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Research Article

Selection criteria and multivariate analysis for identification of Turkey berry (*Solanum torvum*) genotypes for genetic improvement by using correlation and principal components analysis

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Abstract

Loss of biodiversity, which has an impact on both plant development and genetic advancement, disrupts the fundamental services that ecosystems provide to humanity. Variability assessment is a challenging topic. Multivariate statistics can be useful for comparing and evaluating genetic variability. The data of 16 different morpho-physiological variables were subjected to several multivariate approaches, including principal component (PC) and correlation coefficient analysis, in order to assess the diversity of the twenty Turkey berry genotypes. The correlation coefficients discovered through this analysis were used to gauge the strength of the association between the traits. In this study, Pearson correlation analysis revealed a significant correlation between the observed phenotypic traits. Among these traits, number of branches per plant , number of leaves, leaf area, number of flowers per cluster, number of flower cluster per plant, number of fruits per cluster, number of fruit cluster per plant, and fruit diameter exhibited a positive and significant correlation with fresh fruit yield per plant, whereas days of first flowering exhibited a negative and significant correlation with fresh fruit yield per plant. Principal component (PC) analysis revealed that the first three PCs had Eigen values greater than 1, accounting for 81% of the overall variation. For morphological features, PC 1 accounted for the largest variability of 57% of the overall variation, and the lowest contribution (10%) was recorded by PC3. The genotypes St007, St006, St008, St010, St011, St001, St009, St018, St020, St003, St004, and St005 were shown to be more varied and better performers in terms of fresh fruit yield and yield contributing features based on the primary factor scores. According to research findings, the genotypes of Turkey berries identified in this work would serve as useful genetic tools for boosting the productivity of the fruits for upcoming breeding endeavors, especially in light of the unpredictability of climate change.

Keyword: Turkey berry, character association, correlation analysis, principal component analysis and quality parameter.

INTRODUCTION

The adaptability, resilience, and evolutionary potential of plant populations are fundamentally influenced by genetic diversity, or the variation in genetic information within a species. This idea is best illustrated by the intriguing genetic diversity of the turkey berry plant (*Solanum torvum*), which has drawn the interest of scientists and researchers who are trying to understand its potential uses in agriculture, medicine, and conservation. The turkey berry plant is a member of the Solanaceae family and is indigenous to tropical regions of Africa, Asia, and Australia. It is also known by the names *Solanum torvum* and prickly nightshade. Genetic diversity can be seen in the *Solanum torvum* species in morphological characteristics like plant height, leaf shape, flower colour, and fruit size. Genetic variations between populations and geographical areas have an impact on these variations (Choudhary *et al.,* 2017). Exploring the turkey berry plant's genetic diversity is important because it could have useful applications. According to (Jayanthi *et al*., 2015) this knowledge can help plant breeders create improved cultivars for sustainable agriculture. The turkey berry plant's genetic diversity provides hope for the discovery of novel bioactive compounds and their potential therapeutic applications in conventional medicine (Jeyaseelan *et al.,* 2020). By examining its genetic diversity, researchers can unlock the turkey berry plant's untapped potential and promote conservation and agricultural innovation. This study opens the door to a deeper understanding of the species' capacity for environmental adaptation as well as its evolutionary history.

