

Original Research Article

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## Genetic Diversity in Oil Palm Genotypes by Multivariate Analysis

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### ABSTRACT

Genetic diversity was studied in 58 genotypes of oil palm germplasm in Andhra Pradesh and Telangana locations of India. Morphological traits were recorded and subjected to Mahalanobis D2 cluster analysis and principal component analysis (PCA). These 58 genotypes were grouped into eight clusters which show greater genetic diversity in the genotypes. Cluster 7 is the largest one that has 12 genotypes. Intra and Inter cluster distance of clusters was analyzed by D2 and principal component analysis (PCA). According to D2 analysis maximum intra cluster distance was observed in Cluster 5 and minimum in Cluster 4. Maximum D2 inter cluster distance was observed between Cluster 1 and Cluster 6. Similarly in PCA analysis maximum inter cluster distance was observed between Cluster 2 and Cluster 6. These clusters are having greater genetic distance and hybridization of these genotypes with desired traits can develop superior hybrids.

#### Keywords

Genetic diversity, Clusters, D2 analysis, PCA, Oil palm genotypes.

#### Article Info

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### Introduction

Oil palm (*Elaeis guineensis* Jacq) is an important edible vegetable oil crop which produces 4-6 tonnes of crude palm oil/ha. As oil palm crop is introduced in India from Africa, it is growing in India under different climatic conditions like high temperature, low humidity and less rainy days. There is a need

to develop and strengthen the oil palm breeding program in India as there is a demand from the farmers to cultivate good yielding oil palm hybrids. In the cross pollinated crop like oil palm exploitation of heterosis is the main objective to develop high yielding hybrids (Kumar and Singh, 2006).

For strengthening the breeding program broad range of genetic resources collection and its conservation is the preliminary step (Hausmann *et al.*, 2004). Characterization of traits in collected germplasm is the important aspect in crop improvement (Singh *et al.*, 2008; Duran *et al.*, 2009 and Worede *et al.*, 2014). The agro morphological traits which were categorized into qualitative and quantitative traits and their study is the procedure of germplasm characterization. Genetic divergence in the available germplasm is the important requisite for the successful breeding for the selection of parents (Hoisington *et al.*, 1999; Maxted *et al.*, 2002; Rohman *et al.*, 2004; Singh *et al.*, 2008 and Naik *et al.*, 2006). Multi variate analysis such as Mahalanobis D2 cluster analysis and principal component analysis (PCA) were useful to select the diversified genotypes for hybridization (Satish *et al.*, 2005; Sudhakar *et al.*, 2005; Parthasarathy *et al.*, 2005 and Ngah *et al.*, 2015). In the present investigation, genetic diversity was assessed in oil palm genotypes by evaluating the agro morphological traits using cluster and principal component analysis.

## **Materials and Methods**

### **Sample collection and parameters analyzed**

58 oil palm genotypes located in different villages of Andhra Pradesh and Telangana were taken in the present study (Table 1). Randomized block design (RBD) was laid out in 3 replications and 24 morphological traits were recorded in all the genotypes. Morphological biometric observations like height, girth at base, height increment, sex ratio, number of leaves, petiole width, petiole depth, number of leaflets, rachis length, leaflet length (LLL), leaflet width (LLW), leaf area (LA), leaf dry weight (LDW), total leaf dry weight (TLDW), specific leaf weight (SLW), trunk dry matter (TrDM), vegetative dry matter (VDM), total dry matter (TDM)

and yield parameters like bunch number (BN), fresh fruit bunch yield (FFBY), average bunch weight (ABW), bunch dry weight (BDW), bunch index (BI), oil/bunch ratio were recorded as per Corley *et al.*, (1971) and Kushairi *et al.*, (1999) non-destructive method and experiment was conducted during year 2011-2016.

### **Data Analysis**

The Morphological data recorded was submitted to statistical package WINDOSTAT 9.2 (developed by INDOSTAT services Ltd. Hyderabad, India) to carry out the Genetic diversity studies through Mahalanobis (1936) generalized distance (D2) cluster analysis and principal component analysis (PCA) as described by Rao (1952).

### **Results and Discussion**

The analysis of variance revealed significant differences among the 58 genotypes. The 58 genotypes were grouped into eight clusters in D2 analysis. Among the eight clusters, cluster 7 is the largest cluster that consists of 12 genotypes followed by cluster 1 which contains 11 genotypes, cluster 8 with 10 genotypes, cluster 4 with 7 genotypes, cluster 2, 3, 6 with 5 genotypes each and cluster 5 with 3 genotypes (Table 2 and Figure 1).

