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Assessing the genetic landscape of Kapok (*Ceiba pentandra* L. Gaertn) progeny trial: a cluster analysis for sustainable natural fibre resources

Raziya Banoo[1*], M Murugesh[1*], K Vaiyapuri[4], B Rajagopal[3], K B Sujatha[2], J Balamurugan[5], P S Devanand[2]

[1] Department of Agroforestry, Forest College and Research Institute, Tamil Nadu Agricultural University, Mettupalayam 641 301, India

[2] Department of Forest Biology and Tree Improvement, Forest College and Research Institute, Tamil Nadu Agricultural University, Mettupalayam 641 301, India

[3] Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University Coimbatore 641003, India

[4] Department of Agronomy, Tamil Nadu Agricultural University Coimbatore 641 003, India

[5] Agricultural College & Research Institute, Kudumiyanmalai 622 104, India

*Email: drmm1970@gmail.com, raziya.phdfor2021@tnau.ac.in

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Abstract

Ceiba pentandra, commonly known as the kapok tree or silk-cotton tree, exhibits diverse ecological roles, medicinal properties, economic value and cultural significance. In this context, thirty-plus *C. pentandra* (kapok) trees were selected from various locations in the Theni and Dindigul districts of Southern Tamil Nadu based on superior traits by using the comparison tree method. Harvested pods provided seeds for establishing a progeny trial to evaluate seed source variation and other associated studies. Eleven traits were examined, including pod length, pod diameter, pod weight, shell weight, lint weight, floss weight, seed weight, number of seeds, tree height, girth at breast height and number of branches. After two years and seven months, significant variations were observed among the genotypes in terms of biometric parameters and pod attributes of *C. pentandra*. Most characters, including pod weight, pod length, pod diameter and floss weight, exhibited high heritability values and substantial genetic advances as a percentage of the mean. Cluster analysis categorized the thirty genotypes into four clusters. Notably, considering floss weight as a pivotal trait due to its significance as an alternate source of natural fibres, genotypes g28, g29 and g30 (originating from Sirumalai, Dindigul) were identified as superior to other genotypes. These genotypes can be utilized for further research programs to study genetic diversity at the genome level using advanced molecular tools.

Keywords

floss; genotypes; girth; heritability; variation

Introduction

Ceiba species, falling under the family Malvaceae and subfamily Bombacoideae, are trees native to the seasonally dry tropical forests in the Neotropics (including Central America, the Caribbean and South America) (1). The Neotropics region is home to 18 naturally existing *Ceiba* species. Most *Ceiba* species exhibit a height range of 5-20 meters. Notably, *C. pentandra* (2n = 86) (2) stands out as the tallest species, reaching a height between 30 and 50 meters. The cultivated forms of *C. pentandra* may originate from a limited set of parental trees. This view is supported by the observed low diversity among various Asian populations (3-4). It exhibits a diverse range of heights in India, typically between 25 to 40 meters, depending on varying agro-climatic conditions (5). In Tamil Nadu, this species is cultivated predominantly in drier districts, including Coimbatore, Salem, Theni, Dindigul, Dharmapuri and Madurai. Within the various districts of Tamil Nadu, Theni has the most significant extent of cultivation, encompassing approximately 4650 hectares (6). Under optimal conditions, a single tree can produce between 330 to 400 fruits annually, yielding approximately 15 to 18 kg of fibre and around 30 kg of seeds.

Regarding land productivity, a satisfactory fibre yield is around 450 kg per hectare, with exceptional yields reaching up to 700 kg per hectare (7). The global kapok fibre market is projected to reach approximately $975.2 million by 2027, with an expected compound annual growth rate (CAGR) of 4.2% from 2022 to 2027 (8). It is an essential deciduous species with versatile applications. Its flowers serve as a crucial honey source for beekeepers. Kapok floss, known for its excellent buoyancy and water repellence, is utilized in stuffing pillows, mattresses, cushions and naval safety equipment such as life jackets and lifeboats. The fibre also proves valuable for insulating iceboxes, refrigerators, cold-storage facilities, offices and aircraft, acting as an effective sound absorber for acoustic insulation. In healthcare settings, kapok mattresses can undergo dry sterilization without compromising their original quality.

Furthermore, as a notable lignocellulosic plant fibre, kapok is a reinforcement material in polyester matrices through hybridization with glass and sisal fabrics (9). In textile applications, kapok fibres are characterized by their short length and lightweight. To enhance stability and performance, blending kapok fibres with other cellulosic fibres, such as cotton or rayon, is imperative to produce fabrics or yarns. This strategic blending ensures improved quality of the final textile products (10). Blending kapok fibres with cotton or other fabric and yarn manufacturing materials offers an environmentally friendly solution. This approach reduces water and resource usage, effectively lowering the products' carbon footprint. Compared to textiles made solely from cotton or synthetic fibres, this blending strategy represents a more sustainable alternative in textile production (11).

