

Study of genetic diversity and identification of promising accessions of arecanut (*Areca Catechu* L.)

Abstract

The study was undertaken to assess and analysis of genetic diversity and to identify the donor parents with desirable traits among the selected 50 arecanut accessions including exotic and indigenous accessions by principal component analysis (PCA) method. The PCA of vegetative, reproductive, nut and yield characters indicated that the first 13 principal components accounted for 81.41 per cent of the variation among the accessions studied. The characters stem height, length of leaf, number of leaflets on right and left side, number of nodes, number of midribs on right side, male phase (days), female phase (days), intra-spadix overlapping (days), number of tertiary rachillae, fresh fruit weight, husk thickness in fresh fruit, dry kernel weight, dry fruit weight and kernel length were found to be contribute to genetic divergence among the arecanut accessions based on PCA. Based on their performance and genetic divergence, the accessions VTL-12 (Saigon), VTL-18III (BSI), VTL-29IV (Andaman), VTL-29II (Andaman), VTL-85 (Ratnagiri), VTL-73 (Kahikuchi), VTL-78 (Saragoan) and VTL-97 (Wynad) could be useful in arecanut breeding programmes. Accession VTL-56, a dwarf arecanut accession has been exploited in the breeding dwarf hybrids.

Keywords: arecanut germplasm, genetic diversity, cultivars, indigenous, clustering

Volume 3 Issue 2 - 2019

Rajesh B,¹ Ananda KS²
¹P.G. Department of Botany, Alva's College Moodbidri, India

²CPCRI, Regional Station, India

Correspondence: Rajesh B, P.G. Department of Botany, Alva's College Moodbidri, D.K. 574 227, Karnataka, India, Email drrajesh23@gmail.com

Received: February 24, 2019 | **Published:** March 11, 2019

Introduction

Arecanut (*Areca catechu* L.) is one of the main cash crop of South East Asian countries mainly in India. It is popularly known as 'betelnut' or 'supari'. Arecanut crop has mainly grown mainly for its masticatory nuts and also for economic, religious, cultural and medicinal importance in India. The arecanut fruit is mainly used for mastication purpose either alone or in together with leaves of beetle, lime, tobacco, camphor or any spices. It is locally called 'Tambula' where chewing of Tambula is said to increase the production of saliva and gastric juices thus aiding digestion. The fruit of arecanut also an appetizer and a stimulant. Presently arecanut is commercially and enormously cultivated in India, Bangladesh and Sri Lanka. In addition to this, countries like China, Malaysia, Indonesia, Vietnam, Philippines and Thailand also grow supari.² But India is the largest producer in the world. It is a monocot which belongs to the family Palmae.³ Arecanut is a highly cross-pollinated crop. The genus *Areca* includes 76 species spread in South East Asian Islands and important species known are *A. catechu* L., *A. triandra* Roxb., *A. concinna* Thaw., *A. macrocalyx* Zipp. and *A. normanbyii* F. Muel and also one related genera *Actinorhysis calapparia* Wendl. & Drude.^{4,5} However *A. catechu* is the only cultivated species in most of the countries. Earlier work has been resulted in identification of few promising varieties and cultivars.⁶ The study of genetic diversity in any crop like arecanut lead to formulate a better approach for the crop improvement programmes

in future. Hence, the study was carried out to assess and analysis of diversity and to identify the donor parents with desirable traits among the accessions including exotic and indigenous accessions by principal component analysis method.

