, and 6.00% of the total variability respectively. Diversity present in this core collection offers significant insights for enhancing agronomic traits and also enables the selection of promising divergent parents for future hybridization programmes.

Keywords : Diversity, Summer squash, PCA, cluster analysis.

Introduction

Summer squash (*Cucurbita pepo* L.) is a cross-pollinated annual belonging to the cucurbitaceae family cultivated during the summer season. The plant is monoecious and herbaceous, characterized by compact, bushy growth habit. This crop is primarily grown for its tender, immature fruits and thrives well under temperate and mild subtropical climates. The crop is primarily found in America and is believed to

have originated in northern Mexico (Paris, 1996). Asia accounts for half of the total global area dedicated to the cultivation of squash and pumpkin (Al Brifcany, 2015). Squash (*Cucurbita pepo* L.) holds significant economic value. Genus *Cucurbita* is thought to be one of the most primitive genera in the plant kingdom (Tadmor *et al.*, 2005). Archaeological evidence suggest that squash was likely first cultivated in Mesoamerica approximately 8,000 to 10,000 years ago (Roush, 1997; Smith, 1997). It is cultivated in temperate,

subtropical and tropical regions and is widely grown globally for its fruits (Bisognin, 2002). Its economic value is closely linked to its rich nutritional profile, as it contains numerous bioactive compounds, vitamins, minerals, and other essential nutrients that contribute to human health (Kulczyński & Gramza-Michałowska, 2019). It contains high level of carotenoids that contribute to antioxidant and anti-inflammatory activity (Deppe, 2015). Moreover, its minimal calorie content makes it suitable for inclusion in diets aimed at reducing body weight (Fageria *et al.*, 2012). Squash contains Vitamins A, C, niacin and folate along with dietary fiber, which collectively contribute to reducing the risk of cancer, heart-related disorders and inflammatory conditions including asthma and arthritis (Balluz *et al.*, 2005). In addition, it provides substantial amounts of magnesium and phosphorus, minerals that play a crucial role in maintaining bone strength (Gholami *et al.*, 2012). Regular consumption of summer squash has been associated with benefits such as supporting cardiovascular health, aiding digestion and strengthening immune function. With immense health-promoting qualities and its strong market demand, summer squash offers significant potential for improving food security and farmer livelihoods. The efficacy and outcome of any plant breeding initiative with the goal of identifying superior genotypes predominantly rely on comprehending the level of genetic diversity and the extent to which crucial traits are heritable. Acquiring profound understanding of genetic diversity is crucial for attaining sustained progress through selection over time. A noteworthy approach in this context is the application of multivariate statistical techniques such as Mahalanobis D^2 statistics and Principal Component Analysis. Mahalanobis's D^2 statistic approach is a powerful tool to identify desirable and genetically divergent parents and has extensively been utilized to assess diversity [Ullah *et al.* (2015) & Patel *et al.* (2017)]. It estimates the distances between the two populations based on inter and intra-cluster distances and provides insights into the various characteristics of the divergent parents before any hybridization process. PCA serves as an effective statistical approach for simplifying complex datasets by transforming interrelated variables into a reduced number of uncorrelated principal components. This technique highlights the significance of the main determinant of overall variability along each axis of differentiation. Despite considerable medicinal and economic importance of summer squash, there is a noticeable scarcity of studies employing multivariate analysis in Indian summer squash genotypes. To address this gap, the current study was carried out to classify a collection of summer squash genotypes

through multivariate techniques with the aim of identifying genetically diverse parents that could potentially be used to develop superior hybrids in the future.