Thus, diversifying raw materials and embracing eco-friendly manufacturing will help improve both present and future environmental impacts (12). Breeding programs commence by assessing the variability within base populations. This objective can be accomplished by identifying and selecting superior genotypes, often through indirect selection methods. It includes selection based on morphometric and biometric traits like disease-free, with a more significant number of branches, higher pod length and pods with higher floss content. It is followed by calculating parameters like coefficient of variation (genotypic and phenotypic), heritability values and other association studies. The subsequent success of selected materials relies on the stability of the characters under selection. Thus, comprehending the genetic makeup and trait architecture is fundamental for researchers and plant breeders (13). In terms of higher genetic variability, understanding heritability and genetic advancement empowers breeders to efficiently select desired traits, expediting the achievement of breeding objectives. Comprehensive knowledge of variability, heritability and genetic advancement is imperative for the targeted enhancement of traits in any crop (14). Correlation studies enhance our understanding of the relationships between highly heritable traits and economically essential characteristics. These studies also provide insight into the contribution of each variable to the crops' genetic composition, that is, the total genetic makeup of the plant in each population and its variation at the genomic level and chromosomal variation (15). In this framework, the current study investigates the quantitative trait variation in *C. pentandra* seedling progeny trial, utilizing thirty candidates plus trees from diverse locations within the Dindigul and Theni districts of Southern Tamil Nadu.

Materials and Methods

Study area

The research trial was conducted at the Horticulture College and Research Institute in Periyakulam, Theni district (10.07°N, 77.33°E). It is characterized by red-laterite soil and a favourable climate. The region receives northeast monsoon rainfall from October to December, with an annual average precipitation of around 830 mm (16). Summer temperatures in the area range from 26.3°C to a peak of 40°C, while winter temperatures fluctuate between 18°C and 29.6°C.

Cultural practices and experimental design

Tree selection is also the pioneer activity of any tree improvement programme, which identifies potential trees based on their morphometric attributes (13). This study determined the predominant kapok growing area in Southern Tamil Nadu. Candidate plus trees were selected based on superior morphometric traits like trees with a maximum number of branches, better biometric traits and good pod yield and selected using the comparison tree method (Table 1). The pods obtained from the thirty Candidate Plus Trees (CPTs) were harvested. Subsequently, kapok seedling progeny was raised in the nursery in March 2020, followed by transplanting in the main field in September 2020. This planting initiative aimed at a comprehensive evaluation at the Horticultural College and Research Institute, Periyakulam, within the Theni district.

Growth biometrics

After transplanting, the observations at 2 years and 7 months after planting, i.e. May 2023, were taken for variability and association studies. The pods from the progeny, i.e., 2 years and 7 months old, were harvested to measure the required variables: pod length, pod diameter, total pod weight, shell weight, lint weight, seed weight, number of seeds and floss weight. The biometric parameters, i.e., tree height, circumference at breast height and number of branches, were also measured using the following methods outlined (17).

Statistical analysis

The experiment used a randomized blocks design (RBD) with three replications per genotype and ten plants per replication. The spacing adopted was 4m (between rows) and 4m (within rows). Simple statistical measures, such as mean and standard error, were considered in the quantitative data

Table 1. Geographical details of 30 provenances of *C. pentandra*

S.No.	Source	Division	Genotype code	Latitude (^{0}N)	Longitude (^{0}E)
1	Sempatty	Dindigul	g1	10^{0}28'N	77^{0}87'E
2	Vathalakundu	Dindigul	g2	10^{0}15'N	77^{0}74'E
3	Devathanapatty	Theni	g3	10^{0}14'N	77^{0}64'E
4	Kullapuram	Theni	g4	10^{0}06'N	77^{0}64'E
5	HC&RI	Theni	g5	10°7'N	77°35'E
6	Agamalai (Tribal School)	Theni	g6	10°10'N	77^{0}42'E
7	Gudalure	Theni	g7	9°41′N	77°16′E
8	Peryakulam(Sathiyanagar)	Theni	g8	10^{0}12'N	77^{0}54'E
9	Bodi (Meenakshipuram)	Theni	g9	10°0′N	77°23′E
10	Bodi (Anikarapatty)	Theni	g10	10^{0}02'N	78^{0}22'E
11	PKM- Kumbankarai	Theni	g11	10°10′N	77°31′E
12	Audukkam	Dindigul	g12	10^{0}23'N	77^{0}51'E
13	Bodi mettu road	Theni	g13	10°02'N	77°26'E
14	PKM (Puthupatty)	Theni	g14	10^{0}04'N	77^{0}51'E
15	Sirumalai (Thazhakidi)	Dindigul	g15	10^{0}19'N	77°99′E
16	Varusanadu (TWAD) building	Theni	g16	9°43'N	77^{0}30'E
17	Varusanadu(Ganathottam)	Theni	g17	9^{0}72'N	77°51′E
18	Varusanadu (RMEH)	Theni	g18	9°43'N	77^{0}30'E
19	Varusanadu (Petrole bunk1)	Theni	g19	9^{0}72'N	77°51′E
20	Varasanadu (Petrole bunk 2)	Theni	g20	9^{0}72'N	77^{0}51'E
21	Mailadumparai (Govt.SF)	Theni	g21	9^{0}78'N	77°52'E
22	Mailadumparai (Nariyathu)	Theni	g22	10^{0}19'N	77^{0}87'E
23	Varasanadu (Tharmarajapuram)	Theni	g23	9^{0}78'N	77°51′E
24	Varasanadu (Entrance)	Theni	g24	9^{0}72'N	77^{0}52'E
25	Varasanadu (Vaigainagar)	Theni	g25	10^{0}03'N	77°49′E
26	Sirumalai (Thenmalai)	Dindigul	g26	8^{0}96'N	77^{0}05'E
27	Sirumalai (Velanpannai)	Dindigul	g27	10°13'N	78°15′E
28	Sirumalai (Kadamankulam (O.M Farm)	Dindigul	g28	10^{0}16'N	78^{0}91'E
29	Sirumalai (VP P.Mani farm)	Dindigul	g29	10^{0}25'N	77°99'E
30	Sirumalai (VP Anthoni farm)	Dindigul	g30	10°18'N	78^{0}15'E

analyses. R 4.3.2 Statistical software (core package of the software) (18) was used to analyze genetic variability measures: genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance as percent mean. The dendrogram was constructed based on the morphological parameters using square Euclidean distance with the group clustering method.

