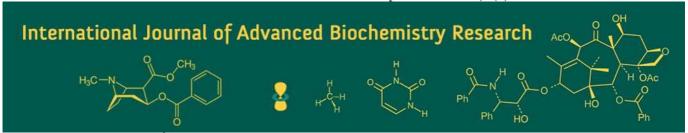
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VM Jambhale

Department of Agricultural Botany, Mahatma Phule Krishi Vidyapeeth Rahuri, Maharashtra, India

GM Karad

Department of Agricultural Botany, Mahatma Phule Krishi Vidyapeeth Rahuri, Maharashtra, India

Adhir Aher

Department of Agricultural Botany, Mahatma Phule Krishi Vidyapeeth Rahuri, Maharashtra, India

DS Thakare

Department of Agricultural Botany, Mahatma Phule Krishi Vidyapeeth Rahuri, Maharashtra, India

Corresponding Author: VM Jambhale Department of Agricultural Botany, Mahatma Phule Krishi Vidyapeeth Rahuri, Maharashtra, India

Assessment of genetic diversity of kenaf genotypes (*Hibiscus cannabinus* L.)

VM Jambhale, GM Karad, Adhir Aher and DS Thakare

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Abstract

Genetic diversity of Kenaf genotypes aimed to evaluate the extent of genetic variability and identify promising genotypes for dry fibre yield improvement. A total of 52 kenaf genotypes were assessed in kharif 2021 using a Randomized Block Design with three replications. Observations were measured for eight quantitative traits including flowering time, plant height, basal diameter, green weight, stick yield, dry fibre yield, and fibre recovery. Analysis of variance showed significant differences among genotypes for all traits studied. Dry fibre yield and fibre recovery exhibited high genotypic and phenotypic coefficients of variation, indicating considerable variability. Heritability estimates were high for most traits, and traits such as dry fibre yield and fibre recovery exhibited both high heritability and high genetic advance, indicating additive gene effects and prospects for improvement via direct selection. Correlation and path coefficient analysis revealed that traits like days to initiation of flowering, plant height, basal diameter, and green weight had significant positive correlations and direct effects on dry fibre yield. Genetic divergence analysis grouped the genotypes into four clusters, with maximum inter-cluster distance observed between Clusters I and II, indicating substantial genetic diversity. Based on cluster means, genetic distances, and trait performance, genotypes such as KIM-02, KIN-256, KIN-233, and KIM-32 were identified as potential parents for future hybridization programs aimed at fibre yield improvement in kenaf.

Keywords: Genetic diversity, Kenaf, fibre yield, heritability, variability, hybridization

1. Introduction

Kenaf (*Hibiscus cannabinus* L.) is an annual, fast-growing, and eco-friendly bast fibre crop belonging to the Malvaceae family. It is one of the most economically important fibre crops after jute and has been traditionally cultivated in Africa and Asia for centuries (FAO, 2013) ^[5]. Though its exact origin remains unclear, historical records suggest that kenaf has been grown since 4000 B.C. in Africa. It is known by different names across regions, including Deccan hemp, Java jute, and Mesta.

Kenaf thrives across a wide latitudinal range (16° S to 41° N) and is grown in India, China, Bangladesh, Indonesia, Malaysia, Vietnam, and parts of Africa and the United States (Webber *et al.*, 2002) ^[20]. Its adaptability to diverse agro-ecological conditions, high biomass yield, and short growing period make it a valuable alternative to traditional fibre crops (Ramesh, 2016) ^[14].

Kenaf consists of two main stem regions: the outer bast and the inner core. The bast, which makes up about 30-35% of the stem by weight, yields long fibres (~2.4 mm) resembling softwood, while the core, around 65-70%, produces short fibres (~0.7 mm) similar to hardwood (Sen & Reddy, 2011) [17]. These fibres are used in various industries such as pulp and paper, textiles, automotive, and construction. Compared to wood, kenaf contains less lignin, requires fewer chemicals for pulping, and produces brighter and stronger paper (Jahan *et al.*, 2007; Kaldor *et al.*, 1990) [8, 10].

The crop's industrial importance extends beyond paper production. Kenaf fibres are increasingly used in composites, ropes, mats, insulation panels, and biodegradable plastics (Arbaoui *et al.*, 2016; Saba *et al.*, 2015) [2, 16]. In the automotive sector, kenaf-based composites offer strength, lightweight properties, and biodegradability, making them ideal for vehicle interiors.

