Regular Article
pISSN: 2288-9744, eISSN: 2288-9752
Journal of Forest and Environmental Science
Vol. 38, No. 1, pp. 12-20, March, 2022
https://doi.org/10.7747/JFES.2022.38.1.12

JFES
Journal of Forest and Environmental Science

Assessing the Performance of *Pongamia pinnata* (l.) Pierre under *Ex-situ* Condition in Karnataka

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Abstract

Pongamia (*Pongamia pinnata* L.) as a source of non-edible oil, is potential tree species for biodiesel production. For several reasons, both technical and economical, the potential of *P. pinnata* is far from being realized. The exploitation of genetic diversity for crop improvement has been the major driving force for the exploration and *ex situ*/*in situ* conservation of plant genetic resources. However, *P. pinnata* improvement for high oil and seed production is not achieved because of unsystematic way of tree improvement. Performance of *P. pinnata* planted by Karnataka Forest Department was assessed based on yield potential by collecting 157 clones out of 264 clones established by Karnataka Forest Department research wing under different research circles/ranges. It was evident that the all the seed and pod traits were significantly different. Further, selection of superior germplasm based on oil and pod/seed parameters was achieved by application of Mahalanobis statistics and Tocher's technique. On the basis of D^2 values for all possible 253 pairs of populations the 157 genotypes were grouped into 28 clusters. The clustering pattern showed that geographical diversity is not necessarily related to genetic diversity. Cluster means indicated a wide range of variation for all the pod and seed traits. The best cluster having total oil content of more than 34.9% with 100 seed weight of above 125 g viz. Cluster I, II, III, IX, XV, XIX, XXI, XXIII, XXVI and XXVII were selected for clonal propagation.

Key Words: *Pongamia pinnata*, Mahalanobis, genetic diversity, cluster analysis, D^2 analysis

Introduction

Worldwide biodiesel production increased from 253.34 million gallons in 2001 to 4.16 billion gallons in 2009, at a compound annual growth rate (CAGR) of 41.9 percent. Supported by governments to increase energy independence and meet rising energy demand, the biodiesel market is expected to produce 11.96 billion gallons of biodiesel in 2020, representing a CAGR of 10.1 percent during 2009 to 2020.

Shortage of edible oil for human consumption in developing countries like India does not favour its use for bio-diesel production. Tree borne oil seeds are not only potential renewable energy source to supplement the increasing energy requirement, but also serves as an alternative source of oil to meet the increasing demand of edible oil globally. Vegetable oils of some tree species like *Pongamia, Jatropha*, Neem, Mahua, Polang, Simarouba, Sal, Kusum, Linseed, Castor, Baigaba etc., are in utilization for the commercial production of biofuels. Usage of Pongamia (*Pongamia pinnata* L.) as a source of non-edible oil, is potential tree species for biodiesel production.

Pongamia pinnata (L.) Pierre, synonymously known as

Received: June 29, 2021. Revised: September 6, 2021. Accepted: September 15, 2021.

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Pongamia glabra Vent., *Derris indica* (Lam) Bennett., *Millettia novo-guineensis* Kane & Hat. and *Cytisus pinnaus* L. is an arboreal legume, belongs to the subfamily Papilionoideae, more specifically the tribe Millettieae. *Pongamia*, popularly known as Karanja, is an important shade tree of India. The *Pongamia* spp. is considered to be native to India (Western Ghats). It is also found in China, Florida, Malaysia, Seyhelles, Philippines and Australia (Daniel 1997).

P. pinnata has been documented to include variable forms with a wide range of pod as well as seed size and shape variations (Council of Scientific & Industrial Research 1969). Seeds contain 30 to 40% oil. Characterization and selection of CPT's (Candidate Plus Trees) is essential for the improvement of this species in addition to experiments on controlled crossing among selected genotypes (Mukta et al. 2009). Under the National Network on Integrated Development of *P. pinnata* in India, about 432 CPTs have been identified from 120 districts of the country (Kureel 2007).

Analysis of phenotypic diversity in germplasm collections can facilitate reliable classification of accessions and its identification with future utility for specific breeding purposes. There are very few studies on phenotypic diversity involving a limited number of germplasm and their suggested use in hybridization with respect to *P. pinnata*.