Results

Variations in traits among the genotypes

The morphological parameters studied across the genotypes showed considerable variation from different regions of the Theni and Dindigul districts (Table 2). *C. pentandra* is mainly planted for its sustainable floss with various end uses. The genotype having a maximum floss weight of 22.75g was recorded in g29, followed by g28 (20.75g) and g30 (17.95g). The minimum floss weight was shown by g13. The maximum values for almost all the remaining traits, including pod length, pod weight**,** shell weight, lint weight, seed weight and number of branches, were also shown by progeny g29. However, maximum plant height and number of seeds were recorded in g8 (6.5m) and g17 (248.33), respectively. The mean pod length values ranged from 13.17 cm (g13) to 36.76 cm (g29). The difference in GBH was non-significant across the genotypes and varied between 21 cm and 39.33 cm.

The genotypic and phenotypic parameters of kapok are furnished in Table 3. All measured traits showed phenotypic variations higher in magnitude than genotypic variations, as genetic and environmental factors influence phenotypic variation. The highest phenotypic coefficient of variation (PCV) (37.49) and genotypic coefficient of variation (GCV) (33.57) were estimated for the pod weight, followed by floss weight with PCV and GCV of 34.26 and 29.39, respectively. The lowest phenotypic coefficient of variation and genotypic coefficient of variation were found for pod diameter (20.17) and girth at breast height (8.60), respectively. This studys' estimated narrow sense heritability ranged from 9.63 for girth at breast height to 81.0 for pod weight. The highest heritability was revealed for pod weight, followed by pod length (80.05) and floss weight (73.61).

High genetic advance as a percent of the mean (GAM) was observed for pod weight (61.93%) followed by floss weight (51.95%), lint weight (42.32%), pod length (40.59%), seed weight (29.33%), number of branches (29.0%), pod diameter (25.24%) and shell weight (24.89%). Moderate GAM was recorded for number of seeds (17.18%) and tree height (16.73%).

Relationship between the morphological attributes

The correlation study depicted a significant and non-significant relationship (either positive or negative) between the traits studied (Fig. 1). Floss weight showed a significantly

Table 2. Variation in morphometric traits across the genotypes in *C. pentandra* progeny trial

