Original Research Article

Exploration of diversity analysis in Avocado (*Persea americana* Mill.) accessions of Lower Pulney Hills of Tamil Nadu, India

Abstract

Avocado (*Persea americana* Mill.) is one of the world's most important subtropical fruit crops. This investigation of genetic diversity would be a first in Tamil Nadu. Morphological diversity in qualitative and quantitative features of avocado genotypes was investigated in this study. The IPGRI descriptor for avocado was used to evaluate twenty accessions for several morphological traits such as tree, leaf, flowering, fruit, seed, and yield traits. The 20 genotypes were classified into ten groups using Mahalanobis D2 statistics. PA-56 and PA-68, which differ in terms of characteristics and distance between the two genotypes, might provide transgressive segregants for choosing desirable traits. Principal component analysis was used to look at the quantitative and qualitative characteristics of the 20 genotypes that were chosen. The total variability of the five PCs was 84.14 percent, whereas the variability of the 13 primary components was 99.99 percent. The genotype with the highest PC score in that PC indicates the maximum values for the variables in that genotype. The genotypes were chosen based on PC values in each constituent that were positive and > 1.0 in each PC. The findings of this research will aid in germplasm management, conservation, and breeding strategies.

Keywords : Avocado, Diversity, genotypes, principal component and descriptors.

Introduction

Butter fruit, popularly known as *Persea americana*, is a flowering plant of the Lauraceae family. Drecher (Drecher, 2013). It has a diploid chromosomal number of 2n= 24 and is considered to have originated in Mexico and Central America (Rohwer, 1999). Its

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nutrient composition is comparable to ripe olives, which contain 2.1 percent protein and 24-26 percent fat on average. Because the fruit has less than 1% sugar, diabetics should eat it as a high-energy diet. It's often used in cosmetics and on the table purpose. Botanically, the fruit is a large berry with a single seed. The avocado was imported to India from Sri Lanka in the nineteenth century (Ghosh et al. 2000). The cultivated crop now comes in three botanical varieties or subspecies. Hereinafter described the Mexican (*P. americana* var. *drymifolia*), Guatemalan (*P. americana* var. *guatemalensis* Wms.) and West Indian (*P. americana* var. *americana* Mill.) races (Scora and Bergh, 1992).

Avocados are extensively produced in the Western Ghats of Tamil Nadu's Lower Pulnuy hills, where they are grown at an elevation of 800-1600 metres above sea level. Avocado plants are heterozygous in nature due to cross pollination. Unfortunately, due to a lack of research on the subject, knowledge on the occurrence of this genetic diversity is currently limited. Avocado diversity was assessed by exploring and characterising it using IPGRI descriptors for qualitative and quantitative traits (Tree, leaf, flowering, fruit and seed characteristics). However, research is being conducted to assess the diversity of seed-propagated avocado cultivated in Lower Pulnuy Hills. The findings of this study will aid in the design of germplasm management and conservation, as well as breeding strategies.

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Materials and Methods

The study was conducted in six locations in Tamil Nadu's Lower Pulnuy hills. This research was carried out in area such as Uthu, Patlakadu, Thandigudi, Peruganal, Thadiyankudisai, Manjal parappu, and TNAU orchard. Which portions of the Western Ghats are located between 800 and 1600 metres above sea level (MSL) at 10 degrees south latitude and 77 degrees east longitude. The areas were chosen because of their number of avocado trees and their closeness, which made traveling between them easier. In this context, old avocado trees grown from seed are referred to as seedlings. Field visits were undertaken with the assistance of locals who were familiar with avocado production sites in a specific area during August 2019 to October 2020. When an avocado tree was identified, we gathered information on the farmer's name, as well as the name of the village, district, and location where the tree was identified. The site's latitude, longitude, and elevation (altitude) were calculated using a Garmin Epic GPS (Global positioning system) mapping & Multisport Watch.

