Combining Ability and Gene Action for Yield Improvement in Kenaf (Hibiscus Cannabinus L.) Under Tropical Conditions Through Diallel Mating Design

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Research Article

Keywords: Hybrid development, combining ability, gene action, diallel analysis, kenaf

Posted Date: December 17th, 2021

DOI: https://doi.org/10.21203/rs.3.rs-1107040/v1

Abstract

Nine morphologically distinct kenaf genotypes were hybridized to produce 36 hybrids following a half diallel mating design. The combining ability and gene action of 15 yield and yield components were assessed in hybrids and their parents across two environments. Except for the mid diameter and plant height traits, there were highly significant differences ($p \leq 0.01$) between both the analysis of variance of environments and the interaction of genotype and environment. For the inheritance of these traits, additive gene effects were considerable, and the expression of these additive genes was heavily influenced by the environment. Significant differences were found for all studied traits for GCA except top diameter, and SCA except plant height and top diameter, implying the presence of both additive and non-additive gene action for the inheritance of the concerned characters. For all features except top diameter and number of nodes, the magnitude of GCA variation was significantly higher than that of SCA variance, indicating the additive gene's predominance. The parental lines P_1, P_3 and P_4 were determined to be outstanding general combiners for fibre yield and yield-related parameters. Considering combining ability and genetic analysis study together, the crosses $P_1 \times P_4$, $P_1 \times P_9$, $P_2 \times P_3$, $P_2 \times P_5$, $P_4 \times P_6$, $P_4 \times P_7$, $P_4 \times P_9$, $P_5 \times P_8$, and $P_7 \times P_9$ were found promising for their heterotic response to higher fibre yield, stick yield, seed yield and and could be useful by adopting proper strategies for future improvement in kenaf breeding programmes.

Introduction

Kenaf (*Hibiscus cannabinus* L.) flowers are capable of both self and cross-pollination, hence due to f insect activity, the percentage of crossing ranges between 2 and 24% (Behmaram et al., 2014). According to Dempsey (1963), the production of a kenaf F_1 generation is 14-43% higher than the parents. China started a hybrid breeding programme in 1978, and hybrid kenaf cultivars were developed and exploited commercially in China (Liu, 2005). According to Li (2000), hybrid kenaf cultivars are extensively grown in China and are gaining favour in India. Hybrid kenaf has received much attention due to its enhanced fiber quality and resistance to force (Aifen et al., 2008). The kenaf stalk's bark includes long fibre strands made up of many smaller bast fibres, whereas the woody core material, which remains after the bark is removed, contains core fibres (Hossain et al., 2011). Whole stalk kenaf fibres, including bast and core, have been found as a promising fibre source for pulp and paper, ropes, twine, coarse, burlap, and fiberboard (Yu and Yu, 2007).

Kenaf seed production is also commercially important because it is a good oil source (16–22%) (Patane and Sortino, 2010). Cooking (flour), lubrication, soap production, cosmetics, linoleum, paints, and varnishes are all possible uses for the seeds (Coetzee et al., 2008). Compared to alternative mating designs, the diallel analysis is an effective method for screening parents for hybrid production. Different varieties of diallel crosses exist, however in terms of the number of reciprocal crossings, half diallel crosses are more manageable for breeders than full diallel analysis (Christie and Shattuck, 1992). Combining ability analysis is an effective tool for identifying superior hybrid parents with high general combining ability (GCA) and progenies with improved specific combining ability (SCA) (Thorat et al., 2021). It's also useful for measuring the genetic worth of parents and crossings in terms of gene activity in quantitative character inheritance, as well as exploitation and breeding tactics (Gaurav et al., 2017).

GCA refers to a parent's average performance in a series of crossings. In contrast, SCA refers to a hybrid combination that is better or worse than expected based on the average performance of the parental inbred lines involved (Chen et al., 2019). Cultivar parents with a high GCA effect have additive gene activity, but they do not always have a favorable SCA in their combination (Santha et al., 2017). Meanwhile, determining the sort of gene action that affects the phenotypes of interest using SCA estimation is useful in genetic research. A high SCA identifies non-additive gene action (Virmani et al., 2003). When measured in terms of average effects (components), SCA effects were bigger than GCA effects, indicating the importance of non-additive gene activity in influencing yield component expression (Pace et al., 1998). For a successful breeding programme, the SCA and GCA data are essential in finding hybrids and parents (Patel et al., 2013).. Strong hybrids are produced by parents who have good general and combining ability (Shattuck et al., 1993).