Genotypes	Pod Length	Pod Diameter	Pod Weight	Shell weight	Lint weight	Seed weight	No. of seeds	GBH	Tree Height	No. of branches	Floss weight
g1	20.57^{hijkl}	3.63^{defgh}	31.09^{hi}	18.17^{fgh}	1.65^{ghijk}	11.07^{efghij}	162.00^{defgh}	21.00^{cd}	4.40^{abcdef}	8.00^{e}	8.15^{hij}
g2	22.20^{fghijk}	3.70^{cdefg}	43.73^{defgh}	$23.11^{bcdefgh}$	1.53^{hijk}	$11.68^{cdefghij}$	160.67^{defgh}	30.00^{abcd}	4.65^{abcdef}	10.67^{e}	11.92^{defghi}
g3	$24.68^{cdefghi}$	3.07^{fgh}	42.98^{defgh}	19.15^{fgh}	1.55^{hijk}	$11.81^{cdefghij}$	172.00^{cdefgh}	33.33^{abcd}	4.93^{abcde}	12.00^{de}	12.32^{defgh}
g4	$23.77^{defghij}$	3.90^{bcdef}	38.83^{efghi}	16.49^{fgh}	1.68^{ghijk}	10.01^{fghij}	167.33^{cdefgh}	21.33^{cd}	3.67^{cdef}	18.00^{bcde}	12.04^{defgh}
g5	18.03^{kl}	3.73^{cdefg}	41.57^{defghi}	19.61^{efgh}	1.87^{efghij}	$14.13^{abcdefg}$	201.67^{abcde}	34.00^{abcd}	5.33^{abcd}	14.33^{cde}	10.17^{fghij}
g6	23.40^{efghij}	3.40^{efgh}	41.09^{defghi}	16.47^{fgh}	$2.14^{bcdefgh}$	$12.66^{cdefghi}$	216.33^{abcd}	35.00^{abcd}	5.90^{abc}	14.33^{cde}	13.93^{cdef}
g7	19.43^{jkl}	2.77^{h}	42.46^{defgh}	20.80^{defgh}	1.57^{hijk}	$12.84^{cdefghi}$	$178.33^{bcdefgh}$	39.33^{a}	6.00^{ab}	14.67^{cde}	9.55^{fghij}
g8	28.30^{cde}	3.10^{fgh}	52.82^{bcde}	30.07^{abcd}	2.58^{abcdef}	$13.95^{abcdefgh}$	$196.00^{abcdefg}$	29.33^{abcd}	6.50^{a}	12.33^{de}	12.90^{defg}
g9	33.60^{ab}	3.91^{bcdef}	65.65^{b}	26.13^{abcdef}	2.60^{abcdef}	15.87^{abcde}	216.00^{abcd}	28.67^{abcd}	5.20^{abcd}	12.33^{de}	15.24^{cd}
g10	21.83^{ghijk}	4.20^{bcde}	33.45^{ghi}	$23.90^{bcdefgh}$	2.80^{abc}	9.48^{ghij}	160.67^{defgh}	23.33^{bcd}	3.17^{def}	10.33^{e}	17.88^{bc}
g11	27.07^{cdef}	3.37^{efgh}	47.29^{defgh}	19.79^{efgh}	$1.96^{defghij}$	16.65^{abc}	199.33^{abcdef}	36.33^{abc}	5.33^{abcd}	12.00^{de}	11.94^{defghi}
g12	28.63^{cd}	3.20^{fgh}	55.50^{bcd}	31.03^{abc}	$2.21^{bcdefgh}$	15.67^{abcde}	160.00^{defgh}	26.00^{abcd}	4.17^{bcdef}	10.00^{e}	11.85^{defghi}
g13	13.17^{m}	2.87^{gh}	25.67^{i}	16.97^{fgh}	1.15^{jk}	7.47^{j}	132.00^{gh}	32.00^{abcd}	4.50^{abcdef}	12.33^{de}	6.58^{j}
g14	28.34^{cde}	2.83^{gh}	46.50^{defgh}	$23.57^{bcdefgh}$	2.66^{abcde}	$12.08^{cdefghij}$	$177.67^{bcdefgh}$	28.33^{abcd}	4.17^{bcdef}	12.00^{de}	19.58^{ab}
g15	18.90^{jkl}	3.50^{efgh}	49.74^{cdef}	22.17^{cdefgh}	$2.10^{bcdefghi}$	15.62^{abcde}	182.67^{bcdefg}	31.67^{abcd}	3.75^{bcdef}	15.33^{cde}	10.66^{efghij}
g16	16.07^{lm}	4.27^{bcde}	40.97^{defghi}	17.96^{fgh}	1.29^{ijk}	15.13^{abcde}	$177.00^{bcdefgh}$	37.33^{ab}	3.67^{cdef}	14.67^{cde}	9.53^{fghij}
g17	19.97^{ijkl}	3.43^{efgh}	36.72^{efghi}	13.77^{h}	1.30^{ijk}	14.85^{abcdef}	248.33^{a}	28.00^{abcd}	4.27^{abcdef}	12.33^{de}	8.50^{ghij}
g18	21.63^{ghijk}	3.60^{defgh}	36.77^{efghi}	34.93^{a}	1.00^{k}	10.91^{efghij}	135.00^{fgh}	23.67^{bcd}	4.67^{abcdef}	9.67^{e}	8.72^{ghij}
g19	21.73^{ghijk}	3.10^{fgh}	44.31^{defgh}	$22.78^{bcdefgh}$	1.82^{fghij}	11.04^{efghij}	$179.33^{bcdefgh}$	22.00^{bcd}	3.60^{def}	14.67^{cde}	15.04^{cde}
g20	$25.00^{cdefghi}$	3.93^{bcdef}	56.65^{bcd}	29.45^{abcde}	2.70^{abcd}	15.64^{abcde}	$190.00^{abcdefg}$	27.00^{abcd}	5.00^{abcd}	13.33^{cde}	11.91^{defghi}
g21	21.33^{ghijk}	3.47^{efgh}	47.56^{defg}	21.77^{cdefgh}	$2.08^{cdefghi}$	18.08^{ab}	238.67^{ab}	36.33^{abc}	5.33^{abcd}	26.00^{abc}	12.38^{defgh}
g22	21.63^{ghijk}	3.50^{efgh}	49.97^{cdef}	22.05^{cdefgh}	2.73^{abcd}	18.73^{a}	230.67^{abc}	29.00^{abcd}	3.67^{cdef}	33.33^{a}	12.30^{defgh}
g23	25.77^{cdefg}	3.47^{efgh}	52.78^{bcde}	26.37^{abcdef}	$2.03^{cdefghi}$	14.94^{abcdef}	206.67^{abcde}	29.00^{abcd}	4.17^{bcdef}	17.67^{bcde}	13.23^{def}
g24	21.67^{ghijk}	3.37^{efgh}	42.21^{defgh}	24.31^{bcdefg}	1.83^{fghij}	$11.16^{defghij}$	142.67^{efgh}	35.00^{abcd}	3.77^{bcdef}	25.33^{abcd}	8.70^{ghij}
g25	12.87^{m}	3.10^{fgh}	31.08^{hi}	15.30^{gh}	1.21^{jk}	8.98^{hij}	157.67^{defgh}	34.33^{abcd}	3.85^{bcdef}	9.67^{e}	7.55^{ij}
g26	25.31^{cdefgh}	3.97^{bcdef}	64.99^{bc}	24.06^{bcdefg}	$2.24^{bcdefgh}$	8.63^{ij}	114.67^{h}	29.00^{abcd}	3.92^{bcdef}	12.33^{de}	12.43^{defgh}
g27	28.37^{cde}	4.74^{b}	33.97^{fghi}	$22.49^{bcdefgh}$	$2.39^{abcdefg}$	$12.97^{cdefghi}$	$175.33^{bcdefgh}$	20.33^{d}	3.67^{cdef}	11.33^{e}	13.67^{def}
g28	29.35^{bc}	5.67^{a}	86.43^{a}	$25.19^{abcdefg}$	2.90^{ab}	16.18^{abcd}	210.00^{abcd}	25.67^{abcd}	3.87^{bcdef}	12.00^{de}	20.75^{ab}
g29	36.76^{a}	4.60^{bc}	98.79^{a}	32.41^{ab}	3.17^{a}	18.80^{a}	180.67^{bcdefg}	29.33^{abcd}	2.40^{f}	29.33^{ab}	22.75^{a}
g30	29.00^{c}	4.43^{bcd}	87.96^{a}	26.48^{abcdef}	2.60^{abcdef}	$13.40^{bcdefghi}$	173.00^{cdefgh}	29.00^{abcd}	2.67^{ef}	12.33^{de}	17.95^{bc}
S.E.	1.4991	0.2673	4.7191	0.95	0.2371	1.4545	18.8471	4.48	0.66	0.99	1.28
C.D.(0.05)	4.1978	0.7484	13.2141	4.33	0.6639	4.0729	52.7746	N.S	1.86	2.80	3.64