The diversity within the species has been increasingly recognized as a tangible, economic resource directly equivalent to a country's mineral wealth, thus they have been referred to as Plant genetic resources. People conserve diversity because they wish to exploit it (Maxted et al. 1997). The exploitation of genetic diversity for crop improvement has been the major driving force for the exploration and *ex situ*/*in situ* conservation of plant genetic resources. Characterization and evaluation of germplasm have been achieved largely on *ex situ* materials and must obviously take place before the choice can be made of what material will be worth using for any particular purpose. Identification of elite with high seed oil content or high seed producing ability or with ability to produce seed oil of desired composition in *P. pinnata* has biodiesel utility.

However, *P. pinnata* improvement for high oil and seed production is not achieved because of unsystematic way of tree improvement and until now there are no reports of multi-locational trial and possibilities of varietal release. Presently our focus is on systematic approach for genetic improvement of *P. pinnata* with following objectives; (a) Assessing the performance of *P. pinnata* planted by Karnataka Forest Department and (b) Selection of superior germplasm based on oil and pod/seed yield performance.

Materials and Methods

Survey and selection of clones

Survey was conducted to collect the pods of all the high yielding clones of *P. pinnata* at fruiting stage from different clonal plantations (by grafting) established by Karnataka Forest Department under different research ranges in

Table 1. Clonal details of *P. pinnata* plantations established by Karnataka Forest Department (KFD) and selected out of available clones

Sl. no.	Range	Location	Number of clones (selected/available)
1	Kolar	Yeshwanthpur B block (Narsapura)	95/134
2	Hoskote	Nelhal C block	8/8
3	Tumakuru	Ankapura	3/5
4	Dharwad	Gungargatti	3/3
5	Haveri/Sirsi	Jangamanakoppa – Karjagi	6/6
6	Bangalore	Bommanahalli	1/4
7	Shimoga	Kesavanakatte – Hittur	5/5
8	Challakere	Somangudda	16/21
9	Mandya	Chikkammanagudda (CM Gudda)	11/18
10	Mysore	Madahalli	9/60
		Total	157/264

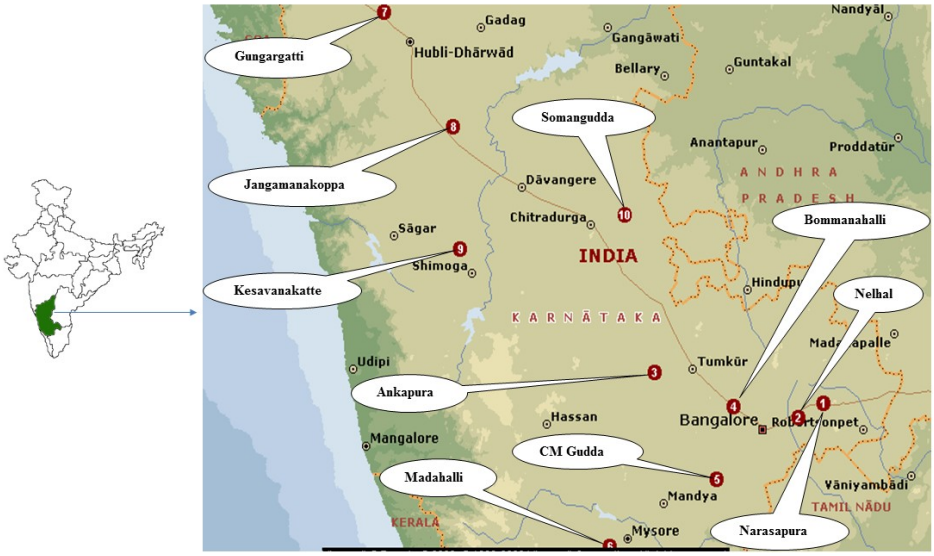

Fig. 1. Selected *Pongamia pinnata* plantations of Karnataka Forest Department for collection of Pods/ Seeds.

Bangalore, Madikeri and Dharwad research circles. After survey of all the pongamia clonal plantations established during 2007-2008, clones having good yield potentiality with good pod set and free from pest & diseases were selected based on the pod/seed yield performance i.e. clones which are able to yield minimum of 2-3 kg of pods per tree. A total of one hundred fifty-seven clones (phenotypically superior trees) were selected by covering a latitude and longitudinal range between 12°12'19.10"N to 15° 32'58.01"N and 75°28'26.02"E to 78°13'30.81"E respectively (Table 1; Fig. 1).

