



Multivariate analysis of oil palm germplasm for vegetative and bunch yield traits

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Oil palm (*Elaeis guineensis* Jacq.) belongs to the genus *Elaeis* and family Palmae (Corley and Tinker, 2003b). Oil palm is one of the most important and the highest edible oil yielding crop among the vegetable oils, giving up to 4.0-5.0 tonnes ha⁻¹ year⁻¹ under good agricultural management practices (Henson and Harun, 2005). Presently, Andhra Pradesh, Karnataka, Tamil Nadu, Mizoram and Orissa are major oil palm growing states in India. Area under oil palm is 3 lakh hectares with production of fresh fruit bunches and crude palm oil being 12.83 lakh million tonnes and 2.17 lakh, respectively during 2015-16 (Anonymous, 2017).

It is being a cross-pollinated crop with variations seen amongst palms with respect to performance. Hence, assessment of individual palms is of utmost important, especially for selection of superior palms (Mandal and Babu, 2008). Accurate evaluation in oil palm is usually hindered by cumbersome data accumulated over many years, the crop being perennial in nature (Obboh and Fakorede, 1990). It is well known that some of these variables may not be adequate for germplasm evaluation, characterization and

management. Both characterization and evaluation provide an effective source of information for genetic diversity and help in understanding patterns of variation in crop species (Rao and Hodgkin, 2002).

Principal components analysis and clustering are mostly used in multivariate technique to classify germplasm materials (Li-Hammeda *et al.*, 2016). Principal component analysis (PCA) explains the general relationship between variables while clustering is an exploratory data analysis tool for grouping accessions (Richard and Wichern, 2007). PCA and cluster analysis (CA) have been used successfully in germplasm evaluation of crops for years as they report relationship and correlation among variables studied (Zafar *et al.*, 2008; Maji and Shaibu, 2012; Odewale *et al.*, 2012; Ahmad *et al.*, 2014). Recently PCA and clustering have been used in characterizing the germplasm at the Malaysian Palm Oil Board (Li-Hammeda *et al.*, 2015). This study aims at using PCA and CA to assess the genetic variability in oil palm germplasm conserved at ICAR-IIOPR. Information obtained from this study will help to select individuals for incorporation into the breeding programmes at ICAR-IIOPR.

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Fifty two oil palm accessions were collected from five locations in India Table 1 and Fig. 1). The seeds were sown, nursed and resulting seedlings were planted in ICAR-IIOPR Field Gene Bank in 2009 for conservation and evaluation. The 52 accessions were laid out in a non replicated block and 150 palms were randomly selected for analysis. The trial was conducted at 16 °81' N latitude and 81 °13' E longitudes with 13.41 meters elevation above MSL. These palms was maintained in well drained red sandy loam soil possessing moderate water holding capacity. The average rainfall in this location was

800-900 mm, with a temperature range of 22-33 °C. Good agronomic practices were carried out from establishment to completion of the trial. Data was collected on number of bunches, Fresh Fruit Bunch (FFB) yield and average bunch weight (2015-2017) and pooled. Vegetative growth measurements were made annually on individual palm basis 10 years after planting and pooled. The vegetative parameters were computed using standard procedure as described by Corley (1976). PCA and CA were used to assess the genetic variability of the 52 accessions using JMP 2009 software.