Table 3. Genetic variability for morphological attributes of *C. pentandra*

S.no.	Traits	PV	GV	PCV	GCV	h^2	GA	GAM
1	**Pod length**	33.79	27.05	24.61	22.02	80.05	9.58	40.59
2	**Pod diameter**	0.54	0.33	20.17	15.72	60.73	0.92	25.24
3	**Pod weight**	337.23	270.42	37.49	33.57	81.00	30.33	61.93
4	**Shell weight**	44.59	18.47	29.17	18.77	41.43	5.69	24.89
5	**Floss weight**	18.84	13.87	34.26	29.39	73.61	6.58	51.95
6	**Lint weight**	0.45	0.28	32.83	25.97	62.58	0.86	42.32
7	**Seed weight**	13.27	6.92	27.29	19.71	52.17	3.91	29.33
8	**Number of seeds**	1687.22	621.58	22.64	13.74	36.84	31.17	17.18
9	**Girth at breast height**	66.90	6.44	27.73	8.60	9.63	1.62	5.50
10	**Tree height**	1.77	0.47	30.74	15.80	26.43	0.72	16.73
11	**Number of branches**	6.39	3.44	26.09	19.16	53.96	2.80	29.00

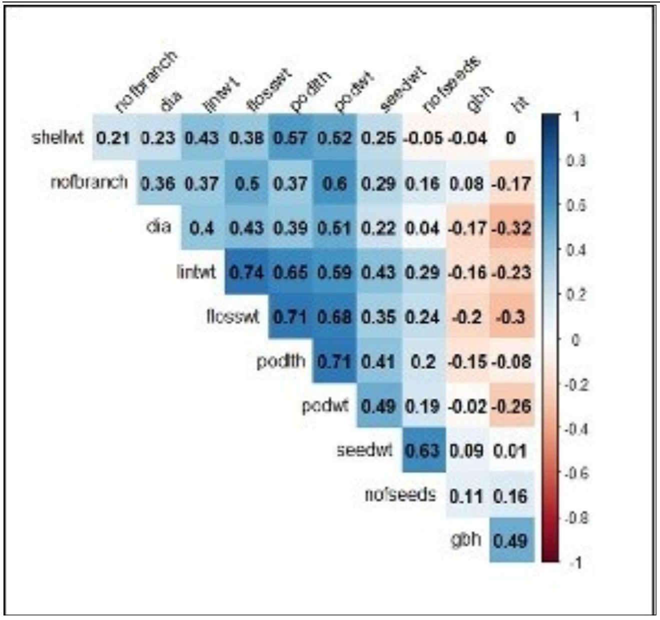

Fig. 1. Karl Pearson's correlation among the attributes of *C. pentandra* Legends: In the above figure, nofbranch = number of branches, dia = pod diameter, lintwt = lint weight, flosswt = floss weight, podlth = pod length, podwt = pod weight, seedwt = seed weight, nofseeds = number of seeds, gbh = girth at breast height, ht = height.

positive relationship with the lint weight (r = 0.74), pod length (r = 0.71) and pod weight (r = 0.68) whereas, negatively correlated with plant height (r = -0.3) and girth at breast height (r = -0.2). Remarkably, the association between pod weight was positively correlated with the maximum number of traits (pod length, floss weight, number of branches, lint weight, shell weight and pod diameter) except with girth at breast height and plant height. Pod diameter negatively correlated with girth at breast height (-0.17) and tree height (-0.32). Number of seeds documented a positive correlation with floss weight (0.24).

Cluster analysis

The comprehensive clustering diagrams for *C. pentandra* were constructed, considering all the quantitative traits (Fig. 2). Cluster analysis was attempted to discriminate the sources based on biometric and pod traits. It assisted in determining the most distant and closest sources for subsequent breeding. Based on Squared Euclidean distances, thirty genotypes were grouped into four clusters based on the attributes measured, showing that selected genotypes had adequate variability (Table 4). Cluster I had twelve genotypes (g1, g2, g3, g4, g10, g15, g18, g19, g23, g24, g26, g27), followed by cluster II with eight genotypes (g5, g6, g7, g11, g13, g16, g17, g25), cluster III with 3 genotypes (g28, g29, g30) and cluster IV with seven genotypes (g8, g9, g12, g14, g20, g21, g22).