The results have clearly indicated that there is no parallelism between the geographic diversity and genetic diversity in oil palm, in accordance with Ngah *et al.*, (2015). Rahman and Al-Mansur (2009) reported that genetic diversity is associated with geographical diversity. Kjaer *et al.*, (2004) and Zulkifli *et al.*, (2012) reported that genetic diversity is associated with geographical diversity. In this study found no association between genetic diversity and geographical location reveals that populations from different locations have genetic similarity that may obtained from

same parent material (Tahir *et al.*, 2013). This results show that the germplasm accessions present in single cluster were genetically similar and that are distributed in different clusters were diversified even though they were collected from different geographical locations.

On the basis of D2 analysis intra and inter cluster analysis was obtained (Table 3). The range of intra cluster distance is from 94.247 (Cluster 4) to 180.169 (Cluster 5) and the maximum intra cluster distance was observed in cluster 5 (180.169), followed by cluster 6 (147.183) and cluster 3 (130.605). The minimum intra cluster distance was observed in cluster 4 (94.247) followed by cluster 7 (95.913) and cluster 2 (115.243). The maximum inter cluster D2 distance was between cluster 1 and cluster 6 (1640.325) which shows greater genetic divergence between these clusters. As these two clusters (cluster 1 and 6) are having greater genetic distance, the genotypes in cluster 1 and

cluster 6 exhibit greater genetic diversity. The hybridization between these genotypes will yields greater variability in the germplasm and develop superior hybrids with desired traits (Arunachalam, 1981; and Ravali, 2017). The minimum inter cluster distance was observed in cluster 1 and cluster 2 (164.048), which shows very narrow range of divergence between the genotypes in these cluster and they are not suitable for hybridization due to inbreeding depression (Kumar and Singh, 2006).

The additional advantage of D2 analysis is the contribution of various characters (Table 4) towards the expression of genetic divergence. This analysis indicated that the height of palm contributed maximum genetic divergence in the material (64.07 %) followed by fresh fruit bunch yield-FFBY (18.45 %). Based on PCA scores the additional advantage in hierarchical cluster analysis is identifying sub-cluster of the major group at different levels so that each small group can be critically analyzed.

**Table.1** List of genotypes and their sources

| S.No | Village          | Genotype | S.No | Village            | Genotype |
|------|------------------|----------|------|--------------------|----------|
| 1    | A Polavaram      | APV      | 30   | Ankannagudem       | ANG      |
| 2    | Annadevarapeta   | ADP      | 31   | Bandivarigudem     | BVG      |
| 3    | Bayyannagudem    | BNG      | 32   | Busarajupalli      | BRP      |
| 4    | Bhimolu          | BMU      | 33   | Chityala           | CHT      |
| 5    | Gavaravaram      | GVM      | 34   | Doramamidi         | DRM      |
| 6    | Jelugumilli      | JLG      | 35   | Eduvadalla Palu    | EVP      |
| 7    | Komatikunta      | KMK      | 36   | Guravaigudem       | GVG      |
| 8    | Kommugudem       | KMG      | 37   | Jaggavaram         | JGV      |
| 9    | Kuntala Gudem    | KTG      | 38   | Kanakadripuram     | KKP      |
| 10   | Lakkavaram       | LKV      | 39   | Kollivarigudem     | KVG      |
| 11   | Lingaraopalem    | LGP      | 40   | Krishnapuram       | KSP      |
| 12   | Mulagalampalli   | MLG      | 41   | P Rajavaram        | PRM      |
| 13   | P Narayanapuram  | PNP      | 42   | Rachanna gudem     | RNG      |
| 14   | R Ganapavaram    | RGP      | 43   | Rudrarajukotagudem | RRK      |
| 15   | Rajavaram        | RJV      | 44   | Bandamcharla       | BMC      |
| 16   | Gudlapalli       | GDP      | 45   | Borrampalem        | BMP      |
| 17   | Kethavaram       | KTV      | 46   | Cherukumili        | CRK      |
| 18   | Laxmanagudem     | LXG      | 47   | Darbhadgudem       | DRB      |
| 19   | Mysannna Gudem   | MNG      | 48   | Devulapalli        | DVP      |
| 20   | Peddipalli       | PDP      | 49   | Gangolu            | GNG      |
| 21   | Pullepudi        | PLP      | 50   | Gopalapuram        | GPP      |
| 22   | Rajupothepalli   | RPP      | 51   | Vegavaram          | VGV      |
| 23   | Ramacherla Gudem | RCG      | 52   | Kamayya Palem      | KMP      |
| 24   | Taduvai          | TDV      | 53   | Makkinavarigudem   | MKV      |
| 25   | Teklavarigudem   | TVG      | 54   | P Ankampalem       | PAP      |
| 26   | Aswaraopeta      | ARP      | 55   | Pangidigudem       | PGG      |
| 27   | Janagareddygudem | JRG      | 56   | Parimpudi          | PRP      |
| 28   | Pedavegi         | PED      | 57   | Ponguturu          | PGT      |
| 29   | Akkampeta        | AKP      | 58   | Pragadapalli       | PGD      |