Table 1 contains information about the collected accessions. Each accession's tree (designated as PA - 51 to PA - 70) was explored from the lower Pulnuy hills and the TNAU Orchard. The observations of the tree, leaf, flower, fruit, seed, and yield characteristics were made using the descriptors developed by the International Plant Genetic Resources Institute (IPGRI; now Bio-diversity International) in 2000.

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The observations were made on five randomly selected fruits from each accession when they were fully mature. The avocado descriptor was used to describe the tree shape, tree age, tree height (m), tree canopy (m2), trunk circumference (cm), leaf blade length (cm), number of flower / inflorescence, fruit length (cm), fruit circumference (cm), fruit weight (g), fruit peel thickness (mm), pulp peel ratio, seed weight (g), seed – pulp ratio, length of seed cavity (cm), length of seed (cm), seed circumference (cm), seed

The clustering groups were constructed based on the neighbour joining approach using a dissimilarity matrix of the 20 avocado genotypes using the R programme – 4.1.2 version. Principal components (PCs) with an eigenvalue greater than one were chosen (Jeffers, 1967), and the PCA was carried out using standardised values from the PAST 3 application. The scree plot was used to visually examine the components that contributed the most to the total variation.

Results and discussion

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Cluster analysis

A cluster analysis splits a natural population of the same species into closely related phylogenetic main groupings and subgroups. The approach groups the population using a set of morphological traits with very consistent criteria. In this study, the properties of the tree, leaves, flowers, fruits, and seeds were used to evaluate the characters. Based on 38 morphological traits, a dendrogram displays the relationships between all avocado trees. Each accession was given a number.

The twenty genotypes were classified into ten groups (Table 2 and Fig 1). Cluster VII had the most genotypes (6), followed by Cluster V (3), Cluster II (2), Cluster IV (2), Cluster VI (2), Cluster I,III,VIII, IX, and each one contributing genotypes. Cluster seven indicates that the same set of planting materials is expected to circulate in the study region and that there should be less morphological diversity in these places. Avocado accessions with comparable morphological characteristics were classified together, so samples like PA-70, PA-62, PA-63, PA-61, PA-69, and PA-51 were grouped together, followed by groups II, IV, V, VI. All the groups are separated at 12% similarity coefficient level. In future, while crossing the genotypes *viz.*, PA-56 and PA-68 which possess variations in the characters and distance between the two genotypes are diverse in nature can give new combination of characters. The genotypes PA-56 and PA-68 showed higher variation since these were propagated through seeds.

Principal component analysis (PCA)

PCA is an effective approach for identifying the fewest number of components, which aids in predicting maximum variability out of total variability (Morrison, 1992). PCA provides the additional feature of ranking genotypes based on PC scores. As a result, avocado genotype variability must be evaluated. The principal component analysis was applied for 20 genotypes collected from different areas of Tamil Nadu's lower pulney hills.

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PCA was used to analyse 20 qualitative and 17 quantitative characters. The data show that there are five principal components with eigenvalues greater than one (Table.3), however there are also thirteen principal components expressed (Table.4). The variability reported in the five PCs was 84.14 percent (Table.3), whereas the variability reported in the 13 principal components was 99.99 percent (Table. 4). Chaimae Nasri et al. (2021) discovered that two principal components with multiple eigenvalues accounted for the majority of the variance in avocado oil.