Materials and Methods

The study was undertaken at Vegetable Experimental Farm, Division of Vegetable Science, Faculty of Horticulture, SKUAST-Kashmir, located in Shalimar, Srinagar, Jammu and Kashmir during the Kharif season of 2023. The site lies at an elevation of 1,685 m above sea level positioned at 34°0.14' N latitude and 74°0.86' E longitude. Soil at the experimental site is alluvial and the irrigation water used for the crop maintained a neutral pH. The region experiences a temperate climate with relatively mild summers. Experimental material involved thirty phenotypically diverse genotypes of summer squash obtained from various sources, including local collections and national institutes such as IIVR, NBPGR, and IIHR. A single factor, Randomized Complete Block Design (RCBD) design with three replications was employed for this experiment. Within each replication five plants per genotype were planted with rows spaced 2 m apart and plants 1 m apart. Standard cultural practices were adopted throughout the crop growth period to ensure optimal plant health.

A comprehensive set of traits were examined including plant height (cm), stem diameter (cm), days to appearance of first male flower, days to appearance of first female flower, node of first female flower, node of first male flower, plant spread (cm), no. of fruits per plant, fruit length (cm), fruit diameter (cm), fruit weight (g), fruit yield/plant (kg), fruit yield /ha (q), TSS (°Brix), Dry matter content (%), Ascorbic acid content (mg 100g⁻¹), Crude fiber content (%), Total carotenoid content (mg 100g⁻¹). For each genotype, observations were made on five healthy plants selected at random across all replications. To evaluate the degree of genetic divergence, Mahalanobis (1936) D^2 analysis was used and the genotypes were grouped into clusters using ward's method. Principal Component Analysis (PCA) was performed in summer squash using thirteen quantitative and five quality characters. PCA is a multivariate statistical technique used to simplify complex data by reducing its dimensions. It identifies few main axis (principal components), For each axis, eigen vectors are determined and component scores for the variables are produced. All statistical analyses and computations were conducted utilizing R software at the Division of Agricultural Statistics, SKUAST-Kashmir, Shalimar.

Results

D₂ analysis (Clustering pattern)

Based on Mahalanobis D² analysis using Ward's method genotypes were categorized into seven clusters. The perusal of data (Table 1, Fig 1) showed that cluster II contained the maximum number of genotypes i.e., 09 subsequently clusters III and VI each had 6 genotypes. Clusters I and V contained 3 genotypes each whereas cluster IV had 2 genotypes. Cluster VII comprised solely one genotype.

Average cluster distance (Intra and Inter)

Table 2 outlines the average intra- and inter-cluster distance (D²) values observed for 30 summer squash genotypes. It is clear from the Table 2 that maximum intra-cluster D² value was observed in cluster IV followed by cluster I, cluster VI, cluster II, cluster III, cluster V, whereas minimum intra-cluster distance (D²) was identified in cluster VII as single genotype was present in this cluster. The inter-cluster distance D² values were highest between clusters VI and VII followed by clusters V and VI, IV and VI, III and VI, II and VI, I and VII and I and VI.

Cluster means

Persual of the data (Table-3 (a) and 3 (b)) revealed that the cluster means for different attributes exhibited pronounced differences across various clusters. Cluster I recorded minimum value for plant height and stem diameter. Cluster II recorded the maximum values for days to appearance of first female flower, fruit diameter and node of first female flower and minimum values for number of fruits per plant, ascorbic acid content and crude fiber. Cluster II recorded maximum value for days to appearance of first female flower, node of first female flower, fruit diameter and minimum values were recorded for number of fruits per plant, ascorbic acid and crude fiber. Cluster III recorded highest mean values for days to appearance of first male flower. Cluster IV exhibited maximum mean value for fruit weight, fruit yield/ha, plant spread, fruit length, fruit yield/ plant and dry matter content and minimum values for node of first female flower, node of first male flower and TSS. Cluster V revealed maximum cluster mean for stem diameter and crude fiber. Cluster VI revealed highest cluster mean value for total carotenoid content and lowest for plant spread. Cluster VII recorded the highest cluster means for plant height, ascorbic acid, TSS and node of first male flower and conversely lowest cluster means were observed for fruit weight, days to appearance of first female flower, days to appearance of first male flower, fruit length, fruit diameter, fruit yield / plant, fruit

yield/ha, dry matter content and total carotenoid content.