Heterosis is a genetic phenomenon caused by heterozygosity and is an important plant improvement measurement. Heterosis for fibre yield is well-known, and hybrid kenaf cultivars have been created and used commercially in China (Liu, 2005). According to Bruce (1910), the presence of heterozygous allelic interaction with one or more loci is explained by overdominance heterosis, whereas dominance heterosis is related with the accumulation of dominant genes from both parents. Epistasis is described by Cordell (2002) as the interaction of genes and non-alleles on a genome (Yang et al., 2018). JianMin et al., (2005) claimed that F_1 heterosis can survive 1.4 - 1.7 generations on average, but that favourable hybrids could last 3 - 4 generations. By selecting genotypes with distinct genetic backgrounds, it will be highly useful for improving the variety of kenaf in the Malaysian tropical environment (Faruq et al., 2013). The primary goal of this research was to identify genotypes (parents and offspring) with good combining ability that could assist future kenaf improvement with high fibre yield.

Materials And Methods

Planting materials. Nine kenaf genotype parents and 36 F_1 hybrids were employed in this study (Table 1). Among the nine genotype, eight mutant lines were developed from V-36 through acute and chronic gamma irradiation by the Malaysian Nuclear Agency in Bangi, Selangor, provided (Supplementary 1), and one was a commercial variety from Bangladesh (Supplementary 1). From February to May 2020, the parents were diallel mated in all possible combinations, barring reciprocals, at Field 10 in University Putra Malaysia to produce 36 F_1 hybrids.

Table 1
Origin and salient features of nine selected kenaf genotypes used as parents for diallel cross

Parent	Accession	Mode of development	Generation	Salient features
P_1	ML5	Acute (300), MNA	M_7	Late maturing cultivar with high fibre yielding green palmate leaves and completely cream flower color with white stigma
P_2	ML9	Acute (300), MNA	M_7	Positive flowering attributes and deep green cordate leaves
P_3	ML36-10	Acute (300), MNA	M_6	Cordate leaves are pale green in color and produce a lot of fibre and stick
P_4	ML36-24	Acute (1300), MNA	M_6	Growing quickly and creating a lot of biomasses with high fibre and stick yield
P_5	ML36-25	Acute (1300), MNA	M_6	Best performer for both seed yield traits (seeds number per pod and 1000 seeds weight)
P_6	ML36-27	Acute (1300), MNA	M_6	Green stem with reddish patches and deep green cordate leaf
P_7	BJRI Kenaf4	Conventional method, BJRI	Check	Purple stem with palmate leaf that develops swiftly and produces several pods per plant
P_8	MLRing4 P2	Chronic, MNA	M_6	Bark thickness is comparatively low and the fibre to stick ratio is intermediate
P_9	ML36-21(2)	Acute (800), MNA	M_6	Green palmate leaves and are far less photosensitive
Legend: MNA = Malaysian Nuclear Agency, BJRI = Bangladesh Jute Research Institute				

Hybridization techniques and raising of F $_1$ seeds in kenaf. Both phenotypic and molecular techniques effectively determined the genetic diversity in the population under research, according to a comparison of clustering based on morphological features and EST-microsatellites markers. Although the genotype clustering changed significantly between the two approaches, the genotypes were generally grouped in the same groupings. As a result, combining phenotypic and molecular data will result in a more accurate summary when selecting parents for hybridization work. Nine genotypes were chosen as parental materials and mated in diallel fashion omitting reciprocals, considering group distances, genetic distances, and other agronomic performance. To achieve flowering synchronization throughout February 2020 to May 2020, pure and healthy seeds were sown in the experiment field three times at 10-day intervals. F_1 seeds were collected after the fruits had ripened, using standard methods for emasculation and pollination.

Step 1. Flowers bloomed early in the morning, and responsiveness lasted until noon. The floral buds of the plants chosen as female parents, which were expected to open the next morning, were emasculated in the afternoon. The corolla was emasculated above the staminal tube with a scalpel blade. The anthers were removed from the staminal tube with forceps. The stigmata of emasculated flower buds were hidden by tubes. The tubes were made using ordinary plastic straws that are commonly used to consume soft drinks. The tubes were cut into 2.5 cm lengths using scissors. To seal one end of the tubes, a heat-sealing machine was used.