Principal component analysis (PCA), correlation analysis, scatterplots, and pie charts are crucial tools for data analysis and visualisation that provide insightful information across a wide range of academic disciplines. By making use of pertinent scientific literature, this introduction seeks to explore the importance of these techniques in scientific research. A statistical technique called correlation analysis measures the strength and direction of a linear association between two variables to quantify the relationship between them. By calculating correlation coefficients like Pearson's correlation coefficient or Spearman's rank correlation coefficient, researchers can determine the strength of a correlation. For instance, correlation analysis was used in a study by (Oyebadejo *et al.,* 2020) to look at the connection between rainfall patterns and agricultural productivity. By converting a high-dimensional dataset into a lower-dimensional space, principal component analysis (PCA) extracts the most insightful features or variables, and is a potent technique used for dimensionality reduction and pattern recognition in multivariate datasets. In a study by (Jafari *et al*., 2021), PCA was used to identify crucial volatile compounds in plant extracts, assisting in the classification and authentication of herbal medicines. A scatterplot is a type of graph that shows the correlation between two continuous variables. It displays the distribution of data points in a Cartesian coordinate system visually, with each dot signifying a different observation. Researchers can spot trends, outliers, and patterns in a dataset by using scatterplots. For instance, scatterplots were used in a study by (Wang *et al.,*2019) to look into the relationship between older adults' physical activity and cognitive function. Scatterplots, pie charts, principal component analysis, and correlation analysis are all important tools that allow researchers to identify patterns, identify meaningful insights, and visually represent data relationships. These techniques enable scientists to conduct thorough analyses, come to sound conclusions, and advance knowledge across a wide range of scientific disciplines.

MATERIALS AND METHODS

Site Description: The field study was carried out in the College Orchard at the Department of Vegetable Science, Horticultural College and Research Institute, TNAU, Coimbatore during 2022–2023 on clay-loam soil. The experimental site is geographically located in 11° N Latitude, 77° E Longitude, at 411m above Mean Sea Level (MSL). The site is situated in the tropical plain topography that receives 830 mm of rain falls annually. The experiment was laid in the randomised block design with three replications. The Turkey berry genotype was sown in a 30-centimetre square with plants and rows spaced apart by 2 metres by 2 metres, respectively. For each genotype, 10 plants were replicated thrice in an area of 60 cents. Twenty genotypes collected from various locations in Tamil Nadu and other Indian states were used in this study. **Table 1** contains a list of the genotypes and their sources. For growing a good crop, all suggested packages of practises were implemented. Days of first flowering information was compiled based on genotype. Data has been collected from season with respect to these characters like plant height (PH), internodal length (INL), the number of branches per plant (NBP), stem girth (SG), the number of stem prickles (NSP), the number of leaves (NL), the leaf area cm^2 (LA), the number of leaf prickles per plant (NLP), days of first flowering (DFF), number of flowers/cluster (NFLC), the number of flower clusters per plant (NFLCP), number of fruits/cluster(NFRC), the number of fruit clusters per plant (NFRCP), fruit diameter (FD), the individual fruit weight (IFW) and the fresh fruit yield (gm/plant) (FFYP). In order to record the observations, five randomly chosen plants from each genotype in each replication were tagged. The data observed were subjected to statistical analysis for one season.

Data Analysis by Statistical Methods and Computers Using Machine Learning Algorithms: The estimates of the mean, variance, and standard error were calculated according to (Panse and Sukathme 1957). The statistical and mathematical 'F' value served as the significance test. Rstudio - 1.3.1093 (https://rstudio.com/) and R-4.1.1 for win (http://CRAN.R-project. org) were used for all the statistical analyses. Differences were deemed significant at p 0.05. The dataset's dimensionality was decreased using PCA without sacrificing crucial information. With the aid of the RStudio (v 4.1.1) software packages "factoextra," and "FactoMineR," latent vectors, eigenvalues, and PCA-biplot are extracted from the PCA and was performed as suggested by (Wickham 2016).

Table 1. List of Turkey berry (*Solanum torvum*) genotypes used in the present study

S.No	Genotypes	Source
1	St001	Himachal Pradesh
2	St002	Tirupur, Tamil Nadu
3	St003	Madurai, Tamil Nadu
4	St004	Trivandrum, Kerala
5	St005	TNAU, Coimbatore,Tamilnadu
6	St006	OUAT,Bhubaneswar, Odisha
7	St007	Theni, Tamil Nadu
8	St008	Haveri, Karnataka
9	St009	Thiruvasur, Tamil Nadu
10	St010	Dindigul, Tamil Nadu
11	St011	Ram Nagar, Tamil Nadu
12	St012	Kolkata, West Bengal
13	St013	Guntur, Andhra Pradesh
14	St014	Ranchi, Jharkhand
15	St015	Nabarangpur, Odisha
16	St016	Patna, Bihar
17	St017	Kannur, Kerala
18	St018	Tiruhelveli, Tamil Nadu
19	St019	IIHR, Bangalore, Karnataka
20	St020	Kanyakumari, Tamil Nadu