Principal Component Analysis

PCA was performed on thirteen quantitative and five qualitative traits of summer squash to determine which traits were the major sources of variation within the germplasm collections. The analysis demonstrated that 6 out of 10 principal components each with an eigen value exceeding 1.00 contributed to 75.20% of the overall variation. Table no. 4 present coefficients characterizing the six principal components of the present data. First principal component (PC1) accounted for 25.00% of the total variation out of 75.20%. PC1 displayed the highest positive loadings from fruit yield/ ha, fruit yield/plant, number of fruits per plant, plant spread, total carotenoid content, fruit weight, ascorbic acid, plant height and crude fiber. PC2 explained 17.25% of the total variance with significant positive loadings from ascorbic acid, total soluble solids, number of fruits per plant and node of first male flower. PC3 accounted for 12.02% of total variation with significant positive contributions from dry matter, fruit diameter and plant spread. PC4 accounted for 8.57% of the total variation, mostly influenced by total carotenoid content and dry matter. PC5 represented 6.34% of the overall variance with the node of the first female flower, stem diameter and TSS as the most significant positive contributors. Finally PC6 accounted for 6.00% of the overall variance, with positive contributions from plant spread, crude fiber, TSS, days to the appearance of the first male flower, fruit diameter and ascorbic acid.

Discussion

Genetic diversity is a crucial element for heritable enhancement in crops and understanding the nature and magnitude of variability is vital for selecting optimal parental lines from existing germplasm to execute a successful breeding programme. The examination of genetic diversity aids in understanding the genetic foundation and breeding potential of the germplasm. Assessing genetic divergence enables breeders to narrow the available gene pool by excluding less promising parental lines, thereby allowing focused evaluation of a limited set of hybrid combinations (Fuzzato *et al.*, 2002). The D² statistics enables to discriminate among different cultivars according to the diversity present (Mahalanobis, 1936). It provides a good understanding of the diverse nature of the populations. The significance of multivariate analysis in measuring the extent of divergence among populations to elucidate their evolutionary trends and evaluate the relative contribution of various

components on overall divergence together with the nature of forces operating at intra- and inter cluster levels, has been notably emphasized (Murty & Qadri, 1966; Anand & Murty, 1968; Mishra *et al.*, 1994). The clusters generated by Ward's approach can be utilized to determine the distances between and within the clusters. These results may provide insight into the different nature of the genotypes within a cluster. Furthermore, the comparative impact of various yield components on overall divergence, as assessed using Mahalanobis D^2 analysis, aids in identifying selection parameters that can serve as criteria for yield enhancement. D^2 clustering suggests that the germplasm assessed in the current study possesses considerable level of genetic diversity. Notably, inter-cluster distances exceeded intra-cluster ones, highlighting substantial genetic divergence across genotypes belonging to different clusters. For effective hybrid development, parental lines should be chosen from genetically distinct clusters that exhibit large inter-cluster distances, and the selected parents must also show superior individual performance for traits that contribute most strongly to overall genetic divergence (Singh *et al.*, 1996). It is clear from the table that maximum intra-cluster D^2 value was observed in cluster IV signifying considerable heterogeneity in the genetic composition of genotypes present in the cluster, whereas minimum intra-cluster distance (D^2) was identified in cluster VII as single genotype was present in this cluster. Inter-cluster distance D^2 values were maximum between clusters VI and VII followed by clusters V and VI which signifies a greater genetic heterogeneity among the genotypes within these clusters. Hybridization between parents from distinct clusters that exhibit the greatest genetic distance is anticipated to obtain a wide spectrum of variation among the segregants (Doddabhimappa *et al.*, 2010). The summer squash genotypes examined originated from a single origin and were distributed across various clusters. The observed diversity among genotypes of common geographic origin may be ascribed to factors such as heterogeneity, genetic architecture of populations, historical selection pressures, developmental traits and the extent of general combining ability (Murty & Arunachalam, 1966).

