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# $D^2$ analysis in avocado (*Persea americana* Mill)

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**Abstract**
Avocado popularly known as butter fruit belonging to the family Lauraceae. Avocado is a great nutrient dense food that provide good amount of vitamins, minerals and other nutrients. The fruit pulp is rich in good fat that reduce the risk of heart disease and hypertension. Avocado being a highly cross pollinated crop due to its protogyny nature, exhibits wider variability. However exploitation of these variability is very meager. A field survey was conducted at Lower Pulney Hills, Western Ghats of Tamil Nadu to identify a superior quality avocado genotypes. More than 100 avocado genotypes were identified and subjected to fruit characterization by using IBPGR descriptor. Among them sixteen avocado genotypes were selected based on fruit size, shape, colour and weight for the present experiment. The experiment was laid out in a Completely Randomized Block Design and replicated thrice. Biometrical observations on fruit length (cm), fruit diameter (cm), peduncle length (cm), peduncle diameter (mm), pedicel length (cm) and fruit weight (g). Nutritive analysis for fat (g), dietry fibre (g), carbohydrate, carotene, vitamin C, calcium and phosphorus were taken from each genotype and subjected to diversity analysis. The results showed that among the 11 clusters, cluster 1 and 2 had the highest number of genotypes. From the results it was observed that the intra cluster values were less than inter cluster values suggested that the study material were homogenous and heterogeneous nature of the genotypes within and between the clusters, respectively. The maximum intra cluster distance was noticed with in cluster 3 and it was followed by the cluster 1 and cluster 2. The cluster mean value results showed that the cluster 11 registered the highest cluster mean values for the traits *viz.*, fruit length, fruit diameter, peduncle length, peduncle diameter, fruit weight and fibre content. The highest contribution in the manifestation of genetic divergence was exhibited by phosphorus and it was followed by vitamin c, calcium and pedicle length.

**Keywords:** Avocado, *Persea americana*, fruit character, nutritive traits, $D^2$ analysis

## Introduction
Avocado (*Persea americana* Mill) also called alligator pear belonging to the family Lauraceae. Avocado fruits have greenish or yellowish flesh with a buttery consistency and a rich, nutty flavor and rightly called as butter fruit. Avocado a great nutrient dense food that provide substantial amounts of vitamins, minerals and other nutrients with relatively few calories. Avocados rich in potassium, dietary fiber, and fats. Avocado pulp rich in oil that consist almost two-thirds (71 percent) monounsaturated fatty acids, the "good fats" shown to lower LDL, or "bad," cholesterol and increase HDL, or "good," cholesterol, because of their "healthy-fat" status, avocados have become a popular food among people following the ketogenic diet. Potassium is a main health component of the fruit that helps promote healthy heart contraction and reduces high blood pressure, avocados are loaded with nutrients such as vitamin C, vitamin K, vitamin B, vitamin E, and vitamin A. Avocados are also a good source of dietary fiber, which helps reduce the risk of heart disease, type 2 diabetes, and obesity, its vitamin C may help reduce skin inflammation, accelerate wound healing, and soothe dry skin. Avocado oil may boost collagen production, further reducing signs of aging (Werman *et al*., 1991) [16]. Avocados are cultivated in tropical and Mediterranean climates of many countries, with Mexico as the leading producer of avocados in 2019, supplying 32 per cent of the world total. In India Avocado is largely cultivated in North-Eastern states and Western Ghats of South India. In Tamil Nadu avocados are commonly found in Pulney hills. Avocado is a highly heterozy-gous diploid species with 12 pairs of chromosomes (Garcia *et al*., 1975) [2]. Avocado is a cross-pollinating species with a reported out crossing ranging from 74 to 96 per cent. Owing to its high cross pollination nature it exhibits wider variability. It was observed that high genetic variation observed with respect to fruit shape, size, colour, flavor, taste, quality etc., Heterogeneous local population of the genus forms an important source of genetic variation (Zeven, 1998) [17].

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In any crop improvement programme evaluation of germplasm is great importance to understand the genetic background and breeding value of the available gremplasm (Singh *et al.,* 2002) [14]. Genetic diversity analysis assists in interpreting the genetic background and breeding value of the germplasm (Joshi *et al*., 2012) [5]. For the selection of parents in hybridization, diversity among parents for the character of interest, estimation of genetic distance is most important as diverse plants are supposed to give high hybrid vigour (Harrington, 1940) [3]. Estimation of genetic divergence also allows breeders to eliminate some parents in downsizing the gene pool available and concentrate their efforts in a smaller number of hybrid combinations (Fuzzato *et al*., 2002).