In a Scree plot graph, the component number was plotted on the X-axis, and the eigenvalues were plotted on the Y-axis (Fig.2a). It explains the percentage of variance associated with qualitative features for each primary component. Gour et al. discovered that PC1 had a maximum variability of 28.068 percent with an eigenvalue of 6.79, which subsequently decreased (2017). The quantitative characteristics were expressed as having more variability in PC1 92.45 percent with eigenvalues of 44201.4. (Fig 2b). The findings can be used to create appropriate selection indices by explaining each PC and understanding the intensity. PCA study on 20 avocado genotypes resulted in the measurement of qualitative and quantitative features based on principal component scores (PC scores). The genotype with the highest PC score in that PC indicates the maximum values for the variables in that genotype. PC value. PC1 components include genotypes (PA - 55, PA - 56, PA - 58, PA - 59, PA - 65, PA - 66), PC2 components include six genotypes with > 1.0 values (PA- 60, PA - 61, PA - 64, PA - 65, PA - 66, PA - 70), and PC3 components include genotypes (PA - 52, PA - 54, PA - 58, PA – 65, PA - 68). The maximum values for the variables in a particular genotype are indicated by the genotype with the highest PC score in that PC. (Table 8) PC1 components was had (PA - 52,PA- 53, PA - 56, PA - 66, PA - 67), PC2 components consist of (PA -51, PA -52, PA -54, PA - 55, PA -56, PA-57, PA - 58, PA -59, PA - 60, PA - 61), PC3 components include genotypes (PA - 56, PA - 57, PA - 58, PA - 59, PA - 60, PA - 61, PA - 62, PA - 67, PA - 69.

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Figure 3 shows a scatter plot including PC1 and PC2 that revealed a distinct pattern of clustering among the 20 avocado genotypes. PA – 60, PA - 65, PA - 55, PA - 53, PA - 67, PA - 62, PA -70 are the genotypes that inhabited the convex of the hull. The maximum variation was observed in Bitterness of pulp, Tree shape, Gloss of fruit skin, Fruit shape. Principal components, scatter plot had PC1 and PC3, maximum variability was noticed accessions PA - 65, PA – 58, PA – 55, PA – 66, PA – 64,PA – 67, PA – 62,PA –70, PA – 52, characters viz., bitterness of pulp, tree shape, length of seed .

Scatter plot incorporating PC1 and PC2 indicated a clear pattern of clustering among the 20 avocado genotypes. The genotypes which occupied the convex of the hull are PA – 52, PA -56, PA - 67, PA - 62, PA - 63, PA - 66, PA - 69, PA - 58. By the results of principal components, scatter plot for PC1 and PC2, the Maximum variation was observed in tree height, trunk circumference, yield, number of flower / inflorescence (Fig. 4) principal components , scatter plot for PC1 and PC3, maximum diversity was noticed accessions PA - 67, PA – 56, PA -60, PA -63, PA -54, PA- 58,PA – 59, characters *viz.*, tree height, trunk circumference, number of flower / inflorescence, yield.

Based on the findings of this study, it is determined that a broad range of variability exists among the genotypes for all of the features in the accessions of PA-56 and PA-68, indicating that there is great possibility for improving avocado genotypes by clonal selection. According to the results of the principal component analysis study, the qualitative and quantitative characteristics of tree shape, fruit shape, leaf shape, tree age, tree height, leaf blade length, number of flower/inflorescence, fruit length, fruit circumference, fruit weight, fruit peel thickness, pulp – peel ratio, yield should be given preference for the selection of superior genotypes.

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Table -1: Details of exploration Avocado (*Persea americana* Mill.) genotypes from Lower pulney hills of Tamil Nadu and Coimbatore.

Accession Number	Name of the genotypes	Source / Location	Tree age (years)	Latitude	Longitude
PA-51	Uthu local	S. Ravi, Uthu	20	10.367	77.980
PA-52	Uthu local	S. Ravi, Uthu	12	10.367	77.980
PA-53	Uthu local	S. Ravi, Uthu	13	10.367	77.980
PA-54	Uthu local	S. Ravi, Uthu	15	10.367	77.980
PA-55	Patlakadu Local	R.Kariyammal, Patlakadu	18	10.225	77.667