Single genotype clusters with unique characteristics may serve as testers in hybridization programs aimed at achieving maximum heterosis. Comparable results were documented by Swain *et al.* (2022), Sajid *et al.* (2022) in summer squash, Lakshman *et al.* (2021) in bitter melon, Verma *et al.* (2020) in pumpkin, Kumar *et al.* (2019) in sponge gourd.

Cluster means also indicate the extent of variations among genotypes that are classified into distinct clusters. Genetic constellation means of various clusters assist in identifying the clusters to be selected for hybridization. The means of clusters and the coefficient of variance illustrate a compelling depiction of nature of diversity (Sardana *et al.*, 1997). Cluster means for different attributes exhibited considerable differences among various clusters. To enhance key divergent traits, genotypes should be selected from clusters with extreme mean values for the respective traits, depending on the specific objective of the breeding scheme. Comparable studies assessing cluster means for characters have been studied by Swain *et al.* (2022), Sajid *et al.* (2022) in Summer Squash, Verma *et al.* (2020) in pumpkin and Kumar *et al.* (2019) in sponge gourd.

The results indicate that there is substantial scope to integrate the superior alleles found in these genotypes using a structured breeding and selection approach to identify and retain desirable recombinants with enhanced yield and improved quality attributes.

Principal Component Analysis (PCA) is an important statistical technique that facilitates the identification of crucial polygenic traits essential for a plant breeding program. PCA offers a method for reducing a complicated data set to a lower dimension, so uncovering the frequently concealed, simplified structures that underlie it. The eigen value of a specific principal component indicates the extent of variation in traits accounted for by that component, which is highly beneficial for subsequent breeding programs. This technique highlights the significance of the largest contributor to the overall variation along each axis of differentiation. Eigen values are frequently utilized to ascertain the number of components to be kept. The sum of the eigen values often corresponds to the number of variables. The six principal components (PC1 to PC6) derived from the original data, with latent roots exceeding one, account for approximately 75.20 % of the total variation. This indicates that these six principal component scores may be utilized to encapsulate the original 18 variables in subsequent data analyses. Chahal & Gosal (2002) noted that characters with the highest absolute values near unity in the first principal component exert a greater influence on grouping than those with lower absolute values around zero. Therefore, in the current study, the classification of genotypes into distinct clusters resulted from the significant influence. First principal component (PC1) accounted for 25.00% of the total variation out of 75.20%. PC1 displayed the highest positive loadings from fruit yield/ ha, fruit yield/plant, number of fruits

per plant, plant spread, total carotenoid content, fruit weight, ascorbic acid, plant height and crude fiber. The remaining attributes contributed minimally to PC1 and were instead allocated to other components. The positive loading indicates the existence of positive correlation trends between the variables and components. Consequently, the aforementioned features that exhibited high positive values contributed more to the diversity and played a crucial role in differentiating the clusters. From the table it can be seen that the most variation was detected in PC1 relative to the other five principal components thus, selecting lines based on the characteristics associated with PC1 may be desirable. Figure 2 illustrates the relation among 18 traits in summer squash genotypes in the first and second principal components. The parameters positioned to the right (towards the value of 1) on the horizontal axis are those that contribute more positively to PC1. The parameters that are positioned more to the left (toward the value -1) on the same axis exhibit a greater negative contribution to PC 1. Conversely, parameters positioned near 1 on the vertical axis exhibit a more favorable contribution to PC 2, while those near -1 on the same axis contribute negatively towards PC2. Figure 3 illustrates the relation among 30 summer squash genotypes depicted by a 2D scatter plot for the 1st two PC'S based on 18 traits. The scatter plot of the principal components indicated that the genotypes were dispersed across all quadrants, signifying a considerable level of genetic heterogeneity among the assessed genotypes, thereby offering a valuable resource for developing enhanced varieties in future breeding programmes. The greater the distance between genotypes, the more genetically distinct they are likely to be, making them suitable for crossing programs aimed at developing high-yielding summer squash varieties in the future. The results of the present study are consistent with those of Martinez *et al.* (2015), who observed six principal components (PC1-PC6) collectively accounting for 85.6 % of total variation in summer squash. Maximum variation was captured by PC1 and PC2, with contributions of 35.6% and 18.4% each and Singh *et al.* (2014) observed six principal components (PC1-PC6) with contribution values of 23.88, 16.81, 13.28, 11.23, 9.38 and 8.61% respectively which together explained 83.19 % of the total variation. Among them, PC1 and PC2 contributed