Material and methods

About 50 Arecanut accessions including exotic mainly South East Asian Countries and indigenous (West Coast, east coast and North east Regions) types have utilized. The study was undertaken in CPCRI, Regional Station, Vittal, Karnataka, India. The experimental palms were planted in RBD with three replications and plot size of eight palms. The details of the study materials (arecanut accessions) are given in Table 1. The palm characters such as morphological, reproductive and yield and its components were subjected to clustering with PCA using the mean values. The PCA was carried out for all the characters and the Principal Component scores were used for Non-Hierarchical Euclidean Cluster analysis (Spark, 1973) of the arecanut accessions. The Non-Hierarchical Euclidean cluster analysis method is a powerful tool in classifying the entries into distinct groups and in discerning divergence among groups based on actual expression of multiple characters. The traits of the palms which contributed for genetic variation, were used for cluster analysis. The inter and intra cluster distances were obtained by calculating the distance between the cluster centres and genetic divergence.

Table 1 Details of materials used in the study

SI No.	Accession	Country of collection	SI. No.	Accessions	Country of collection
1	VTL-1	Fiji-I	26	VTL-73	Kahikuchi-II (Assam)
2	VTL-3	China	27	VTL-75	Nalbari (Assam)
3	VTL-5	Sri Lanka-I	28	VTL-76	Panicha (Assam)
4	VTL-9	Indonesia-IV	29	VTL-77	Saragoan-I (Assam)

Table Continued....

SI No.	Accession	Country of collection	SI. No.	Accessions	Country of collection
5	VTL-11	Indonesia-VI	30	VTL-78	Saragoan-II (Assam)
6	VTL-12	Saigon-I	31	VTL-79	Shelleshella (Assam)
7	VTL-13	Saigon-II	32	VTL-80	Dangapara (West Bengal)
8	VTL-14	Saigon-III	33	VTL-81	Haldibari (West Bengal)
9	VTL-15	Sri Lanka-II	34	VTL-82	Moralpara (West Bengal)
10	VTL-17	Singapore	35	VTL-83	Thargira (West Bengal)
11	VTL-18I	British Solumn Islands-I	36	VTL-84	Kashi and Jayanthi Hills (Meghalaya)
12	VTL-18II	British Solumn Islands -II	37	VTL-85	Ratnagiri (Maharashtra)
13	VTL-18III	British Solumn Islands-III	38	VTL-86	Badarpur-I (Assam)
14	VTL-26	Fiji-II	39	VTL-87	Badarpur-II (Assam)
15	VTL-28I	Saigon-V	40	VTL-88	Badarpur-III (Assam)
16	VTL-28II	Saigon-VI	41	VTL-89	Hylakandi (Assam)
17	VTL-28III	Saigon-VII	42	VTL-90	Cachhar (Assam)
18	VTL-29I	Andaman-I	43	VTL-91	Dauki Hills-I (Meghalaya)
19	VTL-29II	Andaman-II	44	VTL-92	Dauki Hills-II (Meghalaya)
20	VTL-29III	Andaman-III	45	VTL-93	Mowlong-I (Meghalaya)
21	VTL-29IV	Andaman-IV	46	VTL-94	Mowlong-II (Meghalaya)
22	VTL-29V	Andaman-V	47	VTL-95	Jawai-I (Meghalaya)
23	VTL-29VI	Andaman-VI	48	VTL-96	Jawai-II (Meghalaya)
24	VTL-56	Hirehalli Dwarf (Karnataka)	49	VTL-97	Wynad (Kerala)
25	VTL-60	Mohitnagar (West Bengal)	50	VTL-47	S.K. Local (Karnataka)

Results and discussion

The study showed promising results mainly presence of genetic diversity and superior accessions. The obtained mean values of vegetative, reproductive, nut and yield characters were subjected to principal component analysis. About twenty characters have used for non Hierarchical Euclidean cluster analysis in this study as suggested by Spark (1973). The PCA scores of vegetative, reproductive, nut and yield characters indicated that the first 13 principal components accounted for 82.00 per cent of the variation. The latent vectors and latent roots for 43 characters are presented in Table 2. The fruit characters like dry kernel weight (g), fresh fruit weight (g), dry fruit weight (g) and number of nuts per palm recorded high vector values in PC 1 indicating the importance of these characters which