Assessing the performance

After assessment of yield performance in field by selecting superior genotypes with potentiality of yielding minimum 2-3 kg of pods per tree, performance of selected clones were further assessed by collecting few kg of pods by following a random sampling procedure from all the four directions of the crown of each selected tree during fruiting season February-June, 2015. The total pods collected were randomly divided into three replications and each replication consists of 100 pods was selected for recording observations for nine quantitative characters (four pod and 4 seed characters) at Institute of Wood Science and Technology (IWST), Bangalore [latitude: 13°00'42"N, longitude: 77°34' 8" E, altitude 3090 ft msl].

Pod characters

The pods were cleaned and stored in muslin bags at ambient conditions. All lots were dried under similar temperature and humidity conditions to reach constant weight. A total of 300 healthy pods (hundred in each replication) were collected from each clone and observations for four pod characters viz. pod length, pod width, pod thickness were measured using vernier caliper and expressed in mm, while the trait pod weight was measured using electrical balance and average expressed in grams.

Seed characters

Sample of 300 seeds were collected from each clone to make three replications containing 100 seeds per replication and seed morphometric trait viz. seed length, seed width and seed thickness were measured using vernier caliper expressed in mm. The trait 100-seed weight was recorded by weighing 100 pure seed on electrical balance and average value was calculated and expressed in grams. Total oil content in seeds was estimated following the procedure of Sadasivam and Manickam (1992) using soxhlet apparatus and solvent Hexane.

Data analysis

The pod and seed parameters and clonal field biometric data were analysed for Analysis of variance (ANOVA) to

understand the significance of differences between the pods, seeds and clonal traits (Gomez and Gomez 1984).

The morphological variations among 157 clones of *P. pinnata* was estimated based on pod/seed traits using the Mahalanobis D^2 statistics (Mahalanobis 1936) to assess the performance and select the best performing clones. The clusters, derived from distance matrices, were formed according to criterion used by Tocher as described by Rao (1952). This procedure starts with two closely associated genotypes (represented here by plus trees) and finds a third genotype which has the smallest average D^2 from the first two. Next, the fourth is chosen to have smallest average D^2 from the first three, and so on. There is an increase in the average D^2 within a cluster whenever an additional genotype is included. The limit for inclusion of a new genotype corresponds to the minimum generalized distance, above which the newly added genotype has to be considered as outside the former cluster. Average intra and inter cluster distances were determined using GENRES version 3.11, 1994 Pascal Intl. Software and suggested by Singh and Chaudhary (1977).

Table 2. Clustering of *Pongamia pinnata* genotypes

Cluster	Number of accessions	Accessions
I	3	PP001, PP138, PP144
II	2	PP143, PP148
III	2	PP096, PP098
IV	3	PP002, PP008, PP057
V	5	PP003, PP004, PP005, PP066, PP086
VI	3	PP006, PP064, PP078
VII	4	PP007, PP009, PP031, PP116
VIII	2	PP125, PP134
IX	4	PP010, PP011, PP019, PP099
X	15	PP012, PP013, PP014, PP015, PP016, PP017, PP018, PP020, PP021, PP022, PP023, PP024, PP025, PP055, PP157
XI	11	PP026, PP027, PP028, PP029, PP030, PP032, PP033, PP034, PP035, PP050, PP062
XII	3	PP036, PP141, PP145
XIII	3	PP037, PP065, PP104
XIV	30	PP038, PP039, PP040, PP041, PP042, PP043, PP044, PP045, PP046, PP047, PP048, PP049, PP051, PP052, PP053, PP054, PP056, PP058, PP059, PP060, PP061, PP063, PP067, PP068, PP069, PP070, PP071, PP072, PP089, PP108
XV	2	PP076, PP137
XVI	15	PP073, PP074, PP075, PP077, PP079, PP080, PP081, PP082, PP083, PP084, PP085, PP087, PP088, PP118, PP119
XVII	2	PP117, PP126
XVIII	3	PP090, PP091, PP152
XIX	2	PP121, PP142
XX	13	PP092, PP093, PP094, PP095, PP097, PP100, PP101, PP102, PP103, PP105, PP106, PP124, PP132
XXI	2	PP130, PP155
XXII	2	PP135, PP149
XXIII	6	PP107, PP109, PP110, PP111, PP128, PP146
XXIV	11	PP112, PP113, PP114, PP115, PP120, PP122, PP123, PP127, PP129, PP131, PP133
XXV	4	PP136, PP139, PP140, PP147
XXVI	2	PP151, PP153
XXVII	2	PP150, PP154
XXVIII	1	PP156