the most accounting for 23.88% and 16.81% of the variation respectively in bitter gourd. In further support to our findings Sajid *et al.* (2022) stated that the first two components were responsible for 53 % of the phenotypic variability. PC1 and PC2 explained 32.4%, 20.6% of the total variation respectively in summer squash. Kundu *et al.* (2012) detected 6 principal components with Eigen values above 1.0 explaining 80.27% of the total variation in bitter gourd.

Conclusion

Cluster analysis categorized the summer squash genotypes into seven distinct clusters, highlighting varying degrees of genetic similarity and divergence. Cluster II encompassed maximum genotypes while cluster VII consisting of only one genotype, stood out as the most genetically unique. Clusters VI and VII exhibited the maximum inter-cluster distance (D^2) with the next largest distance observed between clusters V and VI, highlighting significant genetic diversity among these clusters. Selection of parents from these clusters characterized by high cluster means and demonstrating superior performance can be utilized in hybridization programs potentially leading to the development of improved, high yielding varieties. PCA further elucidated genetic variability by identifying the key traits contributing to variation among the genotypes. Six principal components with eigen values exceeding 1.0 collectively accounted for 75.20% of the total genetic variability. Principal component analysis highlights the most influential variable contributing to each principal component. The first principal component alone explained 25.00% of the variability, The residual variability of 17.25%, 12.02%, 8.57%, 6.34% and 6.00% was explained by PC2, PC3, PC4, PC5 and PC6 respectively. Key traits such as fruit yield /ha, ascorbic acid content, dry matter, total carotenoids, node of the first male flower and plant spread were identified as significant contributors across different principal components. Thus the PCA results showed substantial genetic variation among the genotypes with specific traits contributing to this variation. These findings offer valuable insights for future breeding programs aimed at yield, quality improvement and overall performance in summer squash.

Table 1: Distribution of Summer Squash (*Cucurbita pepo* L.) genotypes in various clusters based on D² statistics

Cluster number	No. of genotypes	Genotypes
I.	03	SKUA-SQ-01, SKUA-SQ-08, SKUA-SQ -27
II.	09	SKUA-SQ-02, SKUA-SQ-03, SKUA-SQ-04, SKUA-SQ-19,SKUA-SQ-20, SKUA-SQ-21, SKUA-SQ-22, SKUA-SQ-29, SKUA-SQ-30
III.	06	SKUA-SQ-05, SKUA-SQ-07,SKUA-SQ-12, SKUA-SQ-14, SKUA-SQ-15, SKUA-SQ-28
IV.	02	SKUA-SQ-06, SKUA-SQ-17
V.	03	SKUA-SQ-09,SKUA-SQ-13, SKUA-SQ-18
VI.	06	SKUA-SQ-10, SKUA-SQ-11, SKUA-SQ-23, SKUA-SQ-24, SKUA-SQ-25, SKUA-SQ-26
VII.	01	SKUA-SQ-16

Table 2: Average intra-cluster (Diagonal) and inter cluster (Above Diagonal) distance values in Summer Squash (*Cucurbita pepo* L.)

	C1	C2	C3	C4	C5	C6	C7
C1	76.46	102.70	166.53	228.59	253.21	371.23	400.67
C2		51.96	94.33	191.19	177.52	457.11	368.09
C3			47.28	128.48	94.04	530.27	294.46
C4				80.26	127.08	562.72	181.36
C5					26.55	616.76	244.75
C6						58.54	706.37
C7							0

Table 3(a): Cluster means for various growth and yield attributing characters in different clusters of Summer Squash (*Cucurbita pepo* L.)