Kenaf also holds nutritional and ecological value. The leaves are rich in protein and suitable for animal feed, while the seeds produce oil high in omega-3 and omega-6 fatty acids

(Ahmed *et al.*, 2013) ^[1]. Its biomass serves as a renewable energy source and soil amendment. Moreover, kenaf is a phytoremediator capable of absorbing heavy metals from contaminated soils and sequestering large amounts of atmospheric CO₂—up to 10 tons per acre per season (Webber *et al.*, 2002) ^[20].

In countries like Bangladesh, the Bangladesh Jute Research Institute (BJRI) has developed improved kenaf varieties such as HC-2 and HC-95. These are cultivated across nearly 30,000 hectares, significantly contributing to fibre production and rural employment (Miah *et al.*, 2020) [12]. BJRI also maintains over 6,000 germplasm accessions of jute, kenaf, and related species, highlighting the genetic diversity available for breeding.

Despite its potential, genetic improvement in kenaf remains limited. A narrow genetic base restricts breeding progress and stress tolerance. Thus, evaluating existing germplasm for variability is essential. Understanding genetic parameters like genotypic and phenotypic coefficient of variation (GCV and PCV), heritability, and genetic advance helps breeders identify traits under strong genetic control (Burton & Devane, 1953) [3]. Additionally, correlation and path coefficient analysis aid in determining direct and indirect effects of traits on fibre yield.

Cluster analysis, based on Mahalanobis D² statistics, allows classification of genotypes into distinct groups based on trait performance. Genotypes from divergent clusters are suitable parents for hybridization, maximizing heterosis and genetic gain (Rao, 1952) ^[15].

Kenaf's rising industrial relevance, adaptability, and environmental benefits highlight the need for genetic enhancement. Evaluating its genetic diversity provides a foundation for developing improved, high-yielding varieties suitable for various ecological regions and industrial demands.

2. Materials and Methods

The present study entitled "Assessment of Genetic Diversity in Kenaf (*Hibiscus cannabinus L.*) *Genotypes*" was carried out during the Kharif season of 2021 at the Cotton Improvement Project, Department of Agricultural Botany, Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri, Maharashtra, India. The experiment was designed to assess genetic variability, correlations, and divergence among diverse kenaf genotypes using established biometric tools.

2.1 Experimental Site

The experiment was conducted at Rahuri, located at latitude 19°47′ N and longitude 74°50′ E, with an elevation of 495 meters above sea level. The climate is semi-arid with moderately dry weather and hot summers. The soil at the site is deep black cotton soil (Vertisol), well-drained and medium in fertility, suitable for kharif fibre crops. The average annual rainfall ranges between 450-500 mm, typically received from June to September, which supported the crop growth during the experiment.

2.2 Experimental Material

The study included 52 kenaf genotypes, comprising 50 experimental entries and 2 check varieties (HC-583 + and AMC-108 +), sourced from the germplasm collection maintained by the Cotton Improvement Project, MPKV, Rahuri. These genotypes represented wide agro-

morphological diversity with potential differences in flowering behavior, plant vigour, biomass production, fibre recovery, and tolerance to abiotic stresses.

The genotypes, identified by accession numbers (e.g., KIN-232, KIN-256, KIM-02, KIM-35), were chosen based on preliminary evaluation for variability and represent both indigenous and exotic lines.

2.3 Experimental Design and Layout

The experiment was laid out in a Randomized Block Design (RBD) with three replications to minimize the effect of environmental variability and improve the precision of the results. Each genotype was planted in a single-row plot of 4.5 m \times 0.3 m with a row-to-row spacing of 30 cm and plant-to-plant spacing of 5-7 cm. Sowing was done manually on 12th June 2021 using the dibbling method after the receipt of adequate monsoon rainfall.

The field was well-prepared by one ploughing followed by two cross-harrowings and planking to achieve a fine seedbed. Proper land leveling was done to ensure uniform water distribution.

2.4 Fertilizer Application and Crop Management

A basal dose of 60:30:30 kg NPK/ha was applied at sowing. The nitrogen component was split—50% applied at sowing and the remaining 50% top-dressed at 30 days after sowing. All recommended cultural operations including timely weeding, thinning, earthing up, and plant protection measures were carried out to maintain a healthy crop stand. No major pest or disease outbreaks were observed during the cropping season.

Irrigation was not required due to sufficient and welldistributed rainfall throughout the growth period. Crop harvesting was done manually at physiological maturity when lower leaves started yellowing and fibre content was considered optimal.