Results and Discussion

Pursuant to urgent need for production of quality material required for planting in deforested areas and meet the needs of biodiesel industries, evaluation of oil yielding trees germplasm viz. *P. pinnata* in Karnataka is essential. Based on the information from research wing of Karnataka Forest Department, all the clonal plantations established under different research ranges in different research circles were visited to see the growth performance and yield potential. Among all the clonal trial of *P. pinnata*, clonal plantations as mentioned in Table 1 were selected for analysing yield performance and collection of pod & seeds for further analysis. Total of 157 clones of *P. pinnata* were identified and collected from different ranges under research circles under KFD. Analysis of variance for pod, seed and oil traits showed highly significant values, indicating the presence of large range of variability among the selected clones.

Genetic variations in plant species is a gift to mankind as it forms the basis for selection and further improvement. Assessment of genetic divergence in the populations of a species is of paramount significance in purposeful breeding. In fact, an appraisal of the degree of divergence in important traits of a species is of added advantage in this regard, as inter-mating of divergent groups would increase variability and help produce genetically superior planting material required for use in afforestation and reforestation programmes (Chaturvedi and Pandey 2001).

The concept of Mahalanobis genetic distances, among the multivariate distance methods, has been shown to be robust (Dias and Kageyama 1997) because of having vital utility in differentiating well defined plus trees, which is an approach basic and fundamental for estimating the extent of variations among the selected genotypes (Kole and Saha 2009). The more diverse the parents within the overall limit of fitness, the greater the chances of obtaining a higher amount of heterotic expression and a broad spectrum of variability in segregation generations (Kole and Mishra 2002). Owing to large amount of genetic variations encountered in open pollinated trees, it becomes an essential requirement to assess and analyze the extent of this genetic variations in the germplasm of a species through the use of this scientific and advanced biometrical technique viz., multivariate technique based on Mahalanobis D^2 statistics.

In present study selection of superior clones based on oil and seed parameters was carried out using application of Mahalanobis statistics and Tocher's technique. On the basis of D^2 values for all possible 253 pairs of populations the 157 genotypes were grouped into 28 clusters. The clustering pattern showed that geographical variations is not necessarily related to genetic variations (Table 2). This kind of genetic variations might be due to differential adoption, selection criteria, selection pressure and environment (Vivekanandan and Subramanian 1993). This indicated that genetic drift produces greater diversity than the geographic diversity (Singh et al. 1996). Absence of any relationship between genetic diversity and geographical distribution is in accordance with the findings of Kaushik et al. 2007 and Gohil and Pandya 2008 in *Jatropha curcas*.

Cluster XIV had maximum number of 30 genotypes and cluster X & XVI immediately followed accommodating 15 genotypes each. Cluster XXVIII had one genotype and cluster II, III, VIII, XV, XVII, XIX, XXI, XXII, XXVI, XXVII had two genotypes each (Table 2), indicating adequate genetic variability among the clusters under study.

Cluster XXVIII having one genotype and cluster II, III, VIII, XV, XVII, XIX, XXI, XXII, XXVI, XXVII having two genotypes were distinct and unique from others indicating their uniqueness from the breeding point of view. On the contrary, clusters X, XI, XIV, XVI, XX and XXIV included selections from all the locations.

Cluster means indicated a wide range of variation for all the pod and seed traits (Table 3). Cluster XXVI recorded maximum values for two pod traits and four seed traits viz. pod width of 29.01 mm, pod thickness of 11.81 mm, pod weight of 5.17 g, seed length of 25.68 mm, seed width of 20.17 mm and 100 seed weight of 236.47 g. Maximum pod length (55.51 mm), seed thickness (8.28 mm) and total oil content (40.22%) was recorded by cluster XVIII, I and XV respectively. Cluster XXVIII recorded minimum for two pod trait and two seed traits viz. pod thickness (8.60 mm), pod weight (2.45 g), seed width (12.49 mm) and seed thickness (5.39 mm). Minimum pod length of 37.23 mm and pod width of 18.01 was recorded by cluster XII. Lowest total oil content and 100 seed weight was recorded by cluster VII and VIII respectively.