Clusters	Plant height (cm)	Stem diameter (cm)	Days to appearance of first male flower	Days to appearance of first female flower	Node of first female flower	Node of first male flower	Plant spread (cm)	Number of fruits per plant	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	Fruit yield /plant (kg)	Fruit yield /ha (q)
I	55.91	1.78	50.97	56.73	6.86	2.37	92.70	5.69	28.59	7.17	750.01	4.28	211.42
II	59.38	2.224	55.51	60.32	7.25	3.29	87.92	4.33	32.44	7.92	848.98	3.67	174.86
III	65.99	2.24	55.82	58.92	5.94	2.60	92.07	5.07	36.43	7.75	984.02	5.00	244.25
IV	67.13	2.27	50.86	56.06	5.69	2.00	95.34	8.40	36.71	7.66	1011.27	8.50	458.36
V	59.49	2.43	52.93	56.28	5.53	2.15	90.40	7.15	33.43	7.70	936.19	6.69	330.69
VI	59.67	2.22	54.16	58.23	6.74	2.86	84.33	4.81	33.54	7.80	911.91	4.38	218.77
VII	68.94	2.11	50.40	53.87	5.86	3.60	88.5	8.40	18.90	6.34	415.90	3.49	172.80

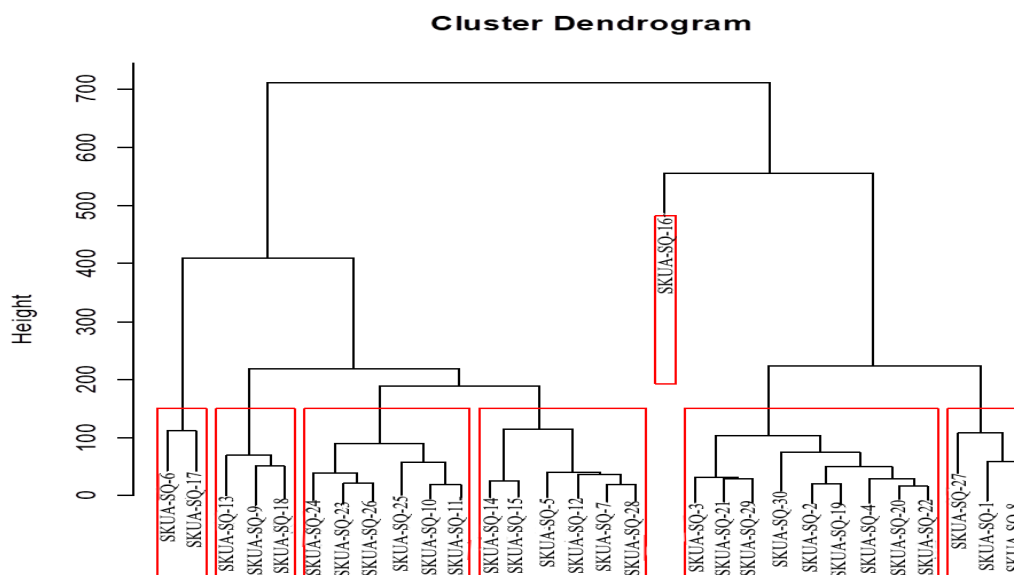
Table 3(b): Cluster means for various quality characters in different clusters of summer squash (*Cucurbita pepo* L.) genotypes (Wards method)

Clusters	TSS (°Brix)	Ascorbic acid content (mg 100g ⁻¹)	Dry matter content (%)	Crude fiber content (%)	Total carotenoid content (mg 100 g ⁻¹)
I	4.13	11.58	6.29	1.78	1.45
II	3.63	11.16	6.55	1.75	1.22
III	4.02	12.51	5.36	1.79	1.40
IV	3.33	12.28	7.25	1.82	1.82
V	4.60	11.90	5.71	2.13	1.84
Vi	4.13	11.77	6.57	1.81	1.89
Vii	4.86	18.08	4.81	1.79	0.24

Table 4: Latent vectors for eighteen traits in summer squash (*Cucurbita pepo* L.)