PA-56	Thandigudi local	S.Moorthy, Thandigudi	22	10.306	77.645
PA-57	Thandigudi local	S.Moorthy, Thandigudi	14	10.306	77.645
PA-58	Peruganal local	S.Murali, Peruganal	14	10.300	77.671
PA-59	Peruganal local	S.Murali, Peruganal	24	10.300	77.671
PA-60	Peruganal local	S.Murali, Peruganal	24	10.300	77.671
PA-61	Thadiyankudisai local	Horticultural Research Station, Thadiyankudisai	16	10.296	77.708
PA-62	Thadiyankudisai local	Horticultural Research Station, Thadiyankudisai	8	10.296	77.708
PA-63	Thadiyankudisai local	Horticultural Research Station, Thadiyankudisai	8	10.296	77.708
PA-64	Manjalparppu local	S.Pradeep, Manjalparappu	8	10.301	77.751
PA-65	Manjalparappu local	S.Pradeep, Manjalparappu	28	10.301	77.751
PA-66	TNAU, Orchard, local	TNAU, Orchard,Coimbatore	30	11.011	76.935
PA-67	TNAU, Orchard, local	TNAU, Orchard, Coimbatore	15	11.011	76.935
PA-68	TNAU, Orchard, local	TNAU, Orchard, Coimbatore	12	11.011	76.935
PA-69	TNAU, Orchard, local	TNAU, Orchard, Coimbatore	12	11.011	76.935
PA-70	TNAU, Orchard, local	TNAU, Orchard, Coimbatore	15	11.011	76.935

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Table 2. Clustering of 20 Avocado genotypes

Cluster	Number of Genotypes	Name of the Genotypes
Cluster I	1	PA - 56
Cluster II	2	PA - 55, PA - 58
Cluster III	1	PA - 64
Cluster IV	2	PA - 54, PA - 60
Cluster V	3	PA - 52, PA- 53, PA - 57
Cluster VI	2	PA - 66, PA - 67
Cluster VII	6	PA - 51, PA - 69, PA - 61, PA - 63, PA - 62, PA -70
Cluster VIII	1	PA - 65
Cluster IX	1	PA - 59

Cluster X	1	PA - 68

Table 3. Eigenvalues, variance, cumulative variability and qualitative characters of avocado genotypes

Principal component	Eigenvalue	Per cent variance	Cumulative variance
1	6.79163	28.068	28.068
2	5.26583	21.762	49.83
3	4.02047	16.615	66.445
4	2.68017	11.076	77.521
5	1.60178	6.6196	84.1406

Table 4. Eigenvalues, variance, cumulative variability and quantitative characters of avocado genotypes

Principal component	Eigenvalue	Per cent variance	Cumulative variance
1	44201.4	92.454	92.454
2	1656.96	3.465	95.919
3	999.43	2.090	98.010
4	553.01	1.156	99.167
5	305.74	0.639	99.806
6	34.61	0.072	99.878
7	20.86	0.043	99.922
8	15.097	0.031	99.954
9	9.802	0.020	99.974
10	4.279	0.008	99.983
11	3.795	0.007	99.991
12	2.004	0.004	99.995
13	1.727	0.003	99.999

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Table 5. Interpretation of PCA for the qualitative traits having values > 0.5 in each PCs.

	PC 1	PC 2	PC 3
Traits	Tree shape Leaf shape Bitterness of pulp	Fruit shape	Bitterness of pulp

Table 6. Interpretation of PCA for the quantitative traits having values > 0.5 in each PCs.

Traits	PC 1	PC 2	PC 3

	Tree age Tree height Leaf blade length Number of flower/inflorescence Fruit length Fruit circumferencre Fruit weight Fruit peel thickness Pulp – Peel ratio Seed weight Length of seed cavity Length of seed Seed circumference Yield	Tree age Tree height Tree canopy Trunk circumference Pulp – Peel ratio Seed weight yield	Tree age Tree height Tree canopy Trunk circumference Number of flower/inflorescence

Table 7: Genotype selection based on PC score in each component with positive values and greater than 1.0 in each PC – Qualitative characters

PC1	PC2	PC3
PA - 55 (4.9904)	PA - 60 (5.2737)	PA - 52 (3.6393)
PA - 56 (1.6045)	PA - 61 (1.6374)	PA - 54 (2.3931)
PA - 58 (2.7251)	PA - 64 (2.0327)	PA - 58 (2.5134)
PA - 59 (5.7829)	PA - 65 (4.0907)	PA - 65 (3.0955)
PA - 65 (1.3762)	PA - 66 (1.6068)	PA - 68 (3.0498)
PA - 66 (2.1367)	PA - 70 (1.2148)	