Step 2. The following morning, between 7 and 9 a.m., pollen from the desired parents was used to pollinate the flowers. The stigma was softly contacted with the desired parents' anther while holding the flower stalk in one hand. The pollinated pistils were quickly capped and tagged with the cross's parents' names. The plastic tubes around the pollinated pistils were removed the next day, allowing the capsules to grow normally.

Step 3. To get the greatest number of fruits feasible, numerous crossings (about 30) were done for each cross combination. Both the hybrids and the parental fruits ripened within two months. F_1 seeds were harvested, cleaned, and sun-dried to a 7-8 percent moisture level before being stored in desiccators with silica gel for use in future planting seasons.

Experimental location. The experiments were carried out at Universiti Putra Malaysia (UPM), Serdang, Selangor, Malaysia, on 3°02′ N latitude and 101°42′ E longitude, with 31 m above sea level. The field evaluation took place in a humid tropical climate across two environments, the first from June 2020 to September 2020 and the second from March 2021 to June 2021.

Experimental design and field layout. To generate a good crop under optimal management, standard kenaf production was applied. The soil for the plant's cultivation was mechanically ploughed, then laddered. Kenaf seeds from 45 entries were planted in peat moss soil in germination trays, consisting of nine parents and 36 F_1s. After two weeks, seedlings were transplanted to a depth of 2 - 2.5 cm in a 60 × 10 m^2 plot with a row spacing of 10 x 30 cm (14 days). The experiment was carried out in a randomised full block design with three replications of planting blocks, with randomization assigned using a table of random numbers (Gomez and Gomez, 1984). NPK Green (15:15:15) and NPK Blue (12:12:17) were applied at the prescribed dose of 450 kg per hectare shortly after seeding and after 40 days of planting. Throughout the cropping season, intercultural operations like weeding, thinning, supplemental irrigations, and plant protection measures were performed appropriately. All the suggested cultural measures for growing a healthy crop were strictly followed.

Data collection. There were a total of seven qualitative and fifteen quantitative features identified. For each genotype per replication, observations were taken from 10 randomly selected plants for each characteristic. At seedling and growth phases in the field, qualitative features such stem color, leaf form, leaf color, and petiole color were observed. The pod shape, seed shape, and seed coat color were observed at the pre-bud and mature stages. Plant height, base diameter, core diameter, middle diameter, top diameter, nodes number, days to first flowering, days to 50% flowering, fresh stem weight with leaves and pods, fresh stem weight without leaves and pods, dry stick weight, dry fibre weight, pods number per plant, seeds number per pod, and 1000 seed weight were among the quantitative data collected (Table 2). Days to first flowering, days to 50% flowering, and pods number per plant were all verified in the field, and residual traits were measured in the lab 90 days after transplanting (Al-Mamun et al., 2020).

Table 2
Quantitative characters studied from nine parents and their crosses

Characteristics	Denotation	Description
Plant height (cm)	PH	Plant height was measured from the base to the tip of the main shoot of 10 randomly selected plants in meter scale at the time of harvest (pre-bud stage, 90 DAS).
Base diameter (mm)	BD	Average base diameter of 10 randomly selected plants was measured at the base of the stem in mm using slide calipers.
Core diameter (mm)	CD	It was measured at the base point of the stem using slide calipers after fibre separated from stem. It was taken at the end of retting period.
Middle diameter (mm)	MD	It was measured at the mid-point between base and top of the stem using slide calipers. It was also taken at the time of harvest.
Top diameter (mm)	TD	It was measured at the top of the stem using slide calipers. It was also taken at the time of harvest.
Number of nodes	NN	Number of nodes of 10 randomly selected plants was counted and averaged then for getting node no/plant.
Days to first flowering	DTFF	It was recorded as the number of days from the date of sowing to beginning of flowering in the population of each genotype.
Days to 50% flowering	D50%F	The number of days to flowering was quantified from planting date to the day when 50% flowering in the population of each genotype.
Fresh stem weight with leaves and pods (g)	FW1	Average fresh stem weight with leaves and pods of 10 plants was recorded using electric balance just after harvest and then per plant basis weight was calculated.
Fresh stem weight without leaves and pods (g)	FW2	Fresh stem weight of 10 randomly selected plants without leaves and pods was taken using electric balance just after harvest and then per plant basis weight was calculated.
Dry stick weight (g)	DSW	It was measured from previously selected 10 plants after extraction of fibre and proper sun drying of stick and the mean was computed.
Dry fibre weight (g)	DFW	Dry fibre weight of randomly selected 10 plants from each plot was taken after retting and proper drying in the sun. Finally, per plant basis weight was calculated.
Number of pods per plant	NF	Number of total pods from first to last pod setting per plant was counted in the field and recorded.
Number of seeds per pod	NS	Number of matured seeds from 10 randomly selected pods per replication was counted and it was then averaged and replication wise recorded.
1000 seeds weight (g)	SW	Weight of 1000 dry seeds (10% moisture) of each genotype for each replication was measured using digital balance and recorded.