**Materials and Methods**
The experiment was conducted at Horticulture Research Station, Tamil Nadu Agricultural University, Thadiyankudisai during 2018. A field survey was conducted at lower Pulney hills, the Western Ghats of Tamil Nadu to identify superior avocado genotypes. More than 100 avocado genotypes were identified and fruits of individual genotypes were collected and subjected to characterization by using IBPGR descriptor. Sixteen superior genotypes of avocado were selected based on the fruit size, shape, colour and weight for the present experiment. The experiment was laid out in a Completely Randomized Block Design and replicated thrice. Biometrical observations on fruit length (cm), fruit diameter (cm), peduncle length (cm), peduncle diameter (mm), pedicel length (cm) and fruit weight (g). Nutritive analysis for fat (g), dietry fibre (g), carbohydrate, carotene, vitamin C, calcium and phosphorus were taken from each genotype and subjected to statistical analysis. Multivariate analysis was done utilizing Mahalanobis $D^2$ statistics (Mahalanobis, 1936) and genotypes were grouped into different clusters following Tocher's method. The inter and intra cluster distance were worked out as per method suggested by Singh and Chaudhary (1985) [12] to find actual divergence within and between the clusters. The contribution of individual characters towards genetic divergence was computed by using the method given by Singh and Chaudhary (1985) [12].

**Results and Discussion**
Sixteen genotypes were chosen for genetic divergence analysis. the results showed that the genotypes differed significantly with regard to the characters studied. Clustering of genotypes was done based on $D^2$ value and displayed marked divergence and grouped in to 11 clusters (Table 2). The cluster 1 and 2 had the highest number of genotypes. The cluster 1 includes the genotypes TKDPA 80, TKDPA 89 and TKDPA 97 and the cluster 2 include the genotypes TKDPA 81, TKDPA 85 and TKDPA 86 respectively. It was followed by the cluster 3 which include two genotypes *viz*., TKDPA 87 and TKDPA 88. Other clusters *viz*., 4, 5, 6, 7, 8, 9, 10 and 11were mono genotypic. The analysis of the Table 2 clearly indicated that clustering pattern there was no parallelism between geographical distribution of genotypes and genetic divergence. Therefore, geographical diversity could not be related to genetic diversity in the material investigated. This is an agreement with results of Singh *et al*. (2006) [13], Reddy *et al.* (2013) [10] and Basavaraj *et al*. (2010) [1]. So selection of genotypes for hybridization to generate diverse new gene combinations should be based on genetic diversity rather than geographic diversity (Pawar *et al*., 2013). It is very difficult to establish the actual location of origin of a genotype.

Inter and intra cluster $D^2$ values among 11 clusters were presented in the table 4. From the results it was observed that the intra cluster values were less than inter cluster values suggested that the study material were homogenous and heterogeneous nature of the genotypes within and between the clusters, respectively as reported by Pawar *et al*., (2013). The information obtained from inter-cluster distances may be used to select genetically diverse and superior genotypes. The genotypes possessing maximum genetic divergence is expected that more heterotic F1 and most promising segregant in segregating generations. Intercrossing of divergent groups would lead to greater opportunity for crossing over, which may release hidden variability (Kumar *et al*., 2010). The intra cluster value ranged from 0.000 (Cluster 4 to Cluster 11) to 3303.27 (Cluster 3). The maximum intra cluster distance was noticed with in cluster 3 (3303.27) and it was followed by the cluster 1 (2864.62) and the cluster 2 (2473.96). The inter cluster $D^2$ values of 11 clusters revealed that the highest inter cluster generalized distance of 12299.39 was recorded between cluster 6 and cluster 9. It was followed by cluster 5 and cluster 9 (10050.35), cluster 9 and cluster 10 (9990.05), cluster 5 and cluster 8 (9863.54). The results suggested that the maximum divergence between genotypes of cluster 6 and cluster 9, cluster 5 and cluster 9, cluster 4 and cluster 10 and cluster 5 and cluster 8 indicating the fact that the genotypes were used in hybridization programme produce superior sergeants. Whereas the lowest inter cluster $D^2$ values were registered between cluster 2 and cluster 7 (2605.66), cluster 1 and cluster 2 (2964.74), cluster 1 and cluster 7 (3323.24), cluster 2 and cluster 5 (3555.81), cluster 1 and cluster 4 (3566.19) and cluster 4 and cluster 5 (3597.15). These results are in accordance with the findings of Veershetty (2004) [15] and Mehta and Asati (2008) [8].