**Table.2** Distribution of 58 genotypes into different clusters as per Mahalanobis D2 analysis

| Cluster | Number of Genotypes | Genotypes  |
|---------|---------------------|--|
| 1       | 11                  | APV, ADP, LGP, CRK, GVG, BVG, DRM, VGV, PGG, KSP, GNG      |
| 2       | 5                   | RRK, DRB, MKV, JGV, PGT                                    |
| 3       | 5                   | GDP, TVG, GVM, BRP, RPP                                    |
| 4       | 7                   | BNG, MLG, KMK, JRG, PDP, TDV, AKP                          |
| 5       | 3                   | RJV, MNG, KTG  |
| 6       | 5                   | BMU, LXG, PLP, GPP, PRM                                    |
| 7       | 12                  | PED, PAP, PRP, RGP, KKP, PGD, BMP, DVP, RCG, PNP, KMP, JLG |
| 8       | 10                  | KMG, KVG, KTV, EVP, CHT, LKV, BMC, ARP, ANG, RNG           |

**Table.3** Intra cluster (bold) and Inter cluster Euclidean<sup>2</sup> values among eight clusters using Wards minimum variance method

|           | 1 Cluster      | 2 Cluster      | 3 Cluster      | 4 Cluster     | 5 Cluster      | 6 Cluster      | 7 Cluster     | 8 Cluster      |
|-----------|----------------|----------------|----------------|---------------|----------------|----------------|---------------|----------------|
| 1 Cluster | <b>119.519</b> | 164.048        | 177.09         | 226.822       | 442.024        | 1640.325       | 1530.418      | 621.552        |
| 2 Cluster |                | <b>115.243</b> | 245.93         | 191.306       | 334.873        | 1353.530       | 1340.588      | 531.929        |
| 3 Cluster |                |                | <b>130.605</b> | 212.75        | 532.697        | 1527.964       | 1254.331      | 470.374        |
| 4 Cluster |                |                |                | <b>94.247</b> | 303.767        | 981.943        | 914.438       | 299.954        |
| 5 Cluster |                |                |                |               | <b>180.169</b> | 951.882        | 1211.797      | 574.752        |
| 6 Cluster |                |                |                |               |                | <b>147.183</b> | 351.993       | 565.267        |
| 7 Cluster |                |                |                |               |                |                | <b>95.913</b> | 350.566        |
| 8 Cluster |                |                |                |               |                |                |               | <b>123.248</b> |

**Table.4** Contribution of 24 characters towards genetic diversity

| S.NO. | Source             | Times Ranked 1st | Contribution % |
|-------|--------------------|------------------|----------------|
| 1     | Height (cm)        | 1059             | 64.07 %        |
| 2     | Girth (cm)         | 9                | 0.54 %         |
| 3     | Height incre (cm)  | 24               | 1.45 %         |
| 4     | Sex Ratio (%)      | 1                | 0.06 %         |
| 5     | No. of Leaves      | 3                | 0.18 %         |
| 6     | Petiole Width (cm) | 5                | 0.30 %         |
| 7     | Petiole Depth (cm) | 0.01             | 0.00 %         |
| 8     | No. of Leaflets    | 4                | 0.24 %         |
| 9     | Rachis Length (cm) | 65               | 3.93 %         |
| 10    | LLL (cm)           | 4                | 0.24 %         |
| 11    | LLW (cm)           | 50               | 3.02 %         |
| 12    | LA sq m            | 3                | 0.18 %         |
| 13    | LDW (kg)           | 3                | 0.18 %         |
| 14    | TLDW (kg)          | 0.01             | 0.00 %         |
| 15    | SLW kg/sq m        | 2                | 0.12 %         |
| 16    | TrDM (kg)          | 8                | 0.48 %         |
| 17    | VDM (kg)           | 0.01             | 0.00 %         |
| 18    | BN                 | 39               | 2.36 %         |
| 19    | FFBY (kg)          | 305              | 18.45 %        |
| 20    | ABW (kg)           | 24               | 1.45 %         |
| 21    | BDW (kg)           | 1                | 0.06 %         |
| 22    | TDM (kg)           | 0.01             | 0.00 %         |
| 23    | BI                 | 0.01             | 0.00 %         |
| 24    | Oil/ bunch %       | 44               | 2.66 %         |