2.5 Data Collection

Observations were measured for eight quantitative traits across all genotypes. Except for flowering time and plant height (which were measured for a plot basis), all traits were measured using data from five randomly selected competitive plants per plot, and the mean values were used for analysis.

2.5.1 The recorded traits were

- 1. Days to initiation of flowering-Number of days from sowing to appearance of the first flower.
- 2. Days to 50% flowering-Number of days from sowing to the date when 50% of the plants had flowered.
- 3. Plant height (cm)-Distance from the base to the tip of the plant using a meter scale.
- 4. Basal diameter (cm)-Stem thickness measured near the soil surface using a Vernier caliper.
- 5. Fresh green weight/plant (g)-Total fresh biomass including leaves and stem.
- 6. Dry fibre yield/plant (g)-Weight of extracted fibre after retting, washing, and drying.
- 7. Stick yield/plant (g)-Weight of non-fibrous stem portion after fibre extraction.
- 8. Fibre recovery (%)-(Dry fibre yield/Fresh green weight) × 100.

Table 1: Quality parameters studied for nine morphological characters

Sr. No.	Genotype	Leaf type	Leaf	Leaf	Phyllotoxy	Leaf	Growth	Branching	Stem colour	Inflorescence
1	KIN-232	Palmately compound	Green	margin Serrate	Whorled	apices Acute	habit Erect	Monopodial	Green	Corymbous
2	KIN-233	Compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Pinkish green	Corymbous
3	KIN-234	Compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
4	KIN-235	Compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
5	KIN-237	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
6	KIN-238	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
7	KIN-242	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
8	KIN-243	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
9	KIN-247	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
10	KIN-254	Simple	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
11	KIN-255	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
12	KIN-256	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Pinkish green	Corymbous
13	KIN-257	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Pinkish green	Corymbous
14	KIN-258	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
15	KIN-259	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Purple	Corymbous
16	KIN-260	Palmately compound		Serrate	Whorled	Acute	Erect	Monopodial	Purple	Corymbous
17	KIN-261	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Purple	Corymbous
18	KIN-262	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Purple	Corymbous
19	KIN-266	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
20	KIN-268	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
21	KIM-01	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
22	KIM-02	Simple	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
23	KIM-03	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
24	KIM-04	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
25	KIM-05	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
26	KIM-06	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
27	KIM-07	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
28	KIM-08	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
29	KIM-10	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
30	KIM-11	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
31	KIM-13	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
32	KIM-14	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
33	KIM-15	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
34	KIM-16	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
35	KIM-17	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
36	KIM-18	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
37	KIM-21	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
38	KIM-22	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
39	KIM-23	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
40		Palmately compound		Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
41	KIM-25	Palmately compound	Pale green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
42	KIM-26	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
43	KIM-28	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Pinkish green	Corymbous
44	KIM-30	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Pinkish green	Corymbous
45	KIM-31	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
46	KIM-32	Palmately compound		Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
47	KIM-33	Palmately compound	Green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
48	KIM-34	Palmately compound		Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
49	KIM-35	Palmately compound		Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
50	KIM-36	Palmately compound		Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
51	HC 583	Simple	Pale green	Serrate	Whorled	Acute	Erect	Monopodial	Green	Corymbous
52	AMC 208	Palmately compound	Pale green	Serrate	Whorled	Acute	Erect	Monopodial	Pinkish green	Corymbous

Additionally, qualitative traits such as leaf shape, leaf margin, phyllotaxy, growth habit, flower color, and branching pattern were recorded using standard descriptors.

2.6 Fibre Extraction and Retting

For fibre yield estimation, harvested plants were bundled and submerged in clean water under anaerobic conditions for retting, a microbial process to separate fibre from the woody stem. After adequate retting (usually 7-10 days), the fibre was extracted manually, washed thoroughly to remove impurities, and sun-dried before weighing.

2.7 Statistical Analysis

The data were statistically analyzed using standard biometric methods to estimate variability, heritability, trait associations, and genetic divergence:

- Analysis of Variance (ANOVA) was performed as per Panse and Sukhatme (1967) to test the significance of differences among genotypes for all traits.
- Genotypic and Phenotypic Coefficients of Variation (GCV and PCV) were calculated using the formulas of Burton and De Vane (1953) [3] to measure the extent of variability.