	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
Plant height (cm)	0.22	-0.03	0.04	-0.66	-0.48	-0.19
Stem diameter (cm)	-0.01	-0.28	-0.01	-0.76	0.48	0.06
Days to appearance of first male flower	-0.60	-0.38	-0.43	-0.04	-0.27	0.33

Days to appearance of first female flower	-0.68	-0.38	-0.28	0.14	-0.04	0.28
Node of first female flower	-0.61	0.01	-0.05	-0.09	0.52	-0.26
Node of first male flower	-0.59	0.20	-0.12	-0.34	0.13	0.18
Plant spread (cm)	0.31	0.10	0.53	0.07	-0.005	0.43
Number of fruits per plant	0.86	0.30	-0.08	-0.06	0.11	0.12
Fruit length (cm)	0.15	-0.85	-0.18	-0.12	-0.03	-0.10
Fruit diameter (cm)	-0.27	-0.55	0.58	-0.05	0.03	0.32
Fruit weight (g)	0.28	-0.87	-0.11	-0.07	-0.03	0.01
Fruit yield/plant (kg)	0.90	-0.30	-0.09	-0.04	0.11	0.09
Fruit yield/ha (q)	0.91	-0.29	-0.04	-0.01	0.12	0.07
TSS (°Brix)	0.10	0.31	-0.41	0.05	0.42	0.34
Ascorbic acid content (mg 100g ⁻¹)	0.27	0.59	-0.12	-0.32	-0.14	0.26
Dry matter content (%)	-0.01	-0.27	0.72	0.23	0.17	0.07
Crude fiber content (%)	0.21	-0.05	-0.49	0.18	-0.08	0.35
Total carotenoid content (mg 100 g ⁻¹)	0.30	-0.24	-0.45	0.35	0.16	-0.28
Eigen value	4.50	3.10	2.162	1.54	1.14	1.08
Variance Percent	25.00	17.25	12.02	8.57	6.34	6.00
Cumulative Percentage	25.00	42.25	54.28	62.85	69.19	75.20



ig. 1: Dendrogram dividing the Summer Squash [*Cucurbita pepo* L.] genotypes into seven clusters by ward's metho

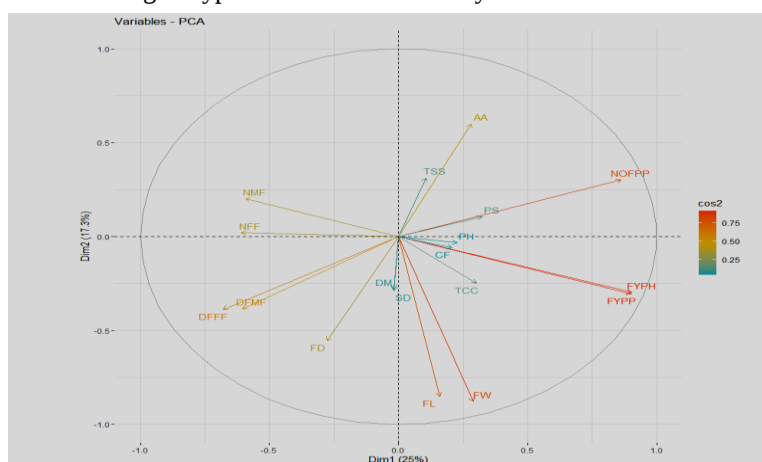


Fig 2: Relationship among different characters of Summer squash (*Cucurbita pepo* L.) genotypes by PCA biplot for first and second PC

PH: Plant height (cm), Sd: Stem diameter (cm), Dtfmf: Days to appearance of first male flower, Dtfff: Days to appearance of first female flower, Nff: Node of first male flower, Nmf: Node of first female flower, Ps: Plant spread (cm), Nofpp: Number of fruits per plant, Fl: Fruit length (cm), Fd: Fruit diameter (cm), Fw: Fruit weight (g), FYPP: Fruit yield/ plant (kg), FYPH: Fruit yield/ ha (q), TSS: TSS ($^{\circ}$ Brix), DM: Dry matter content (%), AA: Ascorbic acid content ($\text{mg } 100\text{g}^{-1}$), CF: Crude fiber content (%), TCC: Total carotenoid content ($\text{mg } 100\text{g}^{-1}$).