Intra-cluster distance D values ranged between 0.00 in cluster XXVIII to 13.8 in cluster XXV having one and

Table 3. Cluster wise mean values of pod and seed traits in *Pongamia pinnata* L.

Clusters	Pod length (mm)	Pod width (mm)	Pod thickness (mm)	Pod weight (g)	Seed length (mm)	Seed width (mm)	Seed thickness (mm)	100 seed weight (g)	Total oil (%)
1	42.88	22.44	11.73	3.77	21.57	15.34	8.28	171.74	37.78
2	47.56	23.17	11.39	4.00	21.80	15.73	7.87	158.37	39.63
3	54.49	25.50	10.50	3.76	17.88	14.14	7.03	127.30	34.92
4	44.18	20.37	9.95	3.26	21.56	14.21	6.57	117.38	33.06
5	54.94	25.03	10.42	4.25	19.85	15.66	7.35	153.14	33.55
6	45.21	21.14	10.27	3.12	21.91	14.50	7.21	152.44	33.94
7	49.11	22.93	10.00	3.38	20.97	14.66	6.92	127.24	32.58
8	46.28	23.06	9.91	3.21	18.48	14.05	6.82	111.48	35.37
9	52.67	26.47	9.98	4.22	21.06	16.61	6.20	167.44	36.36
10	44.72	20.33	10.32	3.07	22.26	13.78	6.64	127.98	34.18
11	45.90	21.89	10.32	3.29	21.08	14.50	6.84	121.17	33.06
12	37.23	18.01	9.76	2.38	21.03	12.54	5.57	92.76	33.14
13	45.14	22.80	11.24	4.33	22.10	15.85	7.02	167.83	34.20
14	47.33	22.20	10.19	3.51	20.97	14.98	6.93	131.32	34.67
15	42.80	18.94	9.11	2.73	21.17	13.59	6.22	146.16	40.22
16	49.29	22.65	10.74	3.69	20.92	15.00	7.47	160.51	33.20
17	47.81	22.03	9.51	3.20	21.01	14.47	6.35	111.74	33.05
18	55.51	25.57	11.14	4.90	22.41	16.47	7.30	187.89	34.44
19	42.97	21.30	10.51	3.43	23.03	15.19	7.19	148.56	36.80
20	51.67	24.17	10.11	3.69	19.67	15.31	7.11	152.22	33.30
21	47.53	19.97	9.37	2.62	20.12	13.02	6.29	163.85	40.13
22	44.13	22.49	9.36	2.73	19.03	13.45	6.64	146.97	34.53
23	47.39	23.00	9.79	3.43	20.58	15.51	6.22	163.04	36.45
24	47.65	22.31	9.64	3.11	19.69	14.25	6.53	153.60	33.06
25	39.22	19.91	10.97	3.08	20.96	13.74	7.53	118.94	33.07
26	49.85	29.01	11.81	5.17	25.68	20.17	8.08	236.47	36.38
27	53.58	26.62	10.83	4.22	20.14	15.93	7.50	210.17	35.68
28	45.99	19.25	8.60	2.45	18.00	12.49	5.39	107.22	34.30
Percent contribution	16.91	0.07	0.11	14.66	5.10	8.22	4.70	4.25	45.97

four genotypes respectively (Table 4). Cluster XXV with 13.8 followed by cluster XI (12.9), XVIII (12.8), XXIV (12.7), XIII (12.5) and VI (12.3) were the most diverse because the genotypes used for breeding programme were from different locations. The divergence within the cluster indicates the divergence among the genotypes in the same cluster. Contrarily cluster XXVIII showed the minimum intra cluster distance (0.00) as it was having only one genotype. Inter-cluster distance ranged from 5.1 between VIII and XVII to 34.4 between XXVI and XXVIII (Table 4). The highest inter-cluster distance 34.4 was followed by 33.2 between cluster XII and XXVI. Inter-cluster divergence suggests the distance (divergence) between the genotypes of different clusters. The tendency of genotypes from diverse eco-geographic regions to group together in the same cluster or scattered distributions of genotypes of same geographic origin in different clusters have been observed in the present study.

The best cluster having total oil content of more than 34.9% with 100 seed weight of above 125 g viz. Cluster I, II, III, IX, XV, XIX, XXI, XXIII, XXVI and XXVII were selected for clonal propagation and establishment of multi-locational trial (Table 5).