Cluster mean values with respect to thirteen quantitative and qualitative characters of sixteen genotypes were presented in the table 3. The results showed that the cluster 11 registered the highest cluster mean values for the traits *viz*., fruit length (18.30 cm), fruit diameter (12.10 cm), peduncle length (17.30 cm), peduncle diameter (9.50 mm), fruit weight (780.03 g) and fibre content (6.58). cluster 7 registered the highest cluster mean values for fat (24.19), carbohydrate (1.75), carotene (10.12) and vitamin C (9.18). Cluster 6 recorded the highest cluster mean value for calcium (26.53) and cluster 9 recorded the highest mean value for phosphorus (62.72). the results suggested that the clusters having high mean values may be selected for transplanting the specific traits through hybridization programme. These type of results also reported by Rai *et al*. (1998) [9], Joshi and Kohli (2003) [14] and Sharma *et al.* (2006) [11].

Contribution of different plant character for genetic divergence is important for the purpose of further selection and choice of parents for hybridization. The contribution percentages of traits under studied towards total divergence are tabulated in Table 1. The highest contribution in the manifestation of genetic divergence was exhibited by phosphorus (25.00) and it was followed by vitamin c (17.50), calcium (10.00) and pedicle length (9.16). Whereas, the lowest contribution in the manifestation of genetic divergence was exhibited by fruit diameter (0.03). The contribution of remaining traits in manifestation of genetic divergence was zero. Similar reports were also made by Lekshmi and Celine (2016) [6] in tomato.

**Table 1:** Contribution of each character to divergence

| Sl. No. | Character | No. of first rank | Per cent of Contribution |
|---|---|---|---|
| 1. | 1 | 0 | 0.0000 |
| 2. | 2 | 1 | 0.0333 |
| 3. | 3 | 0 | 0.0000 |
| 4. | 4 | 5 | 4.1667 |
| 5. | 5 | 11 | 9.1667 |
| 6. | 6 | 5 | 4.1667 |
| 7. | 7 | 7 | 5.8333 |
| 8. | 8 | 9 | 7.5000 |
| 9. | 9 | 10 | 8.3333 |
| 10. | 10 | 9 | 7.5000 |
| 11. | 11 | 21 | 17.500 |
| 12. | 12 | 12 | 10.000 |
| 13. | 13 | 30 | 25.000 |
|  | Total | 120 | 100 |

**Table 2:** Clustering pattern of 16 genotypes of avocado on the basis of $D^2$ statistic

| Cluster No. | No. of Genotypes within cluster | Genotypes in cluster |
|---|---|---|
| 1 | 1,10,16 | TKDPA 80, TKDPA 89, TKDPA 97 |
| 2 | 2,6,7 | TKDPA81, TKDPA85, TKDPA86 |
| 3 | 8,9 | TKDPA87, TKDPA88 |
| 4 | 11, | TKDPA90 |
| 5 | 15 | TKDPA95 |
| 6 | 5 | TKDPA84 |
| 7 | 12 | TKDPA91 |
| 8 | 3 | TKDPA82 |
| 9 | 13 | TKDPA92 |
| 10 | 4 | TKDPA83 |
| 11 | 14 | TKDPA93 |