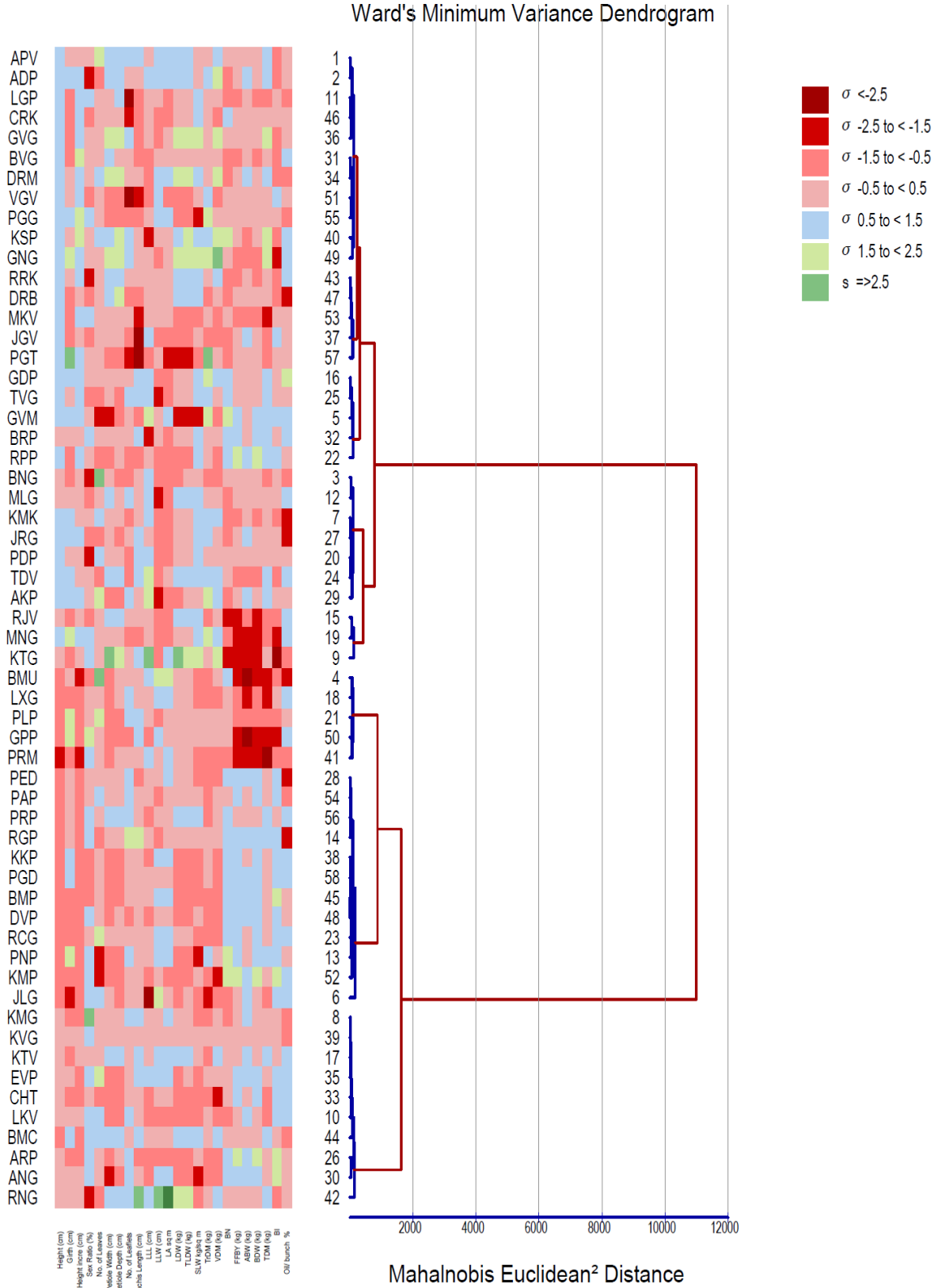
**Table.5** Intra cluster (bold) and Inter cluster distances in principal component analysis (PCA) by Tocher method