contribute for the variations in arecanut accessions studied. The fruit husk thickness (cm) and stem girth (cm) at last exposed node (cm) were important traits in PC 2. The trait stem height (m) and internodal distance (cm) recorded high vector values in PC 3 and length of oldest functional leaf (cm), number of nuts and length of leaf sheath (cm) showed their importance in PC 4. The number of leaflets on right and left side had higher vector ratings in PC 5. Similarly, stem height (m) and number of nodes showed higher vector values in PC 6 indicating the importance of characters which contribute for the variations in the accessions. Similarly, duration of male phase (days) and kernel length (cm) recorded high vector values in PC 7 and number of midribs on right side and recovery of kernel (%) recorded high vector scores in PC 8, which contributed for genetic variation.

Table 2 Latent vectors and latent roots for morphological, reproductive, yield and nut characters of arecanut accessions

Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13
Palm height	0.122	0.052	0.356	-0.010	-0.109	0.282	0.07	0.077	0.075	-0.028	-0.045	-0.016	0.022
Stem height (m)	0.069	0.081	0.360	-0.144	-0.089	0.342	0.071	0.114	0.037	-0.012	-0.025	-0.092	-0.017
Stem girth at fixed mark (cm)	0.053	-0.230	-0.108	0.135	-0.130	0.148	0.016	0.271	0.103	-0.217	-0.023	-0.038	-0.160
No. of nodes	0.028	-0.138	0.195	-0.178	-0.005	0.383	-0.108	0.266	-0.067	0.029	-0.132	-0.213	0.091
No. of leaves	0.127	-0.162	-0.156	0.100	-0.046	0.102	0.125	0.182	-0.187	-0.164	-0.136	0.003	0.059
Internodal distance (cm)	0.045	0.098	0.337	0.160	-0.066	0.016	-0.074	-0.188	0.202	-0.132	0.100	-0.159	0.054

Table Continued...

Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13
Stem girth at last exposed node (cm)	0.075	-0.287	-0.100	0.181	-0.082	0.070	0.115	0.167	0.010	-0.011	0.014	-0.138	-0.052
Length of leaf sheath (cm)	0.210	-0.069	-0.006	0.244	0.099	0.089	-0.069	-0.090	-0.003	-0.126	-0.140	-0.010	-0.012
Leaf length (cm)	0.161	-0.068	0.019	0.352	0.065	0.152	0.023	-0.104	-0.029	-0.186	0.087	0.162	-0.266
Leaf breadth (cm)	0.179	-0.066	-0.059	0.158	0.211	0.029	-0.041	-0.177	-0.069	-0.156	0.028	-0.026	0.308
No. of leaflet (right side)	0.031	-0.125	0.120	-0.010	0.461	0.162	0.143	-0.132	0.090	0.270	-0.043	0.122	-0.039
No. of leaflet (left side)	-0.014	-0.141	0.200	0.036	0.390	0.119	0.204	-0.079	0.065	0.172	0.027	0.286	-0.075
No. of midribs (right side)	0.062	-0.122	0.165	0.017	0.283	-0.182	0.120	0.356	0.104	-0.219	0.030	-0.058	0.109
No. of midribs (left side)	0.028	-0.143	0.175	0.041	0.310	-0.301	-0.052	0.320	0.119	0.020	0.141	0.056	0.000
Length of leaflet (cm)	0.190	0.040	-0.034	0.205	-0.034	0.003	0.100	-0.169	-0.193	0.061	-0.066	-0.207	-0.020
Breadth of leaflet (cm)	0.024	-0.184	-0.147	-0.066	0.196	-0.060	0.149	0.007	-0.163	0.150	-0.152	-0.440	-0.294
Spadix length (cm)	0.194	-0.010	0.087	0.110	-0.100	0.058	-0.120	-0.145	0.146	0.068	0.007	0.039	-0.153
Spadix breadth (cm)	0.128	-0.232	-0.019	-0.157	-0.232	-0.013	0.095	0.070	-0.003	0.087	0.234	0.164	0.029
No. of secondary rachillae/inflorescence	0.153	-0.184	0.065	-0.073	-0.090	-0.138	0.073	-0.048	-0.129	0.049	0.335	-0.059	-0.058
No. of tertiary rachillae/inflorescence	0.147	-0.199	0.028	-0.015	-0.118	-0.106	0.073	0.116	-0.001	0.205	0.415	-0.054	0.009
No. of female flowers/inflorescence	0.183	-0.148	-0.009	-0.039	-0.201	-0.059	0.012	-0.031	0.170	0.235	0.057	0.015	-0.155
Male phase (days)	0.099	0.124	0.155	0.015	-0.080	-0.097	0.388	-0.089	-0.129	-0.026	0.269	-0.075	0.365
Female phase (days)	-0.058	-0.107	-0.136	-0.060	-0.056	0.177	-0.086	-0.141	0.451	-0.113	0.236	-0.019	-0.312
Gap between male and female phases (days)	-0.012	-0.132	-0.091	-0.181	-0.186	0.020	0.367	0.013	0.004	-0.093	-0.292	0.558	-0.001
Intra-spadix overlapping (days)	0.001	-0.094	-0.285	0.081	0.075	0.269	-0.075	-0.052	0.116	0.426	0.018	-0.022	0.211
Inter-spadix overlapping (days)	0.027	-0.098	-0.304	0.031	0.125	0.136	-0.137	0.176	0.145	-0.202	0.092	0.012	0.326
Nut set (%)	0.210	-0.133	0.038	-0.079	-0.029	-0.120	-0.177	-0.136	0.078	-0.032	-0.042	-0.008	0.094
No. of inflorescences/palm/year	0.189	-0.130	-0.006	0.138	-0.093	-0.090	-0.128	-0.051	-0.122	0.125	-0.063	0.115	0.140
No. of harvested bunches/palm/year	0.197	-0.179	0.030	-0.012	-0.059	-0.126	-0.138	-0.043	0.021	0.145	-0.233	-0.086	0.043
Fresh fruit weight (g)	0.231	0.192	-0.087	-0.026	0.095	-0.038	0.027	0.096	0.048	0.081	0.018	0.000	-0.075
Fresh fruit length (cm)	0.187	0.191	-0.030	0.119	-0.039	0.053	0.218	0.053	0.117	0.077	-0.130	-0.118	-0.021
Fresh fruit breadth (cm)	0.199	0.184	-0.10	-0.021	0.180	-0.016	-0.145	0.055	-0.110	-0.036	0.130	0.142	-0.165
Husk thickness (cm)	0.144	0.295	-0.079	0.061	0.003	-0.082	0.011	0.176	0.110	-0.046	-0.011	0.077	-0.034
Dry fruit weight (g)	0.231	0.192	-0.097	-0.107	0.058	0.073	0.059	0.048	-0.034	0.000	0.063	-0.038	-0.064
Kernel weight (g)	0.246	0.103	-0.077	-0.153	0.104	0.047	0.054	-0.058	-0.061	-0.023	0.043	-0.055	-0.043
Kernel length (cm)	0.162	0.103	-0.132	0.009	-0.066	-0.018	0.384	0.055	0.196	0.131	-0.149	-0.051	0.039
Kernel breadth (cm)	0.189	0.095	-0.094	-0.175	0.125	0.122	-0.053	-0.092	-0.179	-0.260	0.213	0.129	-0.138
Dry husk weight (g)	0.158	0.271	-0.101	-0.035	-0.025	0.077	0.066	0.194	0.013	0.035	0.065	-0.013	-0.082
Dry kernel recovery (%)	0.004	-0.205	-0.050	-0.285	0.071	0.192	0.146	-0.317	-0.217	-0.240	0.09	-0.109	0.040
No. of nuts/palm/year	0.245	-0.081	0.096	-0.297	-0.037	-0.068	-0.183	-0.046	0.147	-0.083	-0.176	0.038	0.099
Ripe nut weight/palm/year (kg)	0.199	0.020	-0.014	-0.208	0.059	-0.101	-0.131	-0.002	0.138	-0.004	-0.145	0.016	0.042

Table Continued....

Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13
Chali (dry kernel) weight/palm/year (kg)	0.245	-0.036	0.011	-0.259	0.026	-0.086	-0.081	-0.075	0.072	-0.047	-0.011	-0.001	0.074
Total phenol (mg/g)	0.071	-0.069	0.224	0.040	-0.052	-0.166	-0.103	0.091	-0.361	0.011	-0.190	0.089	-0.316
Eigen Root	12.27	5.87	3.74	2.37	2.23	1.81	1.60	1.45	1.36	1.15	1.05	0.87	0.81
Variance percent	27.27	13.06	8.32	5.27	4.95	4.03	3.56	3.23	3.02	2.56	2.33	1.93	1.81
Cumulative variance percent	27.27	40.33	48.65	53.93	58.89	62.93	66.49	69.73	72.75	75.32	77.66	79.59	82.00

Similarly characters such as duration of female phase (days) and internodal distance (cm) had high vector values in PC 9 while intra-spadix overlapping (days) and number of leaflets on one side showed higher vector scores in PC 10 indicating the importance of these characters. The traits number of secondary and tertiary rachillae per inflorescence were important traits in PC 11 and gap between male and female phases (days) and breadth of leaflet (cm) were important traits in PC 12. In addition to this, the duration of male phase (days) and inter-spadix overlapping (days) had high vector values in PC 13. The PC scores of twenty traits of accessions studied, which contributed to the genetic variations, were utilized for clustering of arecanut accessions in the present study. The PC analysis indicated that the fifty arecanut accessions could be grouped into four clusters and cluster compositions are presented in Table 3. Among the four clusters, cluster IV had maximum number of accessions (20) followed by cluster III (17) and cluster II (12). However, accession VTL-56 (Hirehalli dwarf) clustered separately in cluster I.

Table 3 Cluster composition of arecanut accessions using principal component scores

Cluster No.	Accessions
I (1)	VTL-56
II (12)	VTL-3,VTL-5,VTL-11,VTL-17,VTL-18III,VTL-28III,VTL-29II,VTL-29IV,VTL-29VI,VTL-60,VTL-85,VTL-97
III (17)	VTL-9,VTL-26,VTL-29I,VTL-77,VTL-81,VTL-84,VTL-86,VTL-87,VTL88,VTL-89,VTL-90,VTL-91,VTL-92,VTL-93,VTL-94,VTL-95,VTL-96
IV (20)	VTL-1,VTL-12,VTL-13,VTL14,VTL-15,VTL-18I,VTL-18II,VTL-28I,VTL-28II,VTL-29I,VTL-29III,VTL-47,VTL-73,VTL-75,VTL-76,VTL-78,VTL-79,VTL-80,VTL-82,VTL-83

The mean values of intra and inter cluster distances between cluster are presented in Table 4. The inter cluster distance was maximum (13.206) between the Cluster I and Cluster II followed by Cluster I and