- Broad-sense heritability (h²) and Genetic Advance (GA) were estimated using the procedures described by Johnson *et al.* (1955) ^[9]. Genetic Advance as Percent of Mean (GAM) was also computed to evaluate the efficiency of selection.
- Genotypic and Phenotypic correlation coefficients were calculated to understand the direction and strength of association among traits using the methods of Singh and Chaudhary (1979).
- Path coefficient analysis was performed to decompose the correlation coefficients into direct and indirect effects at the genotypic level following Dewey and Lu (1959) [4].
- Genetic divergence was assessed through Mahalanobis' D² statistics (Mahalanobis, 1936) [11] and clustering of genotypes was done using Tocher's method (Rao, 1952) [15] to group genetically similar genotypes.

Intra-and inter-cluster distances were calculated to assess the extent of genetic variability among genotypes. These statistics were essential to identify genetically divergent parents for future hybridization programs. All statistical analyses were performed using OPSTAT software and Microsoft Excel.

3. Results and Discussion

3.1 Quality Parameters

Fifty-two kenaf genotypes were evaluated for nine qualitative morphological traits such as leaf type, leaf colour, leaf margin, phyllotaxy, leaf apices, growth habit, branching pattern, stem colour, and inflorescence type. Most genotypes showed palmately compound leaves, green coloration, and serrated margins. Whorled phyllotaxy, acute leaf apices, erect growth habit, monopodial branching, and corymbous inflorescence were predominant across the genotypes. This qualitative assessment revealed a narrow variability in morphological descriptors, which are generally stable across environments.

3.2 Analysis of Variance (ANOVA)

Analysis of variance indicated highly significant differences (p < 0.01) among genotypes for six of the eight studied quantitative traits: days to initiation of flowering, days to 50% flowering, plant height, dry fibre yield, stick yield, and fibre recovery. However, basal diameter and green weight showed non-significant variation, indicating limited environmental and genotypic influence on these parameters.

Table 2: Analysis of variance for eight different characters in Kenaf

Sr. No.	Source of Variation	Mean sum of squares						
Sr. No.	Source of variation	Replication (2)	Genotype (51)	Error (102)				
1.	Days to Initial Flowering	4.92	140.24**	1.24				
2.	Days to 50% Flowering	9.40	135.29**	1.14				
3.	Plant Height (cm)	3046.53	2316.14**	446.53				
4.	Basal Diameter (cm)	0.01	0.20	0.06				
5.	Green Weight (Kg/plant)	0.00	0.01	0.00				
6.	Stick Yield (g/plant)	1.46	2.30**	0.74				
7.	Fibre Recovery	132.96	55.62**	4.48				
8.	Dry Fibre Yield (g/plant)	25126.10	5178.46**	628.42				

^{*} and ** indicate significant at 5 and 1 percent level, respectively

These findings indicate substantial genetic variability among genotypes for most traits, which is crucial for effective selection and breeding. Similar results have been reported in earlier studies by Ghosh Dastidar *et al.* (1993) ^[7], Prakash *et al.* (2003) ^[13].

3.3 Mean Performance and Range of Variability

The genotypes exhibited considerable variation for all traits (Table 3). Days to initiation of flowering ranged from 69 to 94 days, with genotype KIN-259 flowering earliest. Days to 50% flowering ranged between 77 to 102 days, with KIN-259 again being the earliest.

Plant height ranged from 183.7 cm (KIN-255) to 362.7 cm (KIM-24), indicating strong diversity. Basal diameter ranged from 0.78 to 2.44 cm; green weight varied between 0.156 to 0.488 kg/plant. Stick yield and fibre recovery ranged from 73.67 to 254.67 g and 5.75% to 10.69%,

respectively. Dry fibre yield showed a wide range from 3.65 to 24.13 g/plant, with KIM-14 being the highest-yielding genotype.

3.4 Genetic Variability Parameters

The estimates of GCV and PCV revealed that fibre recovery and dry fibre yield exhibited high variability. The GCV ranged from 6.91% (days to 50% flowering) to 26.83% (fibre recovery), while PCV ranged from 7.00% to 30.15%. For all traits, PCV was higher than GCV, indicating the influence of environmental factors.

Heritability (broad sense) was highest for days to 50% flowering (97.50%), followed closely by days to initial flowering (97.40%). Dry fibre yield showed high heritability (70.70%) and high genetic advance (67.46), indicating the predominance of additive gene action and suitability for direct selection.