The contribution of individual characters to the diversity has been worked. The seed trait total oil content contributed maximum for genetic diversity as per cent con-

Table 4. Average inter and intra cluster distance of *Pongamia pinnata* L.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVI I	XVI II	XIX	XX	XXI	XX II	XXI II	XXI V	XX V	XX VI	XX VII	XX VIII
I	**10.4**	7.7	15.5	13.4	15.0	12.9	15.9	13.3	15.2	15.0	14.8	18.4	11.3	12.9	14.6	12.6	14.1	15.9	9.0	15.0	17.3	15.0	12.5	16.1	13.6	19.8	13.5	20.4
II		**1.5**	11.9	12.0	10.9	11.1	12.8	11.0	10.6	13.4	12.9	18.5	9.9	10.2	12.8	9.8	11.4	12.4	6.7	11.5	14.4	13.3	9.8	14.0	14.3	17.9	9.2	18.5
III			**1.7**	12.6	8.3	12.3	9.7	7.3	11.9	13.2	12.1	18.3	16.3	10.6	13.7	9.9	8.1	16.0	12.7	8.6	11.4	10.4	12.5	10.8	16.7	26.2	10.6	12.1
IV				**9.8**	14.8	9.8	11.1	8.5	15.9	9.4	10.8	11.3	14.1	10.6	9.7	11.5	7.5	18.8	8.1	13.2	12.2	8.8	12.0	11.8	11.9	26.5	15.6	12.3
V					**8.1**	14.0	11.8	12.1	9.6	15.9	14.1	21.8	14.5	11.9	17.3	10.5	11.6	12.2	13.4	9.6	16.0	14.8	13.0	13.9	18.6	21.2	8.6	17.9
VI						**12.3**	11.4	9.7	15.3	10.6	11.6	14.0	14.2	10.9	10.7	11.0	8.9	17.8	8.6	12.7	12.2	9.7	12.0	12.2	13.2	25.2	14.0	13.9
VII							**10.8**	9.4	13.6	11.7	11.7	16.1	16.1	10.9	12.8	10.9	7.6	17.2	11.4	10.8	12.0	10.3	12.7	11.7	16.0	26.1	13.2	12.6
VIII								**2.5**	14.0	9.8	10.1	12.5	15.0	9.1	8.9	10.0	5.1	18.5	9.2	10.3	9.5	5.9	10.6	9.6	12.5	27.0	13.4	8.9
IX									**8.7**	17.3	15.6	22.6	13.7	12.9	17.7	12.3	13.4	11.6	13.6	11.5	17.2	16.5	12.3	15.8	19.8	18.3	9.1	19.7
X										**10.0**	11.8	11.8	16.1	11.9	9.4	12.6	8.6	20.1	9.6	14.2	11.0	9.0	13.5	12.4	13.4	28.3	16.5	11.8
XI											**12.9**	14.8	15.5	11.7	12.5	12.1	9.2	18.5	10.8	13.0	13.4	10.9	13.2	12.8	14.4	26.4	15.1	13.8
XII												**8.9**	19.7	15.8	10.4	17.5	12.2	26.0	13.3	19.2	14.2	10.9	16.9	15.5	13.6	33.2	22.6	11.8
XIII													**12.5**	13.5	16.9	13.2	14.6	14.0	10.7	15.2	19.3	16.8	12.9	16.9	15.7	17.9	13.5	21.5
XIV														**10.5**	12.3	10.5	8.7	16.0	9.4	11.3	13.1	10.9	11.3	12.3	14.3	23.7	12.5	14.5
XV															**3.2**	13.6	9.3	21.6	8.9	15.1	6.7	7.0	12.7	12.5	13.7	29.2	17.0	9.9
XVI																**9.9**	9.5	14.6	9.9	10.4	13.7	11.6	11.6	12.2	15.0	22.6	10.7	15.6
XVII																	**3.8**	17.5	8.6	9.9	9.6	6.4	10.8	9.5	13.0	26.5	13.2	9.1
XVIII																		**12.8**	15.7	15.0	21.5	20.7	16.0	19.2	21.6	16.1	11.3	24.6
XIX																			**4.3**	12.4	12.1	9.9	9.8	12.3	11.3	22.1	12.8	15.1
XX																				**10.2**	14.0	12.4	12.4	12.6	17.2	23.5	10.5	15.3
XXI																					**4.5**	7.5	14.0	12.2	17.0	30.7	16.0	8.3
XXII																						**5.6**	12.1	10.0	13.0	29.2	15.3	7.3
XXIII																							**11.6**	13.6	15.1	22.0	12.3	16.0
XXIV																								**12.7**	15.5	27.9	14.8	12.3
XXV																									**13.8**	27.3	18.8	17.1
XXVI																										**9.1**	18.7	34.4
XXVII																											**9.2**	19.5
XXVIII																												**0.0**