Cluster IV (12.99). The minimum inter cluster distance was recorded between Cluster II and Cluster IV (3.56). The intra cluster distance was highest in Cluster II (3.588) followed by Cluster IV (3.30) and lowest intra cluster distance was noticed between the accessions in Cluster III (3.01). The cluster means of twenty parameters have presented in Table 5. The Cluster I which included only VTL-56 (Hirehalli dwarf- a natural mutant) had highest mean value for leaflet breadth (5.75cm), female phase (7.28 days), gap between male and female phases (5.73 days), inter-spadix overlapping (3.29 days) and intra-spadix overlapping (1.31 days). The characters such as stem height, number of nodes, internodal distance, length of leaf sheath, length of leaf, male phase, fresh fruit weight, husk thickness, dry fruit weight, kernel weight, kernel length and number of nuts per palm were lowest in Cluster I. The parameters such as stem height (6.40m), number of nodes (50.61), length of leaf sheath (98.63cm), length of leaf (202.22cm), number of leaflets on one side (42.70), number of secondary rachillae (20.58), number of tertiary rachillae (482.85), male phase (23.57 days), dry kernel weight (8.33g), kernel length (2.06cm) and number of nuts per palm (376.07) recorded higher values in Cluster II. Cluster III had maximum values for fresh fruit weight (37.08g), husk thickness (0.69) and dry fruit weight (13.49) and kernel length (2.06cm). Similarly, the internodal distance (16.81cm) was maximum in Cluster IV, while rest of the traits showed moderate values. A list of promising superior arecanut accessions indicating their cluster affinity and their desirable traits which is presented in Table 6.

Table 4 Inter and intra cluster distances between cluster centres

Cluster No.	I	II	III	IV
I	0.00			
II	13.206	3.588		
III	11.703	4.973	3.014	
IV	12.990	3.561	3.781	3.309

Table 5 Cluster mean values for different characters in arecanut

Sl. No	Characters	I	II	III	IV
1	Stem height (m)	1.32	6.40	5.99	6.36
2	Number of nodes	43.00	50.61	44.53	48.56
3	Internodal distance (cm)	2.58	16.19	16.11	16.81
4	Length of leaf sheath (cm)	57.75	98.63	84.08	74.99
5	Leaf length (cm)	146.43	202.22	187.03	174.62
6	No. leaflet on one side	41.00	42.70	38.14	39.17
7	Breadth of leaflet (cm)	5.75	3.62	3.13	3.62
8	No. of secondary rachillae /inflorescence	18.58	20.58	18.63	18.12
9	No. of tertiary rachillae/inflorescence	407.46	482.85	369.27	352.51

Table Continued....

SI. No	Characters	I	II	III	IV
10	Male phase (days)	18.88	23.57	23.55	22.75
11	Female phase (days)	7.28	5.67	5.61	5.84
12	Gap between male and female phases (days)	5.73	3.77	3.52	3.71
13	Intra-spadix overlapping (days)	1.31	0.29	0.21	0.17
14	Inter-spadix overlapping (days)	3.29	1.26	0.83	0.68
15	Fresh fruit weight (g)	12.54	35.62	37.08	24.50
16	Husk thickness (cm)	0.22	0.56	0.69	0.50
17	Dry fruit weight (g)	5.26	13.13	13.49	9.46
18	Kernel weight (g)	3.45	8.33	7.78	5.48
19	Kernel length (cm)	1.85	2.06	2.06	1.76
20	No. of nuts/palm/year	125.75	376.07	268.08	244.76

Table 6 Desirable parameters among the genetically diverse arecanut accessions

SI. No.	Accessions	Origin	Types	Cluster No.	Desirable traits
1	VTL-3	China	Exotic	II	Semi-tall, higher fruit set and high yield
2	VTL-11	Indonesia	Exotic	II	More number of female flowers, higher fruit set, bold kernel higher recovery of dry kernel and yield
3	VTL-12	Saigon	Exotic	IV	Higher fruit set, recovery of dry kernel and yield
4	VTL-18III	Br. Sol. Islands	Exotic	II	Higher recovery of dry kernel and yield
5	VTL-29II	Andaman	Indigenous	II	Higher fruit set, higher recovery of dry kernel and yield
6	VTL-29IV	Andaman	Indigenous	II	More number of female flowers, higher fruit set, higher recovery of dry kernel and yield
7	VTL-56	Hirehalli (Karnataka)	Indigenous	I	Dwarfness and high recovery of kernel
8	VTL-60	West Bengal	Indigenous	II	Higher fruit set, high recovery of kernel, bold kernel and high yield
9	VTL-73	Kahikuchi (Assam)	Indigenous	IV	Bold kernel
10	VTL-78	Saragoan (Assam)	Indigenous	IV	Bold kernel, higher yield
11	VTL-85	Ratnagiri (Maharashtra)	Indigenous	II	Higher recovery of dry kernel and yield
12	VTL-97	Wyanad	Indigenous	II	Semi-tall and higher yield