RESULTS AND DISCUSSIONS

Correlation analysis: The scatter plot, which was created to represent different combinations of independent variables, showed that the groups in **Fig. 1** overlapped to a greater extent. The frequency distribution of each variable was predicted by the histogram with accuracy. The histogram showed the phenotypic frequency distribution of each variable, highlighting the overall similarity in their growth patterns, while the scatter plots showed a consistent linear trend for the majority of the variables. To determine the degree of correlation between the traits under consideration, a Pearson correlation analysis was conducted. The correlation coefficients discovered through this analysis were used to gauge the strength of the association between the traits. Notably, as shown in **Fig. 2**, the Pearson correlation analysis revealed a significant correlation between the observed phenotypic traits. Among these traits, number of branches per plant (NBP), number of leaves (NL), leaf area (LA), number of flowers per cluster (NFLC), number of flower cluster per plant (NFLCP), number of fruits per cluster (NFRC), number of fruit cluster per plant (NFRCP) and fruit diameter (FD) exhibited a positive and significant correlation with fresh fruit yield per plant, in which days of first flowering (DFF) exhibited a negative and significant correlation with fresh fruit yield per plant. The characters number of branches per plant showing r = 0.90, number of leaves r = 0.48, leaf area r = 0.93, number of flowers per cluster r = 0.96, number of flower cluster per plant r = 0.87, number of fruits per cluster r = 0.96, number of fruit cluster per plant r = 0.87, and fruit diameter r = 0.98 with the fresh fruit yield per plant. Whereas days of first flowering r = -0.92 showed a negative correlation with the fresh fruit yield per plant.

The scatter plots consistently displayed a linear trend for most variables, indicating a potential relationship between them. Similarly, the histogram highlighted the phenotypic frequency distribution of each variable, further emphasizing the overall similarities in their growth patterns. These findings suggest that certain traits, such as the number of branches, number of leaves, number of flowers per cluster, and number of fruits per cluster, as well as leaf area and fruit diameter, have a strong positive influence on the fresh fruit yield per plant. On the other hand, delaying the first flowering negatively impacts the fresh fruit yield. These correlations can be useful for understanding and predicting the potential fruit yield based on these phenotypic traits. The results were in close harmony with (Patel *et al.,* 2015) in brinjal and (Konyak *et al.,* 2020) on brinjal. In brinjal (Nayak and Nagre 2013) studied on variation found that there were highly significant differences between the varieties for every character. Fruit length, diameter, and weight significantly positively correlated with fruit yield in the plant and had a high direct effect, according to correlation and path analysis. Fruit length, diameter, and weight are therefore significant characteristics that could be used as selection criteria to increase fruit yield per plant.

