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Genetic diversity in avocado based on qualitative characters

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Abstract
Diversity studies were carried out among 52 avocado accessions using Mahalanobis D^2 statistics and principal component analysis. Based on D^2 analysis avocado accessions were grouped into six clusters. Cluster I consisted of 2 accessions, cluster II had 18 accessions, cluster III had 17 accessions while cluster IV, V and VI consisted of three, eight and four accessions respectively. The study showed 13 principal components that account for 77% of the total diversity in qualitative characteristics across accessions. Crop improvement is likely to result from choosing genotypes from divergent clusters and using them in hybridization programmes.

Keywords: Genetic diversity, Avocado, Principal component analysis and D^2 analysis

Introduction

Avocado (*Persea americana*) is a member of the Lauraceae family, with chromosomal number $2n = 2x = 24$ and a genomic size of 800 Mbp. Avocado is divided into three botanical races: Mexican (*P. americana* var. *drymifolia*), Guatemalan (*P. americana* var. *guatemalensis*) and West Indian (*P. americana* var. *americana*). West Indian avocados originated in the tropical lowlands of southern Mexico and Central America, but Guatemalan and Mexican avocados originated in their respective countries' mid altitude highlands (Crane *et al.,* 2005; Storey *et al.,* 1986) [1, 7]. Because of its nutritional importance, the avocado plant has spread around the world. It includes mono-unsaturated fatty acids, which effectively lower the levels of low density lipoproteins in the blood, so aiding in the prevention of heart disease (Subha and Anitha, 2018) [8].

Avocado being a cross pollinated species and predominance of propagation via seed provides ample opportunities for the selection of outstanding types with desirable horticultural characteristics. Genetic divergence aids in the selection of genetically different parents for use in hybridization programmes. Several methods have been developed for measuring divergence between populations using multivariate analysis. In this context, the present investigation aimed at assessing the genetic diversity using principal component analysis and D^2 analysis.

The aim of principal component analysis is to identify the characteristics that contribute significantly to taxonomic delimitation; whereas cluster analysis and others were targeted at identifying how closely related the species or variations are to one another using phonetic similarities. A hierarchical cluster analysis is also used to explain the dissimilarities among genotypes based on Euclidean distance and to investigate the relationship between them based on their potential characteristics. The multivariate analysis is an effective means of understanding genetic similarities and dissimilarities among the genotypes, where the several different traits are examined simultaneously to understand the clustering mechanism for their utility breeding, commercialization and conservation of plant genetic resources (Kumar *et al.,* 2023) [6].

A morphological technique utilising both cluster and principal component analysis was used to acquire phenomenal insight into the diversity among avocado accessions.

Materials and Methods

The experiment was carried out at ICAR-IIHR-CHES, Hirehalli. The experimental material consisted of fifty two avocado accessions maintained under uniform cultural practices throughout the investigation. All the qualitative morphological characters were recorded as per the standard crop descriptors suggested by IPGRI (1995) [3].

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Statistical analysis: Principal Component Analysis and Cluster Analysis were used to determine genetic divergence among 52 avocado accessions. The XLSTAT 2013.2.04 statistics programme was used to perform principal component analysis. The unweighted pair-group method (UPGMA) in PAST statistics software was then used to infer a dendrogram based on the similarity index (Hammer *et al.,* 2001) [2].

## Results and Discussion
Clustering analysis
The collected accessions were clustered using qualitative morphological features based on the similarity index of the algorithm UPGMA dendrogram. The dendrogram was sorted into six clusters based on similarities and differences in its characteristics (Fig 1). Cluster I had two accessions, Cluster II had eight, Cluster III had seventeen, and Cluster IV, V, and VI had three, eight, and four accessions, respectively.

Principal component analysis: The PCA based on morphological descriptors revealed significant differences among the collected accessions. The accessions were evenly scattered over all four sides of the plot (Fig 2). The first 13 components with Eigen values greater than one accounted for 77.35% of the variation among the accessions studied. The PC1 accounts for the maximum variability (12.67%) in the data, while PC2 with Eigen value of 3.54 accounted for 9.56% of the total variability observed. PC3 had Eigen value of 3.29 and contributed 8.91% to the observed variability. Meanwhile, PC4, PC5 and PC6 had Eigen value 2.87, 2.14 and 2.02 which contributed 7.77%, 5.80% and 5.46% of total variability, respectively.