The characters stem height (m), length of leaf (cm), number of leaflets on right and left side, number of nodes, number of midribs on right side, male phase (days), female phase (days), intra-spadix overlapping (days), number of tertiary rachillae, fresh fruit weight (g), husk thickness (cm) in fresh fruit, dry kernel weight (g), dry fruit weight (g) and kernel length (cm) were found to be contribute to genetic divergence among the arecanut accessions based on PCA. Similar results were reported by Bavappa (1982) in selected arecanut local cultivars.

Non-Hierarchical Euclidean cluster analysis by PCA scores grouped 50 arecanut accessions into four clusters. No separate clusters were formed based on geographic origin indicating the relatedness of indigenous and exotic accessions. Accession VTL-56 (Hirehalli Dwarf a natural mutany) formed a distinct single accession cluster (cluster I) indicating the distinct genetic nature of this accession. The variability was higher in the exotic accessions as they were scattered

in the remaining three clusters irrespective of their origin. In this study, variability observed within and among the accessions collected from Fiji, Indonesia, Sigon and British Solumn Islands (BSI) as these accessions grouped in separate clusters indicating the diversity in their genetic compositions.

The cluster composition indicated the greater resemblance between some of the indigenous collections. Out of 11 accessions collected from Assam (indigenous), six accessions grouped in cluster III and rest of the five accessions grouped in cluster IV. Accessions collected from Meghalaya (indigenous) were grouped in cluster III only indicating the resemblance in genetic architecture of the accessions. Purushotham et al.,⁷ reported that the local cultivars of arecanut in Western ghats, showed close phylogenetic relationship by RAPD markers which corroborates the present result. Similarly, accessions collected from Andaman and Nicobar Islands (6 indigenous accessions) showed their distinctness and the genetic diversity by grouping in separate clusters

(cluster II, III and IV). Interestingly, accessions collected from West Bengal (5 indigenous accessions) were grouped in clusters II, III and IV showing distinctness in their genetic makeup. Cluster III was constituted by mostly indigenous accessions except for two exotic accessions VTL-9 (Indonesia) and VTL-26 (Fiji). Similar results of affinity between indigenous and exotic accessions were also reported by Bharath et al.,⁸ by DNA markers.