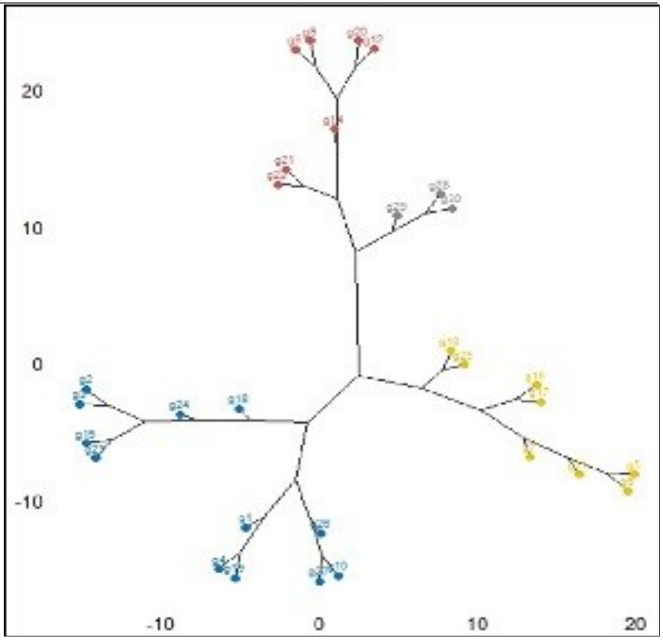

Fig. 2. Cluster dendrogram for 30 genotypes of *C. pentandra* based on all measured traits

Table 4. Genotype composition of different clusters

Cluster number	No. of genotypes	Genotypes
I	12	g1, g2, g3, g4, g10, g15, g18, g19, g23, g24, g26, g27
II	08	g5, g6, g7, g11, g13, g16, g17, g25
III	03	g28, g29, g30
IV	07	g8, g9, g12, g14, g20, g21, g22

Discussion

A comprehensive understanding of the genetic composition of populations and the investigation of genetic parameters are imperative for the proficient administration of genetic resources, constituting the initial phase in any domestication endeavour (19). Variability within core germplasm collections is essential for progressing domestication efforts.

Variation in morphometric traits

Our data depicted considerable differences ($p<0.05$) among thirty genotypes with about eleven morphometric attributes, indicating substantial variation within the studied population. It signified that phenotype. The significant variation observed among trees within very close locations in this study may partly reflect phenotypic plasticity influenced by microsite conditions and genetic differences among individual trees, which can be analyzed further in future using an advanced molecular approach (20). The outcomes presented here align with results reported in previous investigations on *C. pentandra* populations (21). *C. pentandra* tree produces approximately 1,000 to 2,000 pods per year, which yield between 15 and 25 kilograms of seeds (22). The findings indicate substantial genetic variability among genotypes, offering the potential for trait improvement, particularly in floss weight. This underscores the importance of subjecting accessions collected from diverse locations to rigorous selection processes for enhanced genetic traits. Pod length was higher, and pod diameter values were lower than all other genotypes (23). Genotype g29 had the highest pod length, pod weight, shell weight, lint weight, floss weight, seed weight, number of seeds, tree height and number of branches and genotype g13 had the lowest pod length, pod weight, shell weight, lint weight, floss weight, seed weight, number of seeds, tree height and number of branches among all the experimental accessions (Table 2).

Genetic parameters of variation among the traits of *C. pentandra*

The determination of the coefficient of variation serves as a valuable tool in evaluating the magnitude of genetic variability within a population and facilitates comparisons across various traits. The judicious utilization of heritable variation can be optimized with heightened precision by concurrently investigating heritability and genetic advances, thereby enhancing the accuracy of trait analysis. The phenotypic coefficient of variability for all characters was higher than the corresponding genetic coefficient of variability reported in *Jatropha curcas* (24). Heritability is a metric that gauges the efficiency of genotype selection based on phenotypic performance, providing insights into the degree to which observed genetic factors influence traits. Pod length, pod weight, floss weight and lint weight revealed high heritability values of more than 60% and high genetic advance as a percent of the mean (GAM). Similar results with high heritability have also been reported in trees like *Pongamia pinnata*, *Prunus scoparia* and *Prunus elaeagnifolia* (25, 26). Likewise, high heritability and substantial genetic advancement for various growth parameters in *Gmelina arborea* were also noticed (27). The girth at breast height exhibits a diminished heritability value, suggesting a notable influence of environmental factors on this trait.

Character association

The correlation analysis provides a quantitative assessment of the strength and magnitude of associations among various traits, elucidating the degree of relationships within the studied dataset. The correlation matrix among traits revealed positive associations among pod characteristics, such as pod length, pod weight, floss weight and shell and lint weight. Correlation serves as a valuable indicator of the degree of association among seed traits, thus introducing potential supplementary criteria for selection within a breeding program. Focusing on correlated quantitative traits becomes pivotal in improvement programs, as enhancing one characteristic may lead to concurrent correlated alterations in other traits. It aligns with findings in different species, such as dipterocarp species, *Banksia* teak, *Salix* and rubber (28-32).