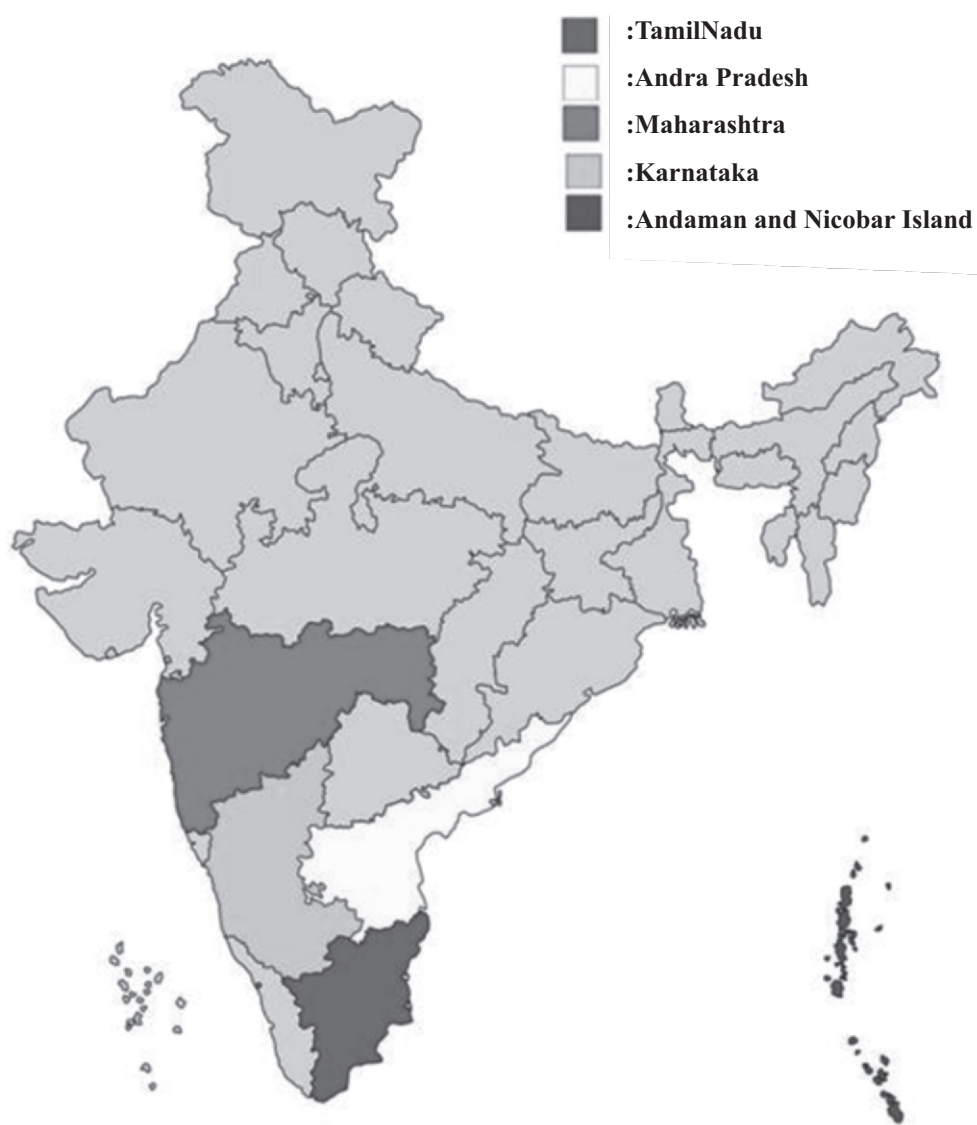
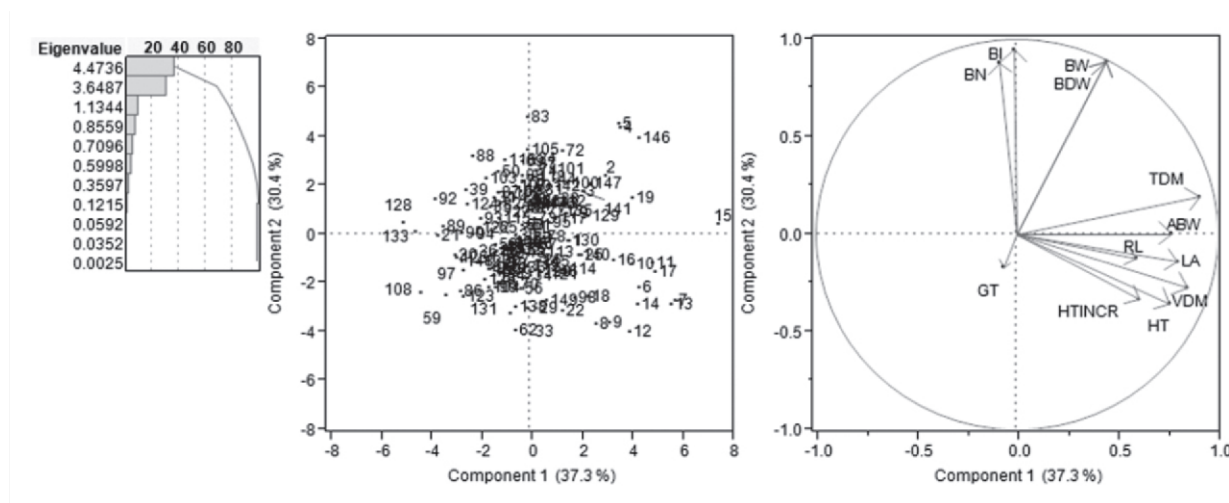


Fig. 1. The map showing the geographical distribution of oil palm genotypes collected from different states in India, which were used in the present study

Table 1. The details of oil palm accessions used for morphological characterization at ICAR-IIOPR, Pedavegi