For each principal component, there are several characters contributing to the total variation. Major contributing characters for the diversity in the principal component one (PC1) was fruit skin pliability (0.644), free space of seed cavity (0.608), nut taste (0.579), general taste (0.578), fruit shape (0.522) and fruit apex position (0.517) while, seed position (-0.577), tree shape (-0.517) and fibre content in the pulp (-0.434) had the highest negative loading. In PCA, characteristics are analyzed in terms of their association and direction of variation. Fruit apex shape (0.610), gloss on fruit skin (0.596), fruiting habit (0.459) was positively correlated with PC2. Trunk surface (-0.597), leaf apex shape (-0.538) and general taste of the pulp (-0.481) decreased in PC2. Moreover in 3, 4, 5 and 6 principal component, trait such as fruit skin surface (0.773), trunk surface (0.539), distribution of branches (0.679) and crotch angle of leaf petiole (0.525) had the highest positive loading, respectively. Fruit skin pliability and fruit apex shape was examined to be best choice which had the highest loading from the principal component one (PC1) and two (PC2), respectively. In principal component analysis (PCA) amount of variation among the genotypes can be attributed to every axis of differentiation by the largest contributor. To aid the visualization of variations among the genotypes, the score of first two principal components were represented graphically in the form of principal component biplot (Fig 2).

Previous research in avocado (Juma *et al*. 2020) [4] and pomegranate (Khadivi *et al*. 2018) [5] found that fruit characteristics were important in differentiating and analysing breeding material. Finally, the accessions exhibited the characteristics of all three horticultural races. The large number of morphological variants in collected accessions allows for the selection of elite genotypes for commercial cultivation as well as the conservation of germplasm with different genes for future breeding projects.
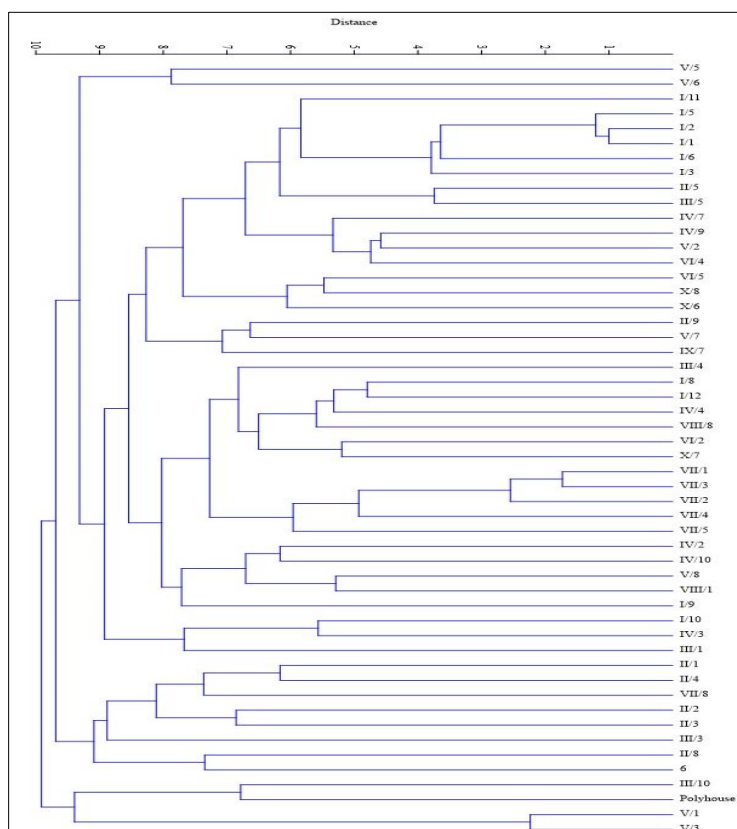
Fig 1: Dendrogram grouping of 52 avocado accessions based on morphological characters.

Table 1: Distribution of avocado accessions in different clusters based on morphological characters.