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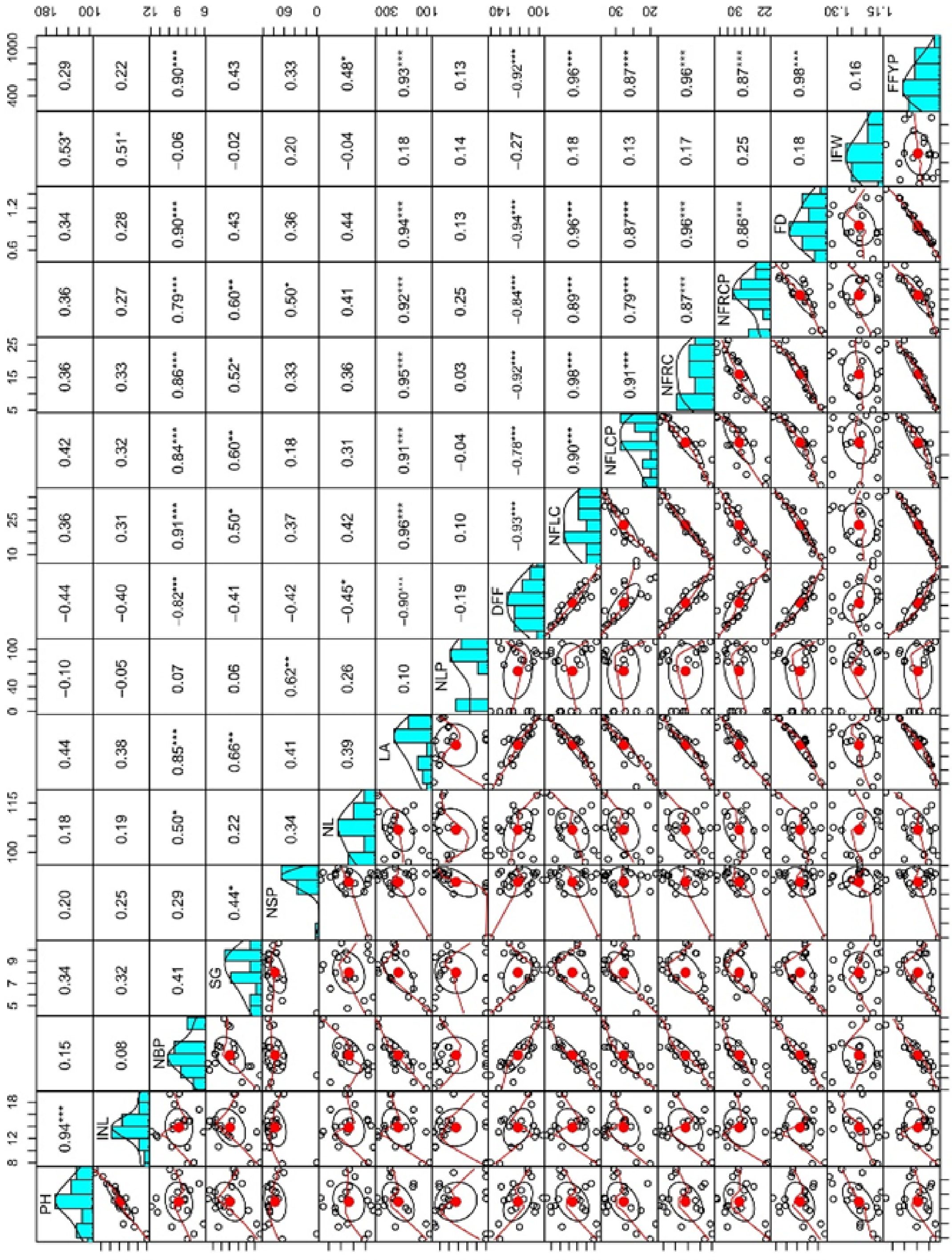

Fig. 1. Scatter plot, Frequency distribution and Correlation coefficient of Turkey berry genotypes

*, ** and *** indicate significant at $p < 0.05$, $p < 0.01$ and $p < 0.001$. (PH - Plant Height, INL - Inter Nodal Length, NBP - Number of branches/plant, SG - Stem Girth, NSP - Number of stem prickles, NL - Number of Leaves, LA - Leaf Area (cm2), NLP - Number of Leaf Prickles/Plant, DFF - Days of 1st Flowering, NFLC - Number of Flowers/Cluster, NFLCP - Number of Flower Cluster/Plant, NFRC - Number of Fruits/Cluster, NFRCP - Number of Fruit Cluster/Plant, FD - Fruit Dimeter, IFW - Individual Fruit Weight (g), FFY - Fresh Fruit Yield (g)/plant)).