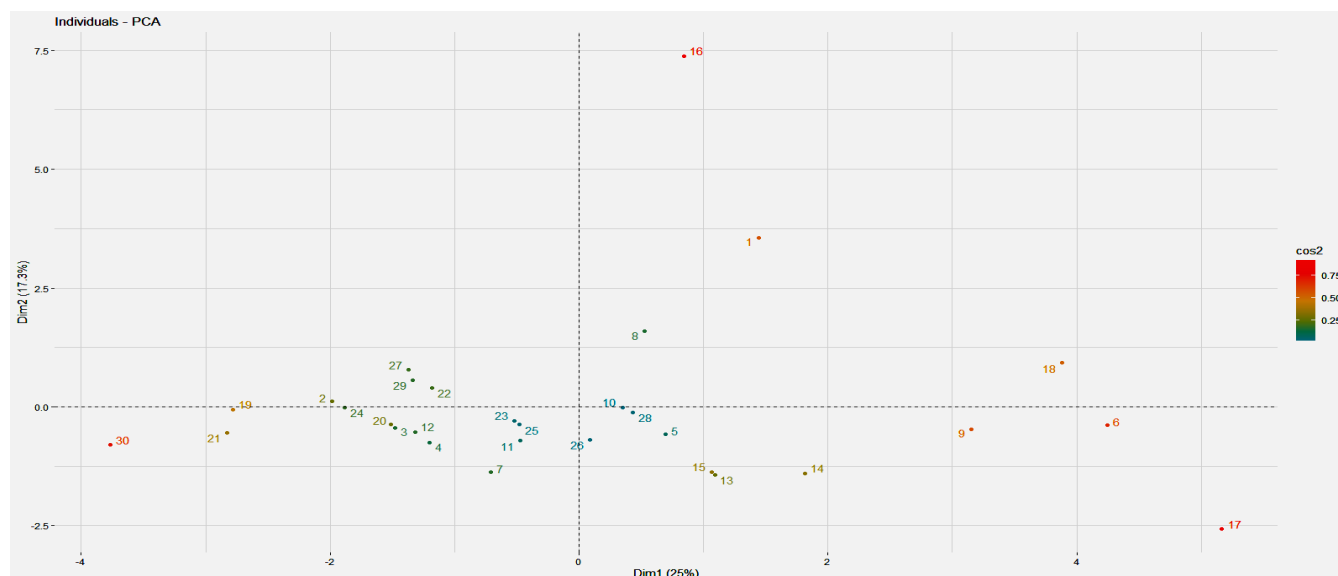


Fig. 3: Distribution of various genotypes among first 2 PC's explaining trait contributions

1-SKUA-SQ-01, 2-SKUA-SQ-02, 3-SKUA-SQ-03, 4-SKUA-SQ-04, 5-SKUA-SQ-05, 6-SKUA-SQ-06, 7-SKUA-SQ-07, 8-SKUA-SQ-08, 9-SKUA-SQ-09, 10-SKUA-SQ-10, 11-SKUA-SQ-11, 12-SKUA-SQ-12, 13-SKUA-SQ-13, 14-SKUA-SQ-14, 15-SKUA-SQ-15, 16-SKUA-SQ-16, 17-SKUA-SQ-17, 18-SKUA-SQ-18, 19-SKUA-SQ-19, 20-SKUA-SQ-20, 21-SKUA-SQ-21, 22-SKUA-SQ-22, 23-SKUA-SQ-23, 24-SKUA-SQ-24, 25-SKUA-SQ-25, 26-SKUA-SQ-26, 27-SKUA-SQ-27, 28-SKUA-SQ-28, 29-SKUA-SQ-29, SKUA-SQ-30

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