Table 8. Genotype selection based on PC score in each component with positive values and greater than 1.0 in each PC – Quantitative characters

PC1	PC2	PC3
PA - 52 (29.325)	PA - 51 (35.181)	PA -56 (1.7008)
PA - 53 (276.89)	PA - 52 (67.609)	PA - 57 (19.388)
PA - 56 (772.11)	PA - 54 (15.34)	PA - 58 (32.725)
PA - 66 (24.012)	PA - 55 (8.5106)	PA - 59 (45.678)
PA - 67 (123.9)	PA - 56 (26.395)	PA - 60 (39.847)
	PA - 57 (28.472)	PA - 61 (43.407)
	PA - 58 (37.359)	PA - 62 (17.292)
	PA - 59 (41.601)	PA - 67 (55.631)
	PA - 60 (47.04)	PA - 69 (4.0045)
	PA - 61 (20.1)	

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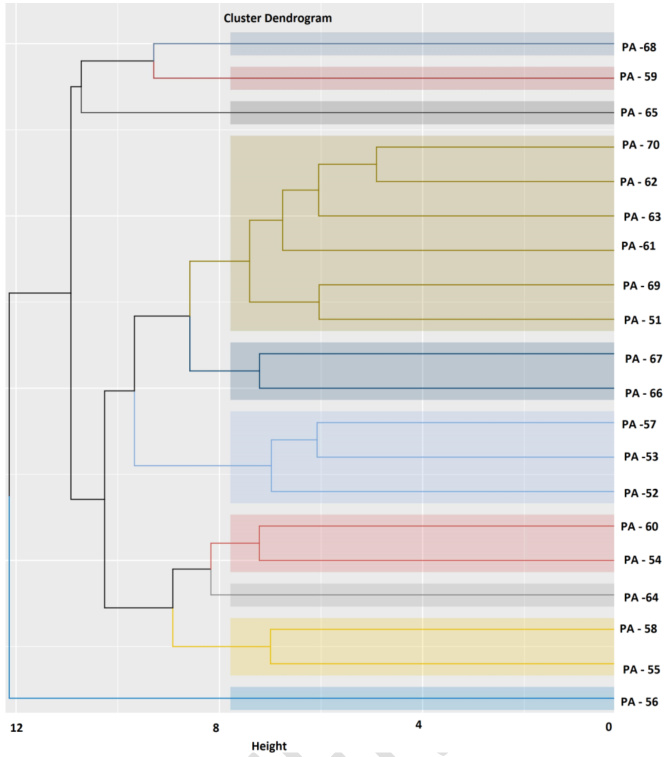


Fig 1. Dedrogram computed based on the neighbour joining algorithm using a dissimilarity matrix of the 20 avocado genotypes