|           | 1 Cluster     | 2 Cluster     | 3 Cluster     | 4 Cluster    | 5 Cluster    | 6 Cluster    | 7 Cluster    | 8 Cluster    |
|-----------|---------------|---------------|---------------|--------------|--------------|--------------|--------------|--------------|
| 1 Cluster | <b>27.900</b> | 414.052       | 108.110       | 491.737      | 139.433      | 138.861      | 140.480      | 383.797      |
| 2 Cluster | 414.052       | <b>62.232</b> | 216.235       | 110.011      | 493.043      | 533.597      | 481.997      | 188.709      |
| 3 Cluster | 108.110       | 216.235       | <b>82.431</b> | 273.295      | 187.422      | 202.525      | 185.182      | 235.754      |
| 4 Cluster | 491.737       | 110.011       | 273.295       | <b>0.000</b> | 408.576      | 441.169      | 455.917      | 87.053       |
| 5 Cluster | 139.433       | 493.043       | 187.422       | 408.576      | <b>0.000</b> | 42.340       | 46.157       | 301.541      |
| 6 Cluster | 138.861       | 533.597       | 202.525       | 441.169      | 42.340       | <b>0.000</b> | 68.174       | 283.859      |
| 7 Cluster | 140.480       | 481.997       | 185.182       | 455.917      | 46.157       | 68.174       | <b>0.000</b> | 328.489      |
| 8 Cluster | 383.797       | 188.709       | 235.754       | 87.053       | 301.541      | 283.859      | 328.489      | <b>0.000</b> |

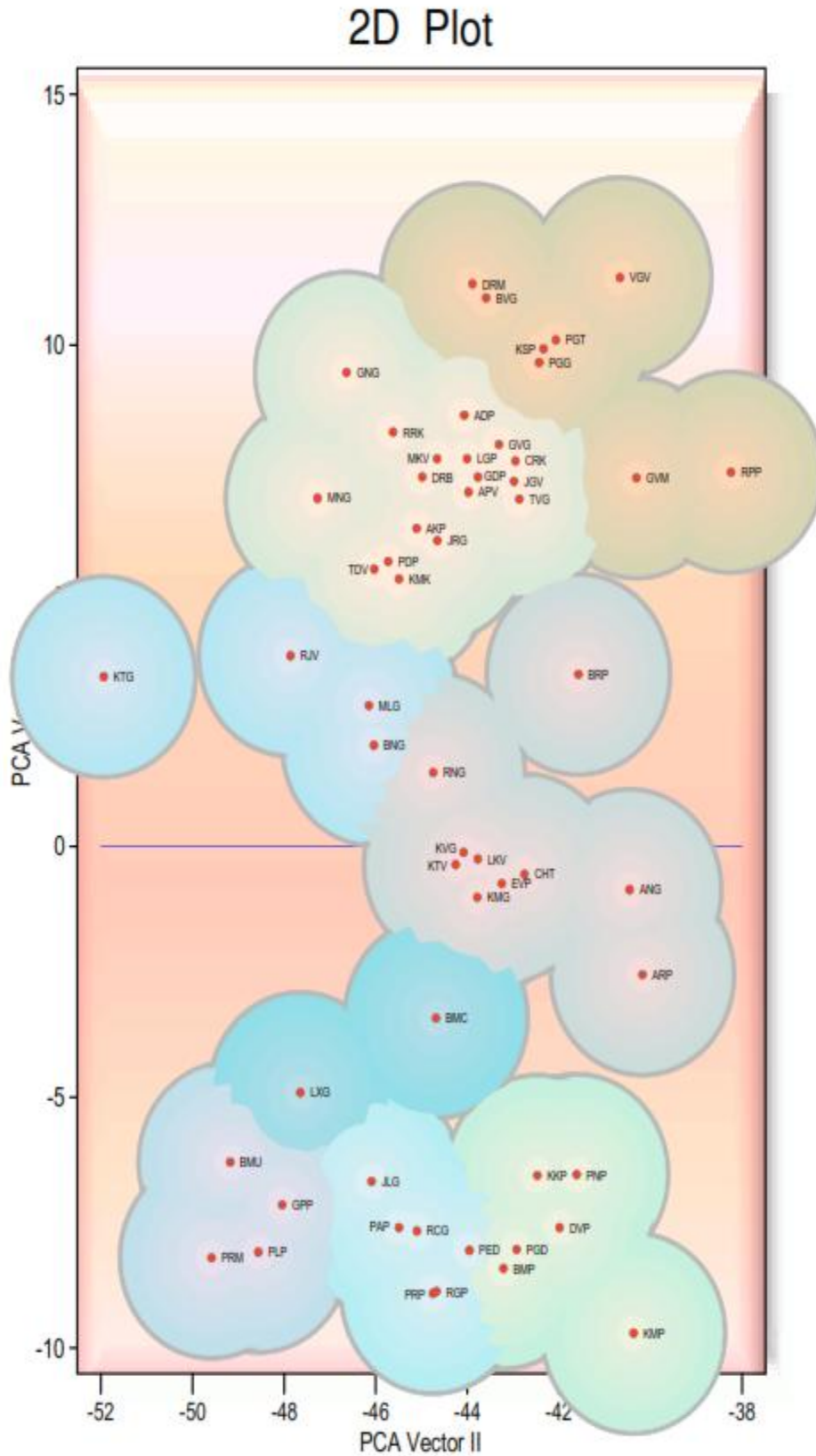
**Table.6** Eigen values, percentage of variability, cumulative percent variability for Eight principal component analysis (PCA)