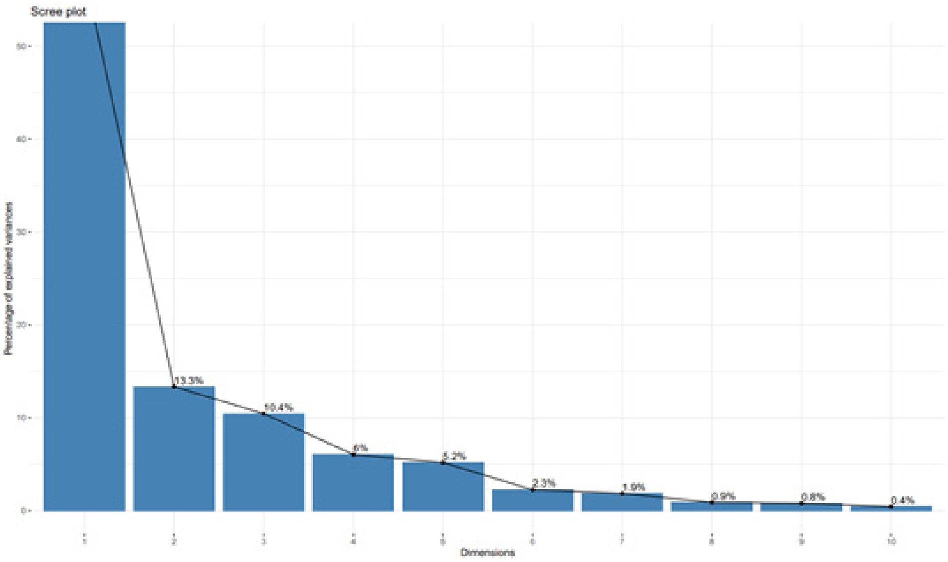

Fig. 2. Scree plot for principal components of 20 Turkey berry genotypes.

Principal component analysis: Multivariate statistical methods like PCA are used to analyse and break down large, complex datasets. The genetic diversity of the Turkey berry genotypes and their relationship to the observed attributes were assessed using PCA, which was based on the correlation between the traits and the pattern of variation in the genotypes. **Fig. 2** shows a scree plot, which is a simple line segment plot that shows the percentage of total variance in the data. The eigenvalues of the correlation matrix were plotted in descending power and components with an eigenvalue of less than one were removed, as suggested by (Brejda *et al.,* 2000)

PC I had the greatest effect on variability (57.86%), which is followed by the PC II (13.34%) and PC III (10.44%). To select traits that can be categorised into main groups and subgroups based on homogeneity and dissimilarity, a PCA biplot analysis can be used. Since these quantitative traits are highly variable, genotypes with high PC1 scores would exhibit high levels of variation in them.

In this data set (**Table 2**), there were three groups of attributes that were found using the PCA biplot that simultaneously considered PC1 and PC2. The PCA biplot showed that the PC1 was primarily responsible for explaining the plant height (0.468), inter nodal length (0.411), number of branches/plant (0.876), stem girth (0.876), number of stem prickles (0.459), number of leaves (0.486), leaf area (0.978), number of leaf prickles/plant (0.160), number of flowers/cluster (0.975), number of flower cluster/plant (0.902), number of fruits/cluster (0.962), number of fruit cluster/plant (0.923), fruit diameter (0.961), individual fruit weight (0.233) and fresh fruit yield (0.954), which together accounted for about 57% of the total variability.

The height of the plant (0.815), the space between nodes (0.815), stem girth (0.087), number of stem prickles (0.144) and individual fruit weight (0.706) were the main contributors to the second main factor, which accounted for about 13% of the total in PC2.

The third principal component, which includes stem girth (0.061), number of stem prickles (0.757), number of leaves (0.328), number of leaf prickles/plant (0.895), number of fruit cluster/plant (0.119) and individual fruit weight (0.101), explained about 10% of the total variability of PC3.

Each quadrant had a wide distribution of accessions (**Fig. 3**). In this data set (**Fig. 4**), two groups of traits were found by using both PC1 and PC2 in the PCA biplot. Internodal distance, plant height and fruit weight were grouped into group I. Group II included leaf area, fruit dimeter, flower cluster size, fruit yield, fruit number, fruit number per plant, fruit number per plant, flower cluster size, and leaf number.