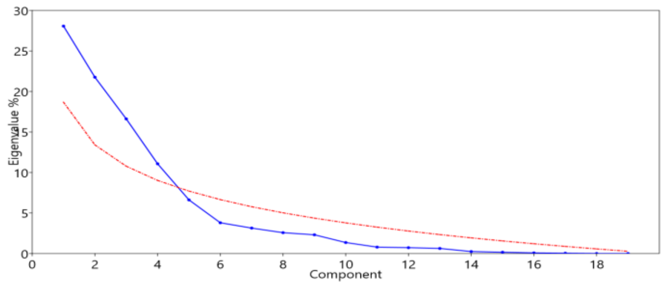


Fig 2a . Scree plot based on eigen values of qualitative characters

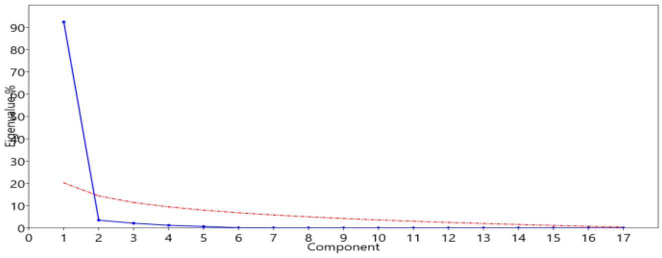


Fig 2b . Scree plot based on eigen values of quantitative characters

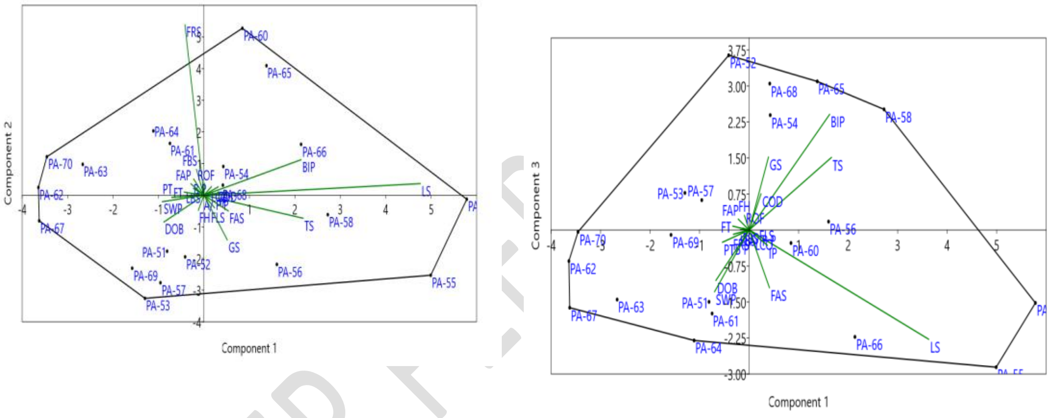
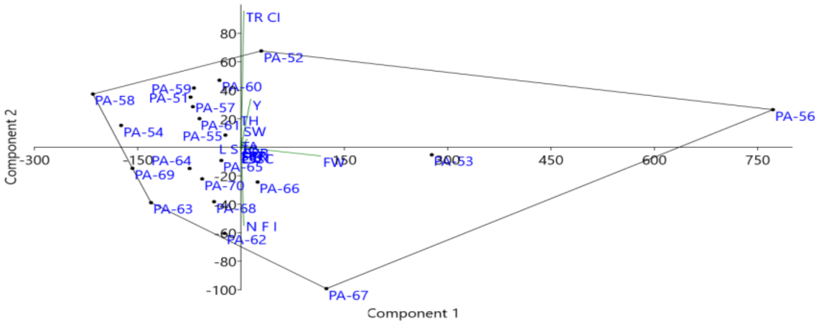


Fig 3. Genotype scatterplot illustrating the relationship between qualitative traits of PC1 and PC2, PC1 and PC3



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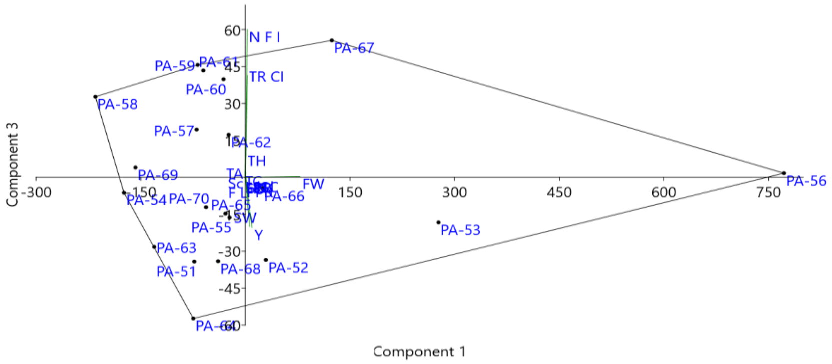

Fig 3. Genotype scatterplot illustrating the relationship between quantitative traits of PC1 and PC2, PC1 and PC3

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