Accession name	Palm No.	Accession name	Palm No.	Accession name	Palm No.	Accession name	Palm No.	Accession name	Palm No.	Accession name	Palm No.
Pune-1	18	G-10	172	ETURU-3	278	AND-17	150	MANG-7	82	NAM-2 (BIG)	27
Pune-1	34	G-10	178	ETURU-4	284	AND-19	33	MANG-7	83	NAM-3	28
Pune-2	40	G-9	181	ETURU-4	287	AND-19	34	MANG-7	169	NAM-3	33
Pune-2	59	G-9	182	ETURU-4	289	AND-19	35	ETURU-1	B2	TG-7	34
Pune-2	60	G-9	183	MN-5	253	AND-19	181	ETURU-1	B6	TG-7	46
LA-1	79	G-7	185	MN-5	254	AND-20	118	ETURU-1	B9	TG-7	48
LA-1	80	G-7	199	MN-5	257	AND-20	171	AND-15	B13	TG-8	56
LA-1	81	G-7	202	NELLORE-1	1	AND-20	172	AND-15	B14	TG-8	57
LA-2	82	Unknown	224	NELLORE-1	131	AND-20	175	AND-15	B16	TG-8	62
LA-2	85	And. 31	230	NELLORE-1	134	AND-21	41	AND-18	B21	TG-9	66
LA-2	88	Unknown	235	NELLORE-1	203	AND-21	196	AND-18	B23	TG-9	71
LA-3	94	And-22	239	NELLORE-1	204	AND-21	197	ANDDURA	B26	TG-9	74
LA-3	95	And-22	240	NELLORE-2	111	AND-21	198	ANDDURA	B28	ANDAMAN	82
LA-4	96	And-14	241	NELLORE-2	112	AND-24	48	AND	B32	ANDAMAN	85
LA-4	97	And-14	242	NELLORE-2	113	AND-24	49	TENERAT3	B33	PISIFERA	88
LA-4	103	MN-3	243	NELLORE-2	114	AND-24	176	TENERAT3	B37	ANDAMAN	
LA-5	104	MN-3	244	NELLORE-2	160	MANG-1	55	TENERAT2	B38		
LA-5	105	MN-3	246	TTD-1	206	MANG-1	108	TENERAT2	B44		
LA-5	106	MN-4	248	TTD-1	208	MANG-1	110	ETURU2	B45		
G-13	141	MN-4	249	TTD-1	210	MANG-1	144	NAM-1	3		
G-13	148	TTHI	260	AND-16	22	MANG-2	60	NAM-1	8		
G-12	152	NELLORE-3	262	AND-16	23	MANG-2	138	NAM-1	13		
G-12	155	NELLORE-4	263	AND-16	95	MANG-2	140	NAM-2	17		
G-11	156	NELLORE-4	264	AND-17	76	MANG-2	193	(SMALL)	19		
G-11	157	NELLORE-4	272	AND-17	78	MANG-6	61	(SMALL)	20		
G-11	161	ETURU-3	273	AND-17	80	MANG-6	62	(SMALL)	22		
G-10	171	ETURU-3	274	AND-17	147	MANG-6	128	NAM-2 (BIG)	26		



HT- Height of palm (cm), HTINR-Annual height increment (cm), GT-Girth of palm (cm), LA- Leaf area (m^2), RL- Rachis length (cm), VDM- Vegetative dry matter (kg), TDM- Total dry matter (kg), BN- Number of bunches/palm, BW- Fresh Fruit Bunches (kg), ABW- Average bunch weight (kg), BI- Bunch index

Fig. 2. The eigen value and scatter diagram plot of oil palm for vegetative and yield traits

The first two PCA components provided a reasonable summary of the data and reported 67.68 per cent of the total variation. The subsequent components explained 9 per cent or less than 9 per cent of variations. The first principal component was the most important which revealed a total variance of 37.28 per cent (Fig. 2). The traits bunch number and bunch index possessed the largest negative loadings, these results corroborating those made by Li-Hammeda *et al.* (2016) from their study on genetic variations in oil palm germplasm for yield, yield components and fatty acid traits using multivariate tools. The total variance of second PC explained an additional 30.40 per cent and positive loadings of the traits FFB, bunch dry weight and total dry matter. Variables that have significant negative as well as positive impact on the PCs can be said to contribute mostly to the genetic diversity, especially those on PC1 are likely to be the source of variation and could be taken into considered as the characters which differentiate the genotypes in the oil palm germplasm (Iannucci *et al.*, 2011; Ahmad *et al.*, 2014). Therefore, these traits can be used in the selection of elite genotypes (Ashfaq *et al.*, 2012). The PCA1 and PCA 2 of scatter plot showed overlapping of 52 accessions and based on these positive loadings, Pune 2-59, Pune 2-60, TG 9-71, AND 19-33 and TTD 1-206 were identified as promising genotypes among 150 genotypes.