|                       | 1<br>Vector   | 2<br>Vector   | 3<br>Vector   | 4<br>Vector   | 5<br>Vector   | 6<br>Vector   | 7<br>Vector   | 8<br>Vector   |
|-----------------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|
| <b>Eigene Value</b>   |               |               |               |               |               |               |               |               |
| <b>(Root)</b>         | <b>9.073</b>  | <b>2.728</b>  | <b>1.628</b>  | <b>1.557</b>  | <b>1.454</b>  | <b>1.180</b>  | <b>1.032</b>  | <b>0.931</b>  |
| <b>% Var. Exp.</b>    | <b>37.805</b> | <b>11.365</b> | <b>6.782</b>  | <b>6.488</b>  | <b>6.057</b>  | <b>4.916</b>  | <b>4.302</b>  | <b>3.880</b>  |
| <b>Cum. Var. Exp.</b> | <b>37.805</b> | <b>49.170</b> | <b>55.952</b> | <b>62.440</b> | <b>68.497</b> | <b>73.413</b> | <b>77.715</b> | <b>81.594</b> |
| Height (cm)           | 0.325         | 0.048         | 0.014         | 0.007         | 0.041         | 0.054         | 0.007         | 0.010         |
| Girth (cm)            | 0.232         | 0.040         | 0.101         | 0.322         | 0.169         | 0.178         | -0.020        | 0.319         |
| Height incre (cm)     | -0.319        | -0.029        | 0.058         | 0.012         | -0.044        | -0.078        | -0.029        | 0.041         |
| Sex Ratio (%)         | -0.203        | 0.092         | -0.067        | 0.258         | 0.238         | -0.119        | 0.041         | 0.130         |
| No. of Leaves         | 0.144         | -0.221        | 0.002         | 0.073         | -0.524        | -0.134        | 0.034         | 0.056         |
| Petiole Width (cm)    | -0.015        | -0.428        | 0.182         | 0.242         | -0.049        | -0.053        | 0.000         | -0.298        |
| Petiole Depth (cm)    | -0.089        | 0.049         | 0.105         | 0.323         | -0.141        | -0.596        | -0.040        | 0.459         |
| No. of Leaflets       | -0.289        | -0.014        | 0.120         | 0.031         | -0.159        | 0.021         | 0.012         | 0.047         |
| Rachis Length (cm)    | 0.044         | -0.222        | 0.589         | 0.072         | -0.024        | 0.169         | 0.104         | -0.116        |
| LLL (cm)              | -0.006        | -0.317        | 0.178         | -0.294        | 0.069         | 0.100         | -0.436        | 0.403         |
| LLW (cm)              | 0.256         | 0.098         | 0.124         | -0.053        | -0.029        | -0.208        | 0.419         | 0.098         |
| LA sq m               | 0.241         | 0.231         | 0.143         | 0.049         | 0.200         | -0.205        | 0.125         | 0.010         |
| LDW (kg)              | 0.312         | 0.010         | -0.089        | -0.036        | 0.039         | 0.066         | -0.032        | -0.078        |
| TLDW (kg)             | -0.100        | 0.176         | -0.425        | 0.250         | -0.110        | -0.021        | -0.257        | -0.255        |
| SLW kg/sq m           | -0.313        | -0.083        | 0.058         | -0.024        | -0.069        | 0.036         | -0.041        | 0.043         |
| TrDM (kg)             | -0.133        | -0.053        | -0.278        | -0.186        | 0.085         | 0.325         | 0.362         | 0.469         |
| VDM (kg)              | -0.092        | -0.154        | -0.080        | -0.475        | -0.139        | -0.307        | 0.409         | -0.112        |
| BN                    | -0.154        | 0.302         | 0.341         | -0.020        | -0.172        | 0.089         | -0.060        | -0.019        |
| FFBY (kg)             | -0.041        | 0.440         | 0.204         | -0.202        | -0.251        | 0.199         | -0.081        | -0.062        |
| ABW (kg)              | 0.132         | -0.006        | -0.194        | 0.163         | -0.571        | 0.154         | 0.068         | 0.088         |
| BDW (kg)              | -0.297        | 0.055         | -0.010        | -0.064        | -0.024        | 0.003         | -0.036        | 0.090         |
| TDM (kg)              | 0.192         | 0.305         | 0.090         | -0.225        | -0.217        | -0.057        | -0.233        | 0.182         |
| BI                    | 0.207         | -0.296        | -0.154        | 0.012         | -0.140        | 0.128         | -0.139        | 0.159         |
| Oil/ bunch %          | -0.130        | 0.080         | 0.077         | 0.340         | -0.110        | 0.385         | 0.380         | 0.077         |