Cluster analysis

As illustrated in the dendrogram, the thirty genotypes were categorized into four clusters based on morphometric attributes (Fig. 2). The third cluster comprises three genotypes (g28, g29 and g30) distinguished by their highest mean value of floss weight and pod weight compared to the remaining genotypes. Cluster II, with 8 genotypes, is characterized by the lowest value for almost all attributes. Three genotypes (g28, g29 and g30) performed better than the rest of the genotypes. The classification of twenty-three accessions of *Moringa oleifera* into clusters was also observed (33). Likewise, 28 populations of *Leucaena leucocephala* were grouped into six clusters (34). A similar pattern of classification in *Acrocarpus fraxinifolius* was revealed (35). The cluster analysis observed that while the chosen populations exhibited ample genetic diversity, those originating from the same geographical region tended to cluster together. The cluster analysis provides a convenient possibility for enhancing improvement through hybridization, involving populations from different clusters in diverse combinations. In the hybridization process, selecting highly divergent parents is paramount to achieving maximum heterosis in the shortest timeframe.

Conclusion

The observed variability within *C. pentandra* collections can be effectively harnessed to develop novel varieties characterized by superior attributes. The morphometric depiction unveiled notable correlations between various pod and biometric traits, which will aid in the prompt identification of fruitful genotypes. Moreover, most of the examined traits exhibited high heritability values, indicating their suitability for establishing kapok descriptors. Additionally, the study underscored the significance of pod traits in distinguishing between various genotypes. The findings of this study demonstrate that the components of variance, coefficient of variations, and heritability estimates obtained can provide valuable guidance for enhancing kapok through targeted improvement efforts. Selection is helpful for improvement in these kapok genotypes. The correlation association showed pod length, pod diameter, number of seeds, pod weight and floss weight. These traits were considered when selecting superior genotypes among the thirty genotypes. Thus, in this study, g28, g29 and g30 were higher floss yielders and can be used for further breeding programmes. To comprehensively understand the genetic makeup of the species, this study recommends supplementing the investigation with molecular characterization techniques. Molecular tools available for kapok can further be leveraged for marker-assisted selection, expediting the progress of evolving breeding agendas.

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Authors' contributions

MM collected plant materials and established a research trial. RB collected the data, took biometric records and drafted the manuscript. MM helped establish the trial. KV and BR assisted in the study's design and helped in the statistical analysis. KBS, PSD and JB provided interpretations and an appraisal of the study.

Compliance with ethical standards

Conflict of interest: The authors declare no conflict of interest.

Ethical issues: None.