Based on their differences, genotypes are dispersed in various ordinates. The length and colour intensity of a vector in a biplot show, respectively, how well the traits are represented and how much they contribute to the principal components. Positive or negative interactions between the traits under study are shown by the angles between the vectors derived from the midpoint of biplots. Larger circles represent the centroid of the associated.

These findings highlight the importance of considering a comprehensive range of traits or variables in future studies to capture a more complete picture of the genetic or phenotypic diversity within the germplasm (**Table 2**). These results were consistent with report of (Nachimuthu *et al.*, 2014). The utilization of a broader set of characteristics can provide a more comprehensive

Table 2. Plant characteristic extracted Eigenvalues and latent vectors connected to the first three main components

	Principal Components		
Variable	**PC1**	**PC2**	**PC3**
Eigenvalue	9.2587	2.1344	1.6710
Variance percent	57.8672	13.3400	10.4442
Cumulative variance percent	57.8672	71.2073	81.6516
Traits		**Latent vectors**	
Plant Height (PH)	0.468	0.815	-0.164
Inter nodal length (cm) (INL)	0.411	0.842	-0.086
Number of branches/plant (NBP)	0.876	-0.366	-0.084
Stem girth (cm) (SG)	0.529	0.087	0.061
Number of stem prickles (NSP)	0.459	0.144	0.757
Number of leaves (NL)	0.486	-0.109	0.328
Leaf area (cm^2) (LA)	0.978	-0.023	-0.069
Number of leaf prickles/plant (NLP)	0.160	-0.038	0.895
Days of 1st flowering (DFF)	-0.941	-0.012	-0.020
Number of flowers/cluster (NFLC)	0.975	-0.115	-0.076
Number of flower cluster/plant (NFLCP)	0.902	-0.069	-0.273
Number of fruits/cluster (NFRC)	0.962	-0.097	-0.153
Number of fruit cluster/plant (NFRCP)	0.923	-0.455	0.119
Fruit diameter (cm) (FD)	0.961	-0.136	-0.059
Individual fruit weight (g) (IFW)	0.233	0.706	0.101
Fresh fruit yield (g/plant) (FFYP)	0.954	-0.186	-0.062

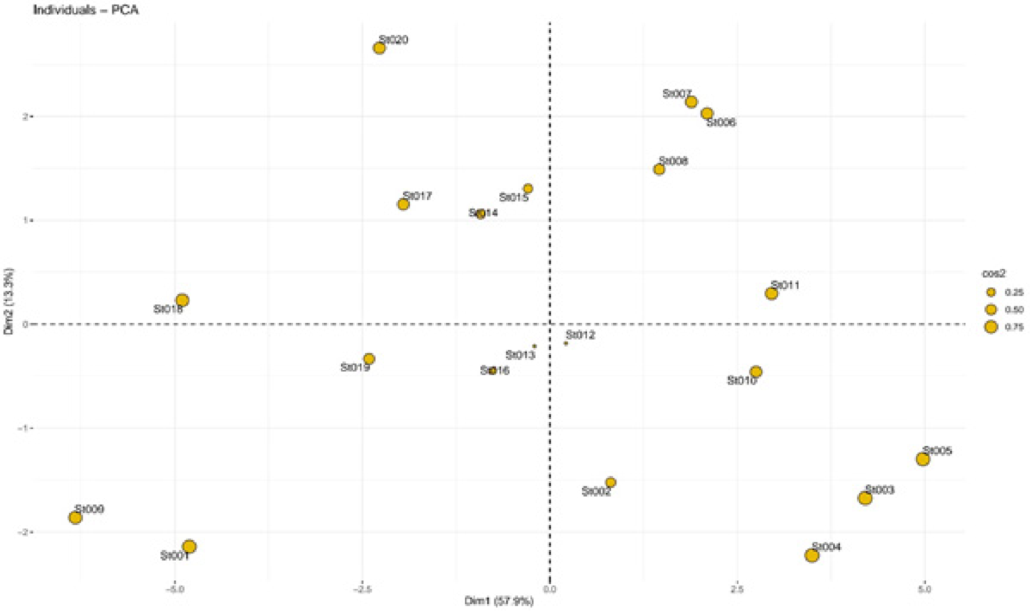

Fig. 3. Principal component biplot showing distribution of twenty Turkey berry genotypes.