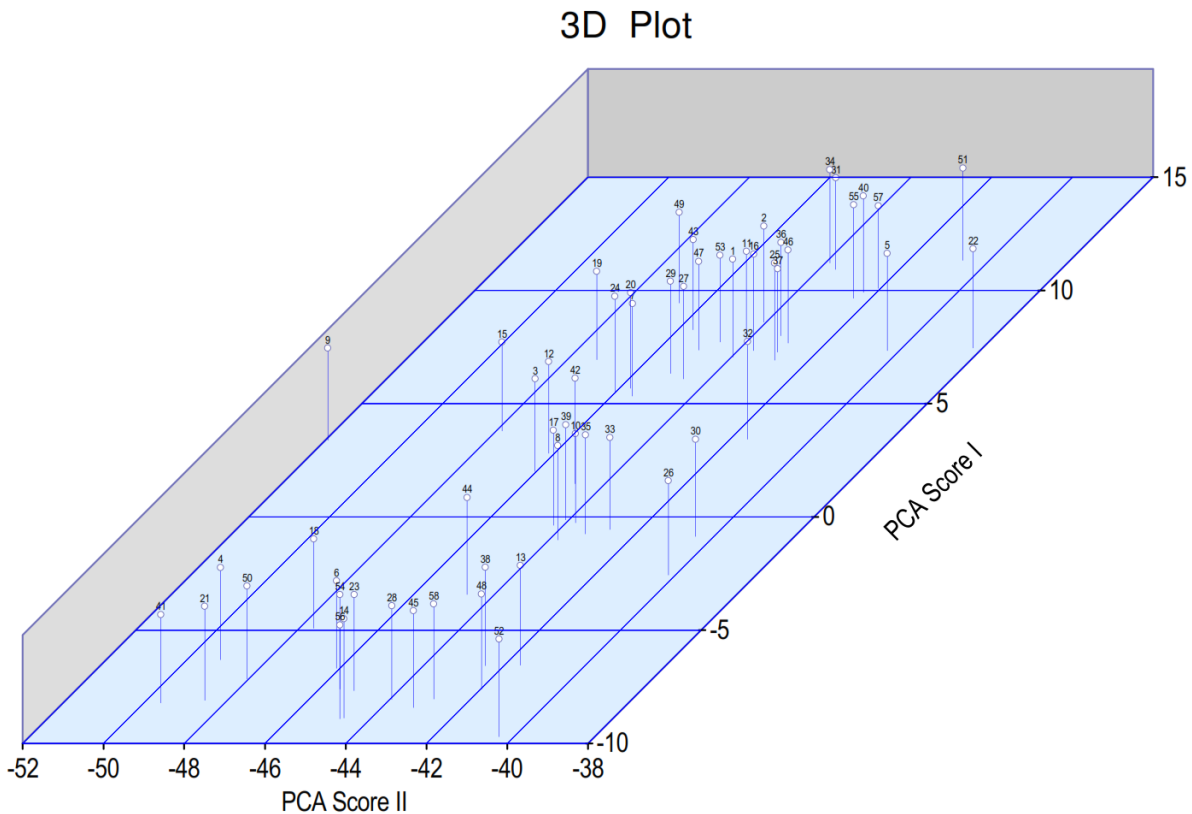
**Fig.1** Distribution of 58 genotypes into different clusters as per D2 analysis-  
Wards minimum variance method