The 150 palms were also examined for two way cluster analysis based on 12 morphological traits data, which separated palms and traits into two major groups. Group A comprised of 56 palms, collected from five states *viz.* Andaman and Nicobar Islands, Maharashtra, Karnataka, Andhra Pradesh and Tamil Nadu, while Group B comprised of 94 palms, collected from Andaman and Nicobar Islands, Karnataka, Andhra Pradesh and Tamil Nadu. Two sub clusters of A1 and A2 divided by group A (Fig. 3). Sub-cluster A1 comprised of genotypes collected from all germplasm collected from Maharashtra, in addition to those from Andaman and Nicobar Islands, Karnataka and Andhra Pradesh, while A2 sub-cluster comprised of genotypes collected from Andaman and Nicobar Islands. The sub cluster B1 and B2 comprised of a majority of germplasm collected from Andaman and Nicobar Islands along with those collected from Karnataka, Andhra Pradesh and Tamil Nadu. The results showed that clustering pattern was not based on geographical origins. Based on the trait specific clustering, eight traits were under Cluster I and four traits were under Cluster II. Cluster I comprised of traits with mixture of strong negative correlation, positive correlation and strongly positively correlated traits, while Cluster II comprised only positively correlated traits. Furthermore, in this study, distribution of the populations was observed

to fall randomly into various clusters from different geographic locations. Hence, there was no association of genetic diversity with geographic distribution. Similarly results have been reported by earlier workers (Kumar and Singh, 2006; Makinde and Ariyo, 2010; Odewale *et al.*, 2012).

Based on PCA analysis genotypes, Pune 2-59, Pune 2-60, TTD1- 206, AND19-33, TG9-71 selected for high FFB, genotypes of Pune 1-34, Pune 2-59, Pune 2-60, LA 4-97, LA 5-106 for high bunch dry weight, genotypes of Pune 2-59, Pune 2-60, LA 4-96, LA 4-97, LA 5-105 selected for high total dry matter, genotypes LA 2-88, LA 3-94, LA 3-95, LA 4-97,

LA 5-106 selected for high average bunch weight among the 150 palms. Based on cluster analysis, mainly two clusters were formed but the clustering was not strictly based on geographical origins. The selected palms can be used in future breeding programmes, as parents for hybridization.

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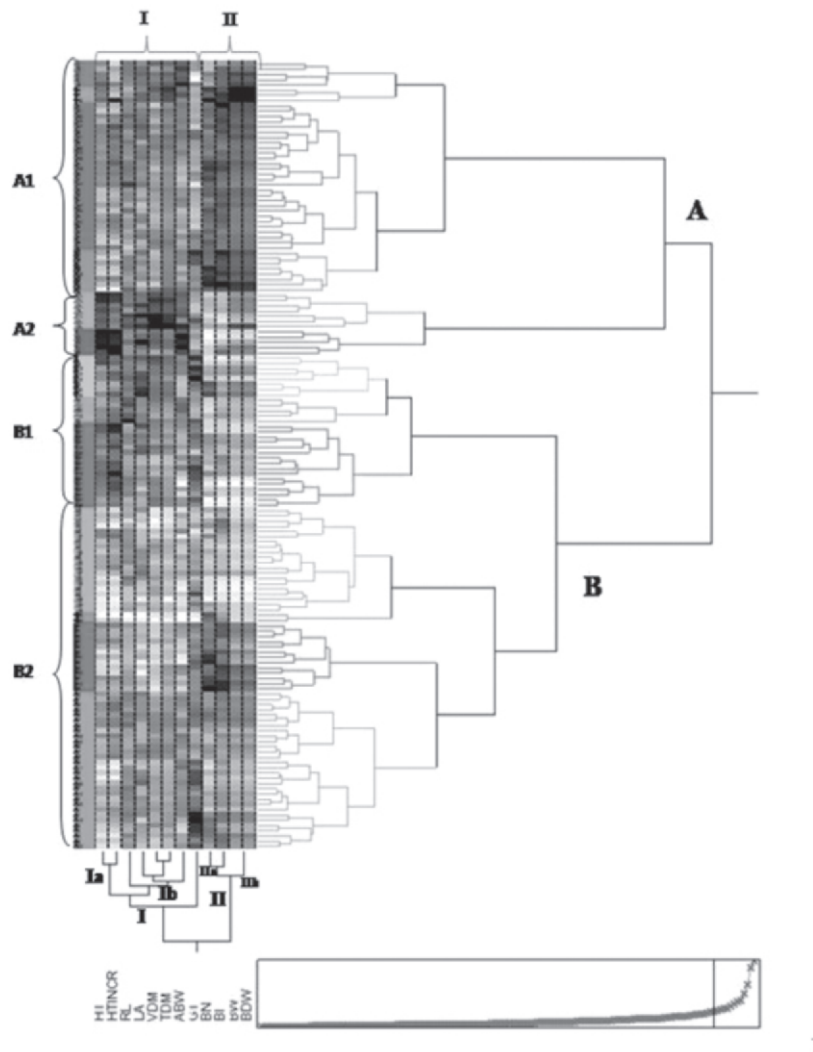


Fig. 3. The dendrogram of oil palm genotypes based on morphological traits

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