Cluster Group	No. of accessions	List of accessions
Cluster I	2	V/5 and V/6
Cluster II	18	I/1, I/2, I/3, I/5, I/6, I/11, II/5, III/5, IV/7, IV/9, V/2, VI/4, VI/5, X/6, X/8, II/9, V/7 and IX/7
Cluster III	17	I/8, III/4, I/12, IV/4, VIII/8, VI/2, X/7, VII/1, VII/2, VII/3, VII/4, VII/5, IV/2, IV/10, V/8, VIII/1 and I/9
Cluster IV	3	I/10, IV/3, III/1
Cluster V	8	II/1, II/4, VII/8, II/2, II/3, III/3, II/8 and 6
Cluster VI	4	V/1, V/3, III/10 and 7
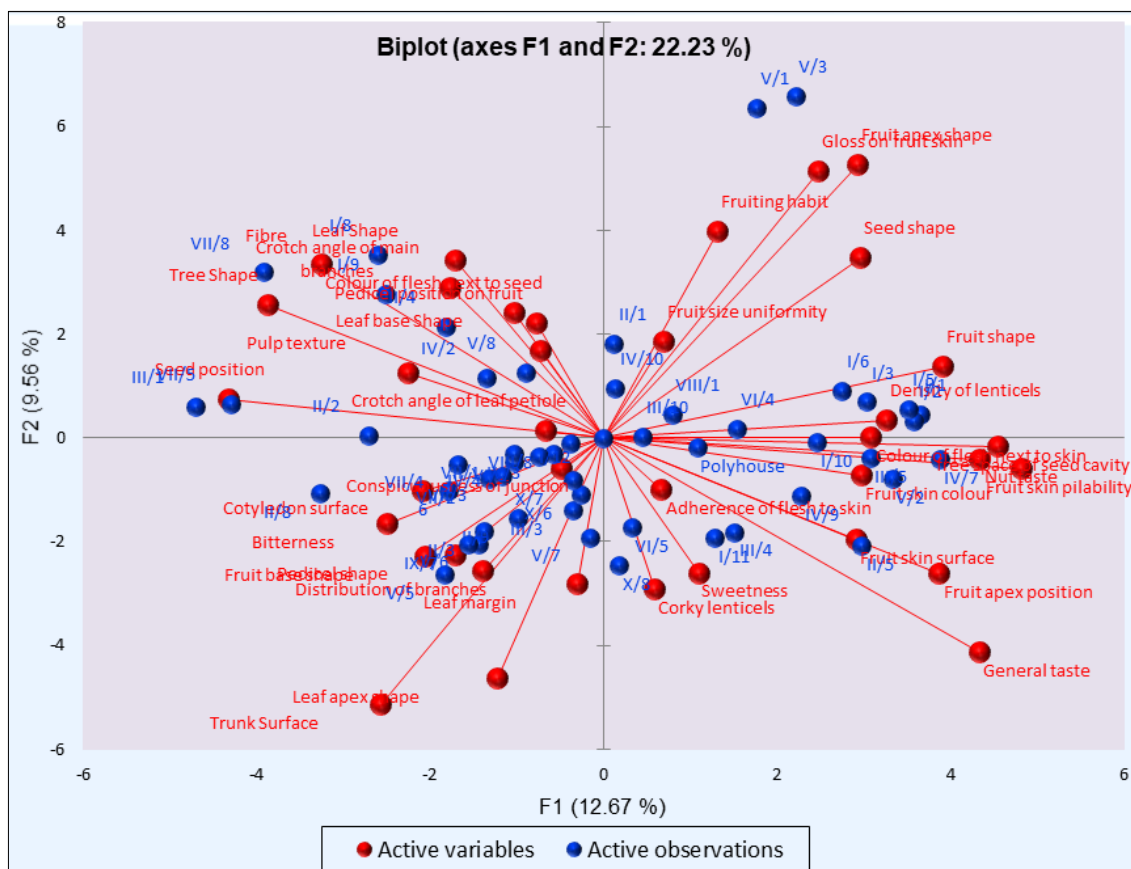
Fig 2: Biplot based on PCA

Conclusion

The study revealed that avocado accessions possessed significant morphological variations with respect to tree and leaf characters. D^2 analysis grouped the avocado accessions into six clusters and PCA was able to capture 77.35% of the variations present in the 52 avocado accessions.

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