**Table 3:** Cluster mean for thirteen characters in avocado

| Cluster | FL (cm) | FD (cm) | Pdnl lth (cm) | Pdnl dia. (mm) | Pdl lth (cm) | F W (g) | Fat | Fibre | CHO | Caro. | Vit.C | Ca | P |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 14.67 | 9.58 | 11.57 | 6.00 | 1.40 | 500.01 | 19.45 | 5.72 | 1.59 | 7.42 | 8.74 | 25.22 | 62.17 |
| 2 | 13.67 | 7.25 | 11.50 | 6.27 | 1.37 | 396.00 | 20.78 | 5.81 | 1.72 | 8.96 | 8.80 | 26.26 | 61.64 |
| 3 | 16.60 | 10.00 | 11.25 | 8.50 | 1.75 | 555.00 | 21.98 | 5.47 | 1.58 | 8.90 | 8.91 | 25.50 | 62.65 |
| 4 | 15.10 | 10.10 | 10.40 | 8.20 | 1.70 | 284.97 | 18.25 | 6.16 | 1.64 | 6.43 | 9.04 | 22.95 | 61.72 |
| 5 | 13.60 | 8.60 | 12.40 | 8.20 | 1.90 | 445.00 | 16.89 | 4.98 | 1.72 | 5.43 | 8.12 | 23.76 | 60.12 |
| 6 | 14.30 | 8.20 | 7.40 | 5.10 | 1.20 | 250.03 | 20.41 | 6.16 | 1.46 | 8.23 | 8.56 | 26.53 | 60.26 |
| 7 | 13.10 | 8.40 | 10.60 | 9.10 | 1.60 | 290.00 | 24.19 | 6.53 | 1.75 | 10.12 | 9.18 | 26.18 | 60.29 |
| 8 | 14.20 | 8.10 | 12.20 | 5.30 | 1.30 | 324.97 | 18.27 | 5.12 | 1.64 | 7.64 | 9.05 | 26.42 | 61.67 |
| 9 | 14.70 | 10.80 | 18.40 | 9.30 | 1.60 | 58.03 | 13.62 | 5.69 | 1.63 | 6.15 | 8.79 | 26.25 | 62.72 |
| 10 | 11.10 | 6.80 | 9.60 | 5.20 | 1.10 | 302.00 | 18.27 | 5.24 | 1.51 | 6.78 | 8.32 | 24.89 | 61.47 |
| 11 | 18.30 | 12.10 | 17.30 | 9.50 | 0.90 | 780.03 | 16.43 | 6.58 | 1.48 | 5.26 | 8.18 | 24.37 | 60.41 |

FL – Fruit length
FD – Fruit diameter
Pdnl.lth – Peduncle length
Pdnl.dia. – Peduncle diameter
Pdl.lth. – Pedicel length

FW – Fruit weight
Fat – Fat
Fibre – Fibre
CHO - Carbohydrate
Caro. – Carotene

Vit. C – Vitamin C
Ca - Calcium
P - Phosphorus

**Table 4:** Inter and Intra cluster $D^2$ values among eleven clusters

| Cluster | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 2864.62 | 2964.74 | 4608.21 | 3566.19 | 4869.36 | 4775.51 | 3323.24 | 5867.15 | 6783.18 | 5765.36 | 5247.99 |
| 2 |  | 2473.96 | 4526.78 | 3747.42 | 3555.81 | 4002.05 | 2605.66 | 4848.56 | 6766.78 | 6720.01 | 5236.65 |
| 3 |  |  | 3303.27 | 4993.01 | 6596.45 | 6950.15 | 5429.83 | 4767.89 | 7719.41 | 5113.63 | 6649.07 |
| 4 |  |  |  | 0.000 | 3597.15 | 4911.79 | 3721.62 | 6196.25 | 7482.55 | 7637.78 | 5632.46 |
| 5 |  |  |  |  | 0.000 | 6565.02 | 4094.50 | 9863.54 | 10050.35 | 8897.05 | 7820.68 |
| 6 |  |  |  |  |  | 0.000 | 4258.50 | 5492.72 | 12299.39 | 8534.74 | 6218.62 |
| 7 |  |  |  |  |  |  | 0.000 | 5791.56 | 7653.16 | 6922.81 | 5550.23 |
| 8 |  |  |  |  |  |  |  | 0.000 | 5453.19 | 5962.49 | 8521.74 |
| 9 |  |  |  |  |  |  |  |  | 0.000 | 9990.05 | 8824.77 |
| 10 |  |  |  |  |  |  |  |  |  | 0.000 | 7341.67 |
| 11 |  |  |  |  |  |  |  |  |  |  | 0.000 |

## Conclusion

From the results of the present study it was concluded that the traits phosphorus, vitamin c, calcium will offer a good scope for improvement through selection and direct selection can be adopted effectively for achieving desirable results. In order to achieve high heterosis or superior recombinants in future, hybridization between genotypes of cluster 6 and cluster 9, cluster 5 and cluster 9, cluster 4 and cluster 10 and cluster 5 and cluster 8 would be more desirable. Since

genotypes with the same geographical origin clustered indifferent groups, it can be concluded that genotypes originating from the same region should be genetically distant. It could be possible to use genetically different genotypes with superior characteristics in avocado breeding

programs aimed to quality improvement.

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