References

1. Gawali AS. Biomass, Carbon sequestration and nutrient storage in *C. pentandra* (L.) Gaertn. stands in agrisilviculture system (Doctoral dissertation, M. Sc. Thesis, Indira Gandhi Agricultural University, Raipur, India). 2003. http://krishikosh.egranth.ac.in/handle/1/5810002097
2. Pezzini FF, Dexter KG, de Carvalho-Sobrinho JG, Kidner CA, et al. Phylogeny and biogeography of *Ceiba* Mill. (Malvaceae, Bombacoideae)-Frontiers in Biogeography 2021;13:e49226. https://doi.org/10.1101/2020.07.10.196238
3. Gibbs PE, Semir J and da Cruz ND. A proposal to unite the genera *Chorisia* Kunth with *Ceiba* Miller (Bombacaceae). Notes Royal Botanical Garden Edinburgh, 2007;45:125-36. https://doi.org/10.18942/bunruichiri.KJ00001077423
4. Baker RM. The intertwined history of the silk-cotton and baobab. In Fields of Change: Progress in African Archaeobotany; Cappers RTJ, Ed.; Barkhuis: Eelde, The Netherlands. 2007;5:1-19.
5. Zeven AC. Kapok tree, *C. pentandra* Gaertn. In: Ferwerda FP, Wit F, editors. Outlines of Perennial Crop Breeding in the Tropics. Landbouwhogeschool: Wageningen, The Netherlands; 1969:269-87.
6. Sudarshan A, Goroji PT. Carbon sequestration potential of kapok (*C. pentandra*) plantations in Theni district of Tamil Nadu, India. Ecology Environment & Conservation. 2014; 20:1287-92.
7. Heuz V, Tran G. Kapok *(C. pentandra)*. Feedipedia, a programme by INRAE, CIRAD, AFZ and FAO. Last updated on July 31, 2019; 18:16. https://feedipedia.org/node/48
8. Townsend T. World natural fibre production and employment. In: Ryszard MK, editor. Handbook of natural fibres. Woodhead Publishing. 2020:15-36. https://doi.org/10.1016/B978-0-12-818398-4.00002-5
9. Reddy GV, Naidu SV, Rani TS. A study on hardness and flexural properties of kapok/sisal composites. J Reinf Plast Compos. 2009;28:2035-044. https://doi.org/10.1177/0731684408091682
10. Yan J, Xu G, Wang F. A study on the quality of kapok blended yarns through different processing methods. J Tex Ins. 2013;104:675-81. https://doi.org/10.1080/00405000.2012.746270
11. Patwary S. Clothing and textile sustainability: current state of environmental challenges and the ways forward. Text Leather Rev. 2020;3:158-73. https://doi.org/10.31881/TLR.2020.16
12. Gomez-Maqueo X, Gamboa-deBuen A. The biology of the genus Ceiba, a potential source for sustainable production of natural fiber. Plants. 2022;11:521 https://doi.org/10.3390/plants11040521
13. Kumar CPS, Raju S, Rajan REB, Muraleedharan A, Suji DB. Studies on genetic variability, heritability and genetic advance in cotton (*Gossypium hirsutum* L.). Plant Arch. 2019;19:934-37.
14. Gnanasekaran M, Thiyagu K, Gunasekaran M. Genetic variability heritability and genetic advance studies in cotton (*Gossypium hirsutum* l.). Electron. J Plant Breed. 2018; 9:377-82.
15. Rani R, Dogra BS, Singh SP, Kumari S, Sharma P. Variability and character association studies for yield and yield contributing characters in cucumber (*Cucumis sativus*) under low hills of Himachal Pradesh. Indian J Agric Sci. 2013;93:801-5. https://doi.org/10.56093/ijas.v93i7.137067
16. Agro Climate Research Centre, Tamil Nadu Agricultural University, Coimbatore, India.2023.
17. Chaturvedi RK, Raghubanshi AS, Singh JS. Growth of tree seedlings in a dry tropical forest in relation to soil moisture and leaf traits. J Plant Ecol. 2013;6:158-70.
18. R Core Team. R. A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. 2023.
19. Metougui ML, Mokhtari M, Maughan PJ, Jellen EN, Benlhabib O. Morphological variability, heritability and correlation studies within an argan tree population (*Argania spinosa* (L.) Skeels) preserved in situ. Int J Agric For. 2017;7:42-51. http://doi.org/10.5923/j.ijaf.20170702.02
20. Brus R, Ballian D, Bogunic F, Bobinac M, Itszojtic M. Leaflet morphometric variation of service tree (*Sorbus domestica* L.) in the Balkan Peninsula. Plant Biosystems-An International Journal Dealing with all Aspects of Plant Biology. 2011;145:278-85.
21. Abengmeneng CS, Ofori DA, Kumapley P, Akromah R, Jamnadass R. Estimation of heritability and genetic gain in height growth in *C. pentandra*. Afr J Biotechnol. 2015; 14:1880-885. eISSN: 1684-5315
22. Gomez-Maqueo X, Gamboa-deBuen A. The biology of the genus Ceiba, a potential source for sustainable production of natural fiber. Plants. 2022; 11:521 https://doi.org/10.3390/plants11040521
23. Gawali A. Studies on growth and floss yield of *C. pentandra* (L) Gaertn. stands in sub humid tropics. Asian J Plant Sci Res. 2015; 4:37-39.
24. Gawali AS, Wagh RS, Sonawane CJ. Genetic Variability in Growth and Seed Traits of Jatropha curcas L. Germplasm for Genetic Tree Improvement. Forest Res. 2016;5:171. http://doi.org/10.4172/2168-9776.1000171
25. Divakara BN, Das R. Variability and divergence in *Pongamia pinnata* for further use in tree improvement. J. For. Res. 2011; 22:193-200. https://doi.org/10.1007/s11676-011-0149-9
26. Ansari A, Gharaghani A. A comparative study of genetic diversity, heritability and inter-relationships of tree and nut attributes between *Prunus scoparia* and *P. elaeagnifolia* using multivariate statistical analysis. Int J Hortic Sci Technol. 2019;6:137-50. http://doi.org/10.22059/ijhst.2019.276425.282
27. Kumar A. Growth performance and variability in different clones of *Gmelina arborea* Roxb. Silvae Genetica. 2007;56:32-6. http://doi.org/10.1515/sg-2007-0005
28. Kenzo T, Ichie T, Watanabe Y, Yoneda R, et al. Changes in photosynthesis and leaf characteristics with tree height in five dipterocarp species in a tropical rain forest. Tree Physiology. 2006;26:865-73. https://doi.org/10.1093/treephys/26.7.865
29. Drake PL, Froend RH, Franks PJ. Smaller, faster stomata: scaling of stomatal size, rate of response, and stomatal conductance. Journal of Experimental Botany. 2013;64:495-505. https://doi.org/10.1093/jxb/ers347
30. Huang G, Liang K, Zhou Z, Yang G, Muralidharan EM. Variation in photosynthetic traits and correlation with growth in teak (*Tectona grandis* Linn.) clones. Forests. 2019;10:44. https://doi.org/10.3390/f10010044
31. Singh NB, Sharma JP, Huse SK, Thakur IK, et al. Heritability, genetic gain, correlation and principal component analysis in introduced willow (*Salix* species) clones. Indian Forester. 2012; 138:1100.

32. Ariff EARE, Abdullah S, Suratman MN. The Relationships between Height and Stomatal Conductance, Chlorophyll Content, Diameter of Rubber Tree (*Hevea brasiliensis*) Saplings. In The 12th Symposium of the Malaysian Society of Applied Biology. Engineering and Industrial Applications (ISBEIA), Kuala Terengganu. 2012;1-4.
33. Drisya Ravi RS, Nair BR Siril EA. Morphological diversity, phenotypic and genotypic variance and heritability estimates in *Moringa oleifera* Lam.: a less used vegetable with substantial nutritional value. Genet Resour Crop Evol. 2021;1-16. https://doi.org/10.1007/s10722-021-01183-8
34. Pande PK, Kumar A, Ravichandran S, Naithani S, Kothiyal V, Kishore PBK, Raturi A, Gautam P, Dobhal S, Sharma S. Genetic analysis of growth and wood variations in *Leucaena leucocephala* (Lam.) de Wit J For Res. 2013;24:485-93. https://doi.org/10.1007/s11676-013-0343-z
35. Ashwath MN, Sathish BN, Deepthi NL, Devagiri GM, et al. Geographic and within tree variation for wood properties in *Acrocarpus fraxinifolius* wight and arn. populations. Journal of Scientific and Industrial Research. 2021;80:1049-055. https://doi.org/10.56042/jsir.v80i12.44915