(PH - Plant Height, INL - Inter Nodal Length, NBP - Number of branches/plant, SG - Stem Girth, NSP - Number of stem prickles, NL - Number of Leaves, LA - Leaf Area (cm^2), NLP - Number of Leaf Prickles/Plant, DFF - Days of 1st Flowering, NFLC - Number of Flowers/Cluster, NFLCP - Number of Flower Cluster/Plant, NFRC - Number of Fruits/Cluster, NFRCP - Number of Fruit Cluster/Plant, FD - Fruit Dimeter, IFW - Individual Fruit Weight (g), FFY - Fresh Fruit Yield (g)/plant)).

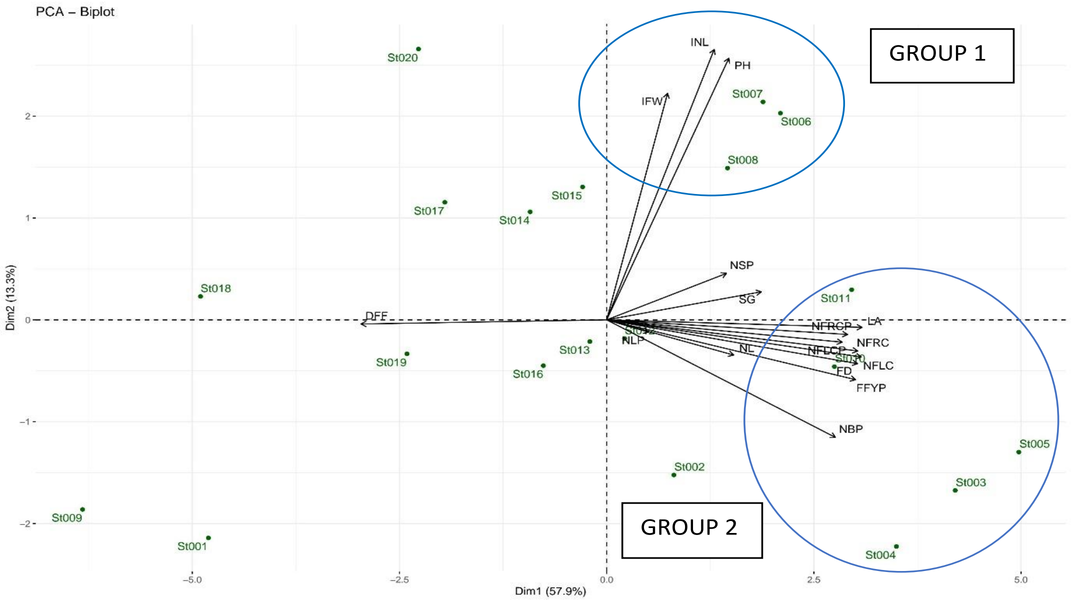

Fig. 4. Biplot of twenty Turkey berry genotypes based on different quantitative traits.

(PH - Plant Height, INL - Inter Nodal Length, NBP - Number of branches/plant, SG - Stem Girth, NSP - Number of stem prickles, NL - Number of Leaves, LA - Leaf Area (cm^2), NLP - Number of Leaf Prickles/Plant, DFF - Days of 1st Flowering, NFLC - Number of Flowers/Cluster, NFLCP - Number of Flower Cluster/Plant, NFRC - Number of Fruits/Cluster, NFRCP - Number of Fruit Cluster/Plant, FD - Fruit Dimeter, IFW - Individual Fruit Weight (g), FFY - Fresh Fruit Yield (g)/plant)).

understanding of the factors driving variation and enable researchers to make more informed decisions regarding breeding programs, conservation strategies, or other agricultural applications. The order of decreasing relevance was described by (Abraha *et al.,* 2015).