The maximum inter cluster distance was observed between Cluster I which comprised only accession VTL-56 (Hirehalli Dwarf) and Cluster II having promising cultivars (VTL-3 (China), VTL-11 (Indonesia), VTL17 (Singapore), VTL-60 (West Bengal) and VTL-85 (Ratnagiri)), indicating that their members are distantly related and it would be useful to attempt hybridization between the two groups. Similarly, the inter cluster distance was higher between Cluster I and Cluster IV indicating their distant genetic relationship. The lowest inter cluster distance was observed between Cluster II and Cluster IV, indicating their genetic resemblance. The intra cluster distance was very less in the Cluster III which was constituted by indigenous accessions except VTL-9 (Indonesia) and VTL-26 (Fiji) indicating the genetic closeness among the accessions. The higher intra cluster distance was noticed in Cluster II comprising of promising cultivars (VTL-3 (China), VTL-11 (Indonesia), VTL17 (Singapore), VTL-60 (West Bengal) and VTL-85 (Ratnagiri)) and other accessions indicating their divergence among the accessions. Among these, VTL-60 (West Bengal) and VTL-85 (Ratnagiri) were indigenous in origin while the rest of the accessions were exotic types. Interestingly, the present study indicated that Cluster III (intra cluster distance) and inter cluster distance between Cluster III and Cluster IV indicated that the closeness of the genotypes. So, accessions grouped with cluster III is less diverged from Cluster IV. Among these accessions studies, some promising accessions and cultivars evolved as varieties and released for cultivation as reported by Ananda et al.⁶ Similarly, reported. The present study indicated the maximum divergence among the exotic accessions. In earlier studies also, it has been reported that the majority of the species of *Areca* have been observed in Malay Archipelago, the Philippines and other East Indies Islands, and believed that the center of origin of *A. catechu* is likely to be around this region (Raghavan, 1957). Similarly, the centre of maximum variation of the arecanut is believed to be the East Indies group of Islands where majority of the species of *Areca* have been reported.¹⁰ The highly divergent accessions could be exploited in hybridization depending upon the objectives of the breeding programme in arecanut. Based on their performance and genetic divergence, the accessions VTL-12 (Saigon), VTL-18III (BSI), VTL-29IV (Andaman), VTL-29II (Andaman), VTL-85 (Ratnagiri), VTL-73 (Kahikuchi), VTL-78 (Saragoan) and VTL-97 (Wynad) could be useful in the arecanut breeding programmes. Accession

VTL-56, a natural mutant dwarf accession has been exploited in the breeding dwarf hybrids and resulted in identification of promising dwarf (HD I & HD II) hybrids through from hybridization between high yielding tall varieties and local cultivars. The promising superior cultivars/ accessions identified in the study could also be exploited for further breeding programme mainly for identification of location specific varieties and dwarf hybrids.

Acknowledgments

None

Conflicts of interest

The author declares there are no conflicts of interest.

References

1. Rao MM. Introduction. In: The Arecanut Palm-Monograph. Bavappa KVA, Nair MK, Prem Kumar T, editors. Central Plantation Crops Research Institute, Kasaragod. 1982. p. 1–7.
2. Balasimha D, Rajagopal V. Introduction. In: Arecanut-Monograph. Balasimha D, Rajgopal V, editors. Central Plantation Crops Research Institute, Kasaragod, Kerala, India. 2004. p. 1–6.
3. Linnaeus, C. *Species Plantarum* 2 Vol. Stockholm, 1753.
4. Murthy KN, Pillai RSN. Botany. In: The Arecanut Palm. Bavappa KVA, Nair MK, Prem Kumar T, editors. Central Plantation Crops Research Institute, Kasaragod. 1982. p. 11–49.
5. Ananda KS. Botany. In: Arecanut-Monograph, Balasimha D, Rajagopal V, editors. Central Plantation Crops Research Institute, Kasaragod. 2004. p. 7–50.
6. Ananda KS, Nagaraja NR, Chowdappa P. Arecanut Varieties and Hybrids released by ICAR- CPCRI. *Indian Journal of Arecanut, Spices and Medicinal Plants*. 2016;8(4):16–21.
7. Purushotham B, Narayanaswamy P, Simon L, et al. Genetic relationship between Arecanut cultivars (*Areca catechu L.*) determined by RAPD. *The Asian and Australian Jn. Plant Science and Biotechnology*. 2008;2(1):31–35.
8. Bharath BG, Ananda KS, Rajith J, et al. Studies on genetic relationship and diversity in Arecanut (*Areca catechu L.*) germplasm utilizing RAPD Markers. *Jn Plantation Crops*. 2015;43(2):117–125.
9. Raghavan V. On certain aspects of the biology of arecanut (*Areca catechu L.*) and utilization of its by-products in industry. D. Phil. Thesis. Gauhati University. 1957. p. 186.
10. Bharath BG, Ananda KS, Rajith J, et al. Studies on genetic relationship and diversity in Arecanut (*Areca catechu L.*) germplasm utilizing RAPD Markers. *Jn Plantation Crops*. 2015;43(2):117–125.