Table 3: Mean Performance of fifty-two Kenaf genotypes studied for eight characters

Sr. No.	Genotypes	Days to initial	Days to 50%	Plant height	Basal diameter	Green weight		Fibre	Dry fibre yield
51. 110.	<u> </u>	flowering	flowering	(cm)	(cm)	(kg/plant)	(g/plant)	recovery	(g/plant)
1	KIN-232	93	99	349.00	2.19	0.437	176.40	8.51	16.40
2	KIN-233	93	101	351.33	2.02	0.404	194.67	8.43	17.87
3	KIN-234	93	99	346.00	2.10	0.420	197.33	8.19	17.67
4	KIN-235	92	99	355.00	1.93	0.387	186.67	7.82	16.00
5	KIN-237	92	98	323.67	1.76	0.352	125.33	7.44	10.07
6	KIN-238	93	99	349.67	2.15	0.431	236.00	7.44	19.13
7	KIN-242	93	100	329.00	1.79	0.357	162.67	7.21	12.53
8	KIN-243	83	92	319.33	1.65	0.329	104.00	7.99	9.07
9	KIN-247	84	91	324.67	1.72	0.344	138.67	7.48	11.20
10	KIN-254	90	97	313.33	2.00	0.400	185.33	10.69	21.20
11	KIN-255	76	84	183.67	0.78	0.156	73.67	5.82	4.60
12	KIN-256	94	101	353.67	2.42	0.484	156.33	8.94	14.87
13	KIN-257	92	99	348.67	2.44	0.488	240.00	9.12	23.80
14	KIN-258	71	79	318.00	1.97	0.393	215.33	8.89	21.07
15	KIN-259	69	77	318.67	1.72	0.344	136.00	8.54	12.47
16	KIN-260	75	83	293.33	1.78	0.356	132.67	7.99	11.60
17	KIN-261	73	81	289.00	1.78	0.376	109.33	7.99	8.70
18	KIN-262	72	80	275.00	1.54	0.308	88.33	7.61	7.20
19	KIN-266	74	81	298.00	1.58	0.316	114.67	7.60	9.13
20	KIN-268	92	100	307.67	2.01	0.403	210.67	7.10	15.93
21	KIM-01	92	99	307.00	1.99	0.399	190.00	7.94	16.20
22	KIM-02	94	101	292.00	1.88	0.376	184.00	7.75	15.33
23	KIM-03	92	99	323.00	2.06	0.412	190.00	8.06	16.60
24	KIM-04	93	101	330.67	2.08	0.416	202.00	8.57	18.87
25	KIM-05	92	99	343.67	2.15	0.431	223.33	7.70	18.53
26	KIM-06	92	99	343.33	2.13	0.448	228.67	7.46	18.40
27	KIM-07	92	99	350.33	2.29	0.459	202.67	8.42	18.73
28	KIM-08	92	99	334.00	1.87	0.437	210.00	7.22	16.73
29	KIM-10	92	100	353.00	1.94	0.373	151.33	7.22	12.73
30	KIM-10	93	100	329.67	1.94	0.384	188.67	7.93	16.27
31	KIW-12 KIM-13	92	97	334.33	1.92	0.389	108.67	6.28	7.27
32	KIM-13	93	99	348.00	2.27	0.389	233.33	9.43	24.13
33	KIM-14	93	100	311.67	1.79	0.455	164.00	8.35	14.93
34	KIM-15	91	100	333.67	2.00	0.337	153.00	8.10	13.80
35	KIM-17	92	99	351.67	2.13	0.400	146.00	7.95	12.53
-									
36	KIM-18	92 92	101 99	330.67	1.94	0.388	206.67 190.67	7.65	17.07
37	KIM-21			332.33	1.87	0.373		8.96	18.87
38	KIM-22	92	98	333.67	2.02	0.404	210.67	8.91	20.73
40	KIM-23	92 92	98 99	321.67	2.09	0.417 0.452	254.67	7.93	21.87
	KIM-24	92	99	362.67	2.26		236.93	8.75	22.13
41	KIM-25			339.00	2.05	0.409	199.33	8.04	17.47
42	KIM-26	93	101	307.33	1.75	0.349	153.33	7.35	12.13
43	KIM-28	93	100	328.67	1.86	0.372	162.67	7.60	13.27
44	KIM-30	92	100	316.00	1.82	0.364	158.67	7.44	12.73
45	KIM-31	93	101	327.00	2.01	0.403	176.40	8.26	15.80
46	KIM-32	93	102	321.33	1.99	0.397	164.00	7.58	13.47
47	KIM-33	92	98	328.67	1.76	0.353	158.67	8.17	14.13
48	KIM-34	92	99	337.00	2.03	0.407	208.00	7.18	15.93
49	KIM-35	93	100	332.67	2.01	0.403	174.67	9.08	17.40
50	KIM-36	93	100	342.67	1.93	0.385	218.67	5.75	13.20
51	HC 583	92	100	309.00	1.91	0.383	206.67	6.28	13.53
52	AMC 208	92	101	347.67	2.19	0.437	208.00	8.64	19.40
	Mean	89	97	326.00	1.95	0.389	177.85	7.95	15.39
	S.E.	0.64	0.62	12.20	0.14	0.03	14.47	0.49	1.22
	C.D. @ 5%	1.81	1.72	34.22	N.S.	N.S.	40.59	1.39	3.43
	CV	1.25	1.10	6.48	12.35	14.31	14.09	10.85	13.75