According to (Prasad *et al.,* 2023) the first four components accounted for 94.75 percent of the total variation, with principal component 1 (PC1) accounting for 55.96 percent and PC2 for 20.97 percent, according to principal component analysis and genotype by trait biplot analysis. The high yielding genotypes with additional yield characteristics discovered in this study would be an excellent source of genetic material for the development of premium tobacco varieties.

By understanding the major components contributing to the variability (**Fig. 4**), researchers can focus on specific traits that have a significant impact on the overall variation. This knowledge can be valuable for breeding programs, genetic studies, or agricultural management practices, as it helps identify important traits for selection and improvement. There were 16 principle components (PCs) in total, but only three of these were considered significant because their eigenvalues were higher than 1. The remaining non-significant PCs (eigenvalue 1) lacked sufficient interest to merit further investigation. In the turkey berry germplasm measured for various morphological features, these three PCs accounted for 81.651% of the variation (**Table 2**). These outcomes matched those of (Nachimuthu *et al.,* 2014). However, only 18.34% of the total morphophysiological diversity for this collection of Turkey berry genotypes was provided by the remaining 13 components. Furthermore, the main component analysis demonstrated that a limited number of traits cannot fully account for the heterogeneity in germplasm accessions. The order of decreasing relevance was described by (Abraha *et al.*, 2015). In 25 forage and 45 grain sorghum genotypes for dual purposes, the first four main components also had eigenvalues greater than one (Chikuta *et al.,* 2015). (Sasipriya *et al.,* 2022) found three principal components with eigenvalues greater than one and accounting for 78% of the population's overall variability were identified by principal component analysis (PCA).

(Mujaju and Chakauya, 2008) found a significant contribution from the first PCs to overall variability after looking at a number of features. Principal component analysis aims to resolve the entire variation of a set of characteristics into linear, independent composite traits in order to maximise the diversity in the data (Johnson 2012). Fruit width, fruit weight, and fruit yield per plant were identified as significant traits that contributed to the genotypes' divergence by (Malik *et al.*, 2011).

The best cultivars for number **of bolls** per plant were chosen from PC-1, which has the best variability and a high Eigen value, in the context of high variance, as previously presented by (Amna *et al.,* 2013). PC-1 is crucial and reliable for examining the wide range of variation among various traits. In order to produce superior genotypes for desired traits, breeding techniques may benefit from the information (Malik *et al.,* 2011). According to (Patel *et al.,* 2018) six components of PCA (PC-1 to PC-6) explained 70.73% of the variation in traits across all brinjal genotypes. In which, out of these six principal components, PC-1, PC-2, and PC-3, explained 21.11%, 13.07%, and 11.32% of the total variation respectively.

The key findings of the data showed a significant correlation between the phenotypic traits that were observed. Among these characteristics, the number of branches per plant, the number of leaves, the area of the leaves, the number of flowers per cluster, the number of flower clusters per plant, the number of fruits per cluster, the number of fruit clusters per plant, and the diameter of the fruit all showed positive and significant correlations with fresh fruit yield per plant, whereas the number of days since first flowering showed negative and significant correlations with fresh fruit yield per plant. Principal component (PC) analysis revealed that the first three PCs had Eigen values greater than 1, accounting for 81% of the overall variation. For morphological features, PC 1 accounted for the largest variability of 57% of the overall variation, and the lowest contribution (10%) was recorded by PC3. Based on the primary factor scores, it was determined that the genotypes St007, St006, St008, St010, St011, St001, St009, St018, St020, St003, St004 and St005 were more diverse and better performers in terms of fresh fruit yield and yield contributing features. Thus, the findings of this study revealed a high level of genetic diversity in the population along with the traits that contribute to this diversity, which has enormous potential for use in the improvement of Turkey berries. The present findings will assist in using these genotypes for Turkey berry genetic improvement.

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