**Fig.2** Two dimensional plot of 58 genotypes and their relative positions based on PCA scores



**Fig.3** Three dimensional plot of 58 genotypes and their relative positions based on PCA scores



On the basis of principal component analysis (PCA) by Tocher method (Table 5) the maximum intra-cluster distance was observed in cluster 3 (82.431) and minimum in cluster 1 (27.90). Similarly the maximum inter-cluster distance was observed between cluster 2 and 6 (533.60) while the least being between cluster 5 and 6 (42.34).

Rahman and Al-Mansur (2009) reported that higher genetic diversity with higher inter and intra cluster distances in cluster and closeness of the genotypes by minimum inter and intra cluster distances. PCA will show the major contributor of the total variation at each distinct point. The principal factor (PF) will be obtained by PCA method and it does not require the assumption of normal distribution of population. The major principal component can be determined by Eigen value. The first 7 principal components (PCS) greater than one

Eigen value and they together explained 77.71% of total variability among 58 genotypes (Table 6). The first principal component or Vector (PC1) accounted maximum towards variability (37.80%) followed by PC2 (11.36%), PC3 (6.78%), PC4 (6.48%), PC5 (6.05%), PC6 (4.91%), PC7 (4.30%) and PC8 (3.88%).

PC1 has major positive association with Height of the palm (0.325), Girth at base (0.232), number of leaves (0.144), leaflet width-LLW (0.256), leaf area-LA (0.241), leaf dry weight-LDW (0.312), total dry matter-TDM (0.192) and respectively. PC2 has significant positive association with leaf area-LA (0.231), total leaf dry weight-TLDW (0.176), bunch number-BN (0.302), fresh fruit bunch yield-FFBY (0.440), total dry matter-TDM (0.305), respectively. PC3 has significant positive association with petiole



width (0.182), rachis length (0.589), bunch number-BN (0.341), and fresh fruit bunch yield-FFBY (0.204), respectively. PC4 has significant positive association with Girth at base (0.322), sex ratio (0.258), petiole depth (0.323), oil to bunch ratio (0.340), respectively. PC5 has significant positive association with sex ratio (0.238), Girth at base (0.169), Leaf area-LA (0.200), respectively.

PC6 has significant positive association with oil to bunch ratio (0.385), fresh fruit bunch yield-FFBY (0.199), average bunch weight-ABW (0.154), trunk dry matter-TrDM (0.325), rachis length (0.169), Girth at base (0.178), respectively. PC7 has significant positive association with leaflet width-LLW (0.419), vegetative dry matter-VDM (0.409), trunk dry matter-TrDM (0.362), respectively. PC8 has significant positive association with Girth at base (0.319), petiole depth (0.459), leaf let length-LLL (0.403), trunk dry matter-TrDM (0.469), respectively. All the genotypes were plotted (2D and 3D) for first principal components (PCS) to observe the relationship between 58 genotypes (Figure S 2 and 3).

In conclusion, due to Genetic drift and selection pressure the genotypes of same geographical location clustered with other genotypes that are in different geographical location. This shows that there is no parallelism between genetic diversity and geographical location. From D2 and PCA analysis the maximum cluster distances in intra and inter clusters genotypes are having greater genetic diversity and they can be useful for hybridization to develop superior genotypes with desired traits. Similarly PCS or vectors that are having greater positive significance towards fresh fruit bunch yield-FFBY, oil to bunch ratio and bunch index-BI can be selected to develop superior genotypes with desired traits.

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