Table 4: Estimates of variability parameters for Dry Fibre Yield and yield contributing characters in fifty-two kenaf genotypes

Characters	Mean	Range	Genotypic variance	variance	Genotypic coefficient of variance (%)	of variation	Heritability (bs) (%)		Genetic advance as percentage of mean (%)
Days to initial flowering	89	69-94	46.33	47.58	7.61	7.71	97.40	13.84	15.46
Days to 50% flowering	97	77-102	44.72	45.85	6.91	7.00	97.50	13.60	14.05
Plant height (cm)	326.0	183.7-362.7	623.20	1069.73	7.66	10.03	58.30	39.25	12.04
Basal diameter (cm)	1.9	0.8-2.4	0.05	0.11	11.32	16.75	45.70	0.31	15.76
Green weight (Kg/plant)	0.4	0.2-0.5	0.00	0.01	10.86	17.97	36.50	0.05	13.52
Stick yield (g/plant)	177.9	73.7-254.7	0.52	1.26	9.06	14.14	41.10	0.95	11.98
Fibre recovery	7.9	5.8-10.7	17.05	21.53	26.83	30.15	79.20	7.57	49.19
Dry fibre yield (g/plant)	15.4	4.6-24.1	1516.68	2145.10	21.90	26.04	70.70	67.46	37.93

Similar findings were reported by Johnson *et al.* (1955) ^[9], and Senapati *et al.* (2006) ^[18, 19], confirming that fibre yield and associated traits are heritable and responsive to selection.

3.5 Correlation Analysis

Correlation analysis revealed that dry fibre yield had significant positive correlations at both genotypic and phenotypic levels with:

• Days to initiation of flowering (G = 0.577**, P = 0.476**)

Days to 50% flowering (G = 0.564**, P = 0.472**)

- Plant height (G = 0.630**, P = 0.511**)
- Basal diameter (G = 0.864**, P = 0.605**)
- Green weight (G = 0.889**, P = 0.562**)
- Stick yield (G = 0.461**, P = 0.056)

These results suggest that improvement in any of these traits may result in higher fibre yield. Significant correlations between these traits themselves indicate close physiological relationships that can be exploited during selection.

Table 5: Estimates of genotypic & phenotypic correlation coefficients among Dry Fiber Yield and yield contributing characters in fifty-two kenaf genotypes

Sr.	Character		Days to initiation	Days to 50%	Plant height	Basal diameter	Green weight	Stick yield	Dry fibre
No.	No.		of flowering	flowering	(cm)	(cm)	(g/plant)	(g/plant)	yield (g/plant)
1	Days to initiation of	G	1.00	0.994**	0.636**	0.678**	0.935**	0.044	0.577**
1	flowering	P	1.00	0.984**	0.475**	0.461**	0.771**	0.037	0.476**
2	Days to 50% of	G		1.00	0.617**	0.659**	0.726**	0.04	0.564**
2	flowering	P		1.00	0.475**	0.458**	0.449**	0.024	0.472**
2	2 8 4 1 1 4 4	G			1.00	0.935**	0.934**	0.546**	0.630**
3	Plant height (cm)	P			1.00	0.771**	0.701**	0.173	0.511**
4	4 B 11	G				1.00	1.02**	0.722**	0.864**
4	Basal diameter (cm)	P				1.00	0.911**	0.259**	0.605**
5	Green weight	G					1.00	0.658**	0.889**
3	(g/plant)	P					1.00	0.228**	0.562**
_	C4: -1: -1.1 (- /-14)	G						1.00	0.461**
6	Stick yield (g/plant)	P						1.00	0.056
7	Dry Fibre Yield	G							1.00
/	(g/plant)	P							1.00

3.6 Path Analysis

Path coefficient analysis revealed that fibre recovery had the highest positive direct effect (1.417) on dry fibre yield, followed by days to 50% flowering (0.361) and plant height (0.273). These traits also showed significant correlations with fibre yield, indicating a true relationship and indicating

they are ideal for selection.