Table 5. Details of the selected clones for multi-locational trials (MLT)

Research ranges	Locations	Selected clones	Code	Code on layout map
Kolar	Yeshwanthpur B-block	K – 1	PP001	1
		K – 11	PP010	2
		K – 12	PP011	3
		K – 20	PP019	4
		H – 58	PP076	5
Mandya	CM Gudda	BK – 1	PP138	6
		MK – 15	PP144	7
		MK – 1	PP143	8
		MR – 6	PP146	9
		BK – 5	PP142	10
Challakere	Somangudda	NKT – 7	PP128	11
		NKT – 9	PP130	12
		Rayapura	PP137	13
Hoskote	Nelhal C block	NC – 1	PP096	14
		NC – 3	PP098	15
		NC – 4	PP099	16
Shimogha	Kesavanakatte	G – 32	PP121	17
Mysore	Madahalli	M – 33	PP155	18
		M – 15	PP151	19
		M – 20	PP153	20
		M – 14	PP150	21
		M – 25	PP154	22
Dharwad	Gungargatti	S – 14	PP107	23
Haveri/Sirsi	Jangamanakoppa	TD – 2	PP110	24
		TD – 3	PP111	25

tribution and rank total, 45.97 and 5630 respectively. The character contributing maximum diversity can be given more emphasis for the purpose of fixing priority of parents in hybridization program.

Cluster XI, XVIII, XXIV, XIII and cluster VI with high intra-cluster distance were the most diverse and the divergence within the cluster indicates the divergence among the genotypes in the same cluster (Table 4). Hence, best suited for within group hybridization. Cluster means indicated crosses involving under cluster I, II, III, IX, XV, XIX, XXI, XXIII, XXVI and cluster XXVII may result in substantial segregates and further selection for overall improvement of species. In general, the cluster XXVI and XXVIII exhibited high and low mean values respectively for most of the characters (Table 3). It is also suggested that for creating variability and developing the best selection a large number of divergent lines, instead of few should be used in the hybridization. Earlier studies, in crop plant had indicated that inter-mating of divergent groups would lead to greater opportunity for crossing over which would release latent variation by breaking up predominantly repulsion linkage (Thoday 1960) and utilization of diverse parents in breeding was also stressed by (Singh et al. 1981). Accordingly the use of superior clusters in its afforestation and reforestation programmes. As we know the picture today is that the demand for forest products is increasing as rapidly as the forests are vanishing. Hopefully such knowledge will aid propagators, geneticists and tree improvement specialists in enhancing the quality and productivity of the forest ecosystems in meeting the pressing market demand.

Conclusion

Performance of *P. pinnata* planted by Karnataka Forest Department was assessed based on yield potential by collecting 157 clones out of 264 clones established by

Karnataka Forest Department research wing under different research circles/ranges. Selection of superior clone/CPT based on oil and pod/seed parameters was achieved by application of Mahalanobis statistics and Tocher's technique. On the basis of D^2 values for all possible 253 pairs of populations the 157 genotypes were grouped into 28 clusters. The clustering pattern showed that geographical variations is not necessarily related to genetic varitions. Cluster means indicated a wide range of variation for all the pod and seed traits. The best cluster having total oil content of more than 34.9% with 100 seed weight of above 125 g viz. Cluster I, II, III, IX, XV, XIX, XXI, XXIII, XXVI and XXVII were selected for clonal propagation and establishment of multi-locational trial.

Acknowledgements

The authors wish to thank the Director, IWST for providing all necessary facilities for this study. Authors are grateful to Group Coordinator Research and Head of the Divisions for providing necessary guidance and support for this study. The authors like to extend sincere thanks to the officials of Karnataka State Forest Department for granting permission to conduct the study in their *Pongamia pinnata* plantations and for extending help and support during the field work.

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