Some traits like green weight (-0.145) and stick yield (-0.559) had negative direct effects but still showed positive correlation with fibre yield due to indirect contributions via other traits like fibre recovery and plant height.

Table 6: Estimates of genotypic direct (diagonal) and indirect effects (above and below diagonal) of component characters on Dry Fibre Yield in Fifty-two kenaf genotypes

Characters	Days to initial				Green weight			Dry fibre yield
	flowering	flowering	(cm)	diameter (cm)	(Kg/plant)	(g/plant)	recovery	(g/plant)
Days to initial flowering	-0.419	0.359	0.173	-0.060	-0.110	-0.020	0.659	0.577**
Days to 50% flowering	-0.417	0.361	0.168	-0.059	-0.105	-0.024	0.641	0.564**
Plant height (cm)	-0.267	0.223	0.273	-0.084	-0.135	-0.306	0.926	0.630**
Basal diameter (cm)	-0.285	0.238	0.255	-0.090	-0.148	-0.404	1.297	0.864**
Green weight (Kg/plant)	-0.319	0.262	0.255	-0.090	-0.145	-0.368	1.297	0.889**
Stick yield (g/plant)	-0.018	0.015	0.149	-0.065	-0.090	-0.559	1.034	0.461**
Fibre recovery	-0.195	0.163	0.178	-0.080	-0.133	-0.409	1.417	0.939**

Residual effects = 0.015

These findings agree with earlier reports by Ghosh Dastidar and Bhaduri (1983) ^[6], Dewey and Lu (1959) ^[4], and Senapati (2006) ^[18, 19], who observed strong direct effects of fibre-related traits on yield.

3.7 Genetic Diversity and Clustering

The 52 genotypes were grouped into four clusters using Mahalanobis' D² statistics and Tocher's method. Cluster I was the largest with 43 genotypes, followed by Cluster II (6

genotypes), Cluster III (2 genotypes), and Cluster IV with only one genotype (KIN-255).

Inter-cluster distances ranged from 5.49 to 12.14. The highest divergence (D = 12.14) was between Clusters I and II, indicating that genotypes from these clusters are genetically distant and can be exploited in future hybridization programs. The minimum distance (D = 5.49) was observed between Clusters II and IV.

Table 7: Grouping of 52 genotypes of kenaf into different clusters based on D2 values

Cluster No.	Number of genotypes	Name of Genotypes	Origin
		KIN-232, KIN-233, KIN-234	
		KIN-235, KIN-237, KIN-238	
		KIN-242, KIN-254, KIN-256,	
		KIN-257, KIN-268, KIM-01,	
		KIM-02,KIM-03, KIM-04,	
		KIM-05, KIM-06, KIM-07,	
		KIM-08, KIM-10, KIM-12,	
I	43	KIM-13, KIM-14, KIM-15,	
		KIM-16, KIM-17, KIM-18,	
		KIM-21, KIM-22, KIM-23, KIM-24, KIM-25, KIM-26,	CRIJAF Barrackpore
		KIM-28, KIM-30, KIM-31,	
		KIM-32, KIM-33,KIM-34,	
		KIM-35, KIM-36, HC 583,	
		AMC 208	
II	6	KIN-258, KIN-259, KIN-260, KIN-261, KIN-262, KIN-266	
III	2	IN-243, KIN-247	
IV	1	KIN-255	

Table 8: Average intra (bold) and inter-cluster D2values for eight clusters in fifty-two kenaf genotypes

Cluster	I	II	III	IV
I	4.67	147.38	31.92	117.94
	(2.16)	(12.14)	(5.65)	(10.86)
II		7.45	51.41	30.14
11		(2.73)	(7.17)	(5.49)
111			3.61	40.70
III			(1.90)	(6.38)
IV				0.00
I V				(0.00)

3.8 Cluster Mean and Trait Contribution

Cluster means revealed that Cluster I had the highest values for plant height, basal diameter, green weight, and dry fibre yield, making it the most promising for fibre yield improvement. Cluster IV had the lowest performance in all traits.

Table 9: Mean values of the eight clusters for eight characters in fifty-two kenaf genotypes

Cluster No.	Days to Initial Flowering	Days to 50% Flowering	Plant Height (cm)	Basal Diameter (cm)	Green Weight (Kg/plant)	Stick Yield (g/plant)	Fibre recovery (%)	Dry Fibre Yield (g/plant)
I	92	100	333.26	2.02	0.40	7.99	16.40	189.20
II	72	80	298.67	1.70	0.33	8.09	11.69	132.73
III	84	91	322.00	1.68	0.33	7.77	10.13	121.33
IV	76	84	183.67	0.77	0.17	5.83	4.60	73.73
Mean	81	89	284.40	1.54	0.31	7.42	10.71	129.25

Trait contribution to genetic divergence showed that days to initial flowering contributed the most (32.28%), followed by

stick yield (21.42%) and dry fibre yield (18.25%), while fibre recovery and green weight contributed the least.

Contribution % Sr. No. Character Number of times appearing first in the ranking Days to initial flowering 428 32.28 Days to 50% flowering 2 14.86 3 Plant height (cm) 91 6.86 4 Basal diameter (cm) 57 4.3 5 Green weight (Kg/plant) 18 1.36 6 Stick yield (g/plant) 284 21.42 7 Fibre recovery 09 0.68 Dry fibre yield (g/plant) 8. 242 18.25 Total 100

Table 10: Percent Contribution of different characters

4. Summary and Conclusion

This study, titled "Genetic Variability Studies in Kenaf (*Hibiscus cannabinus* L.)" was conducted during the kharif season of 2021 at the Cotton Improvement Project, Department of Agricultural Botany, MPKV, Rahuri. The study aimed to assess genetic variability, estimate heritability and genetic advance, examine trait correlations and path coefficients, and evaluate genetic divergence among 52 kenaf genotypes to identify promising lines for future breeding programs.

The experiment was laid out in a randomized block design (RBD) with three replications. A total of eight quantitative traits were studied: days to initiation of flowering, days to 50% flowering, plant height, basal diameter, green weight, stick yield, dry fibre yield, and fibre recovery percentage.

4.1 Variability, Heritability, and Genetic Advance

Significant variation was observed among the genotypes for most traits. The widest range of variation was recorded for plant height, followed by dry fibre yield and stick yield, indicating a broad genetic base. The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all traits, indicating that environmental factors had a notable influence.

High GCV and PCV were observed for dry fibre yield and fibre recovery, while moderate values were recorded for traits such as plant height, green weight, and stick yield. Days to initiation and 50% flowering exhibited low GCV and PCV. Heritability in the broad sense was high for days to initiation of flowering (97.40%), days to 50% flowering (97.50%), fibre recovery (79.20%), and dry fibre yield (70.70%). These traits also showed high genetic advance as a percentage of the mean, indicating the predominance of additive gene action and the potential for effective genetic improvement through direct selection.

4.2 Correlation and Path Analysis

Dry fibre yield showed a significant positive correlation with most other traits at both genotypic and phenotypic levels, excluding stick yield, which had a weak or non-significant association. This suggests that simultaneous improvement of traits like plant height, basal diameter, and green weight would likely enhance fibre yield.

Path coefficient analysis revealed that fibre recovery had the highest positive direct effect on dry fibre yield, followed by days to 50% flowering and plant height. Traits like green weight and stick yield exhibited negative direct effects but still contributed indirectly through their associations with key traits. This analysis supports the selection of traits with both significant correlation and strong direct effects for improving fibre yield.

4.3 Genetic Divergence and Clustering

The genetic divergence study grouped the 52 genotypes into four clusters. Cluster I had the maximum number of genotypes (43), while Cluster IV had only one. The highest inter-cluster distance (12.14) was recorded between Clusters I and II, indicating wide genetic diversity that can be exploited for hybridization.

5. Conclusion

Based on variability, heritability, trait associations, and genetic divergence, traits like flowering time, fibre recovery, and dry fibre yield emerged as promising targets for improvement. Genotypes such as KIM-02, KIN-256, KIN-233, KIM-32, KIM-26, KIM-04, KIM-22, KIM-35, KIN-242 showed superior performance and are recommended for use as parents in future kenaf breeding programs aimed at enhancing fibre yield and overall productivity.

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