Statistical analysis. A combined analysis of variance (ANOVA) was performed on all data (yield, yield components, and seed characters) using SAS (Statistical Analysis Software) version 9.4 (SAS Institute Inc., Cary, NC, USA). Simultaneously, the LSD test was employed to compare means at a significance level of 5%.

Estimation of heterosis. Two types of heterosis were calculated and expressed as percentages: relative heterosis (MP) and heterobeltiosis (BP) (Mather and Jinks, 1971). The amount of heterosis was determined by comparing the mean of F_1 hybrids to the mid parental value for a given trait using the formula below (Rai, 1979). The following formula was used to calculate the magnitude of heterosis of the derived F_1 over mid-parents and better parents.

i) Mid-parent heterosis = $[(F_1\text{-}MP)/MP]$ x100 (relative heterosis)

Where, F_1 = mean value of the F_1

MP = mean value of two parental involves in F_1 i.e $(P_1 + P_2)/2$

The significance of relative heterosis was tested using t-test (Wynne et al., 1970).

$t = F_1ij - MPij/(3/8\sigma e)^{1/2}$

Where, F_1ij = mean of the ij^{th} F1 cross

MPij = mid-parent value for ij^{th} cross

σ^2e = estimate of error variance

ii) Better parent heterosis = $[(F_1\text{- }BP)/BP]$ x100 (heterobeltiosis)

Where, F_1 = mean value of the F_1

BP = mean value of better parent

The significance of relative heterosis was tested using t-test (Wyne et al., 1970).

$t = F_1ij – BPij/(1/2\sigma^2_e)^{1/2}$

Where, F_1ij = mean of the ij^{th} F_1 cross

BPij = Better value for ij^{th} cross

σ^2_e = estimate of error variance

Result

Using nine parents and 36 F_1s, researchers attempted to evaluate the relative impact of general and combining skills and the type of gene action and genetic parameters affecting yield and important features. To identify and select superior genotypes that are less sensitive to photoperiodism and indeterminate flowering, researchers used a total of 22 qualitative and quantitative features linked with the plant, flower, fibre yield, pod, and seed.

Qualitative variation. Qualitative characteristics assessment provides information on highly diverse or uniform character, which can be quite different or very consistent. Table 3, supplementary figure 1 and Figures 1, 2 and 3 show the variation observed among the seven qualitative traits, revealing that plant, leaf, and flower characteristics differed significantly.

Table 3
Characteristics of selected parents' growth stages and the F_1 kenaf population

Parents/Hybrids	Stem color	Leaf shape	Leaf color (Lamina)	Petiole color	Pod shape	Seed shape	Seed coat color
P_1	Green	Palmate	Green	Green	Ovoid	Triangular	Ash gray
P_2	Green	Cordate	Deep green	Green	Ovoid	Triangular	Ash gray
P_3	Grp	Cordate	Pale Green	Green	Ovoid	Triangular	Ash gray
P_4	Grp	Cordate	Deep green	Green	Ovoid	Sub-reniform	Brownish
P_5	Grp	Cordate	Green	Green	Globular	Triangular	Ash gray
P_6	Grp	Cordate	Deep green	Green	Elongated	Triangular	Bfb
P_7	Purple	Palmate	Green	UrLg	Ovoid	Triangular	Ash gray
P_8	Grp	Cordate	Deep green	Green	Globular	Triangular	Ash gray
P_9	Grp	Palmate	Green	Green	Elongated	Triangular	Ash gray
$P_1 \times P_2$	RaGb	Palmate	Green	Green	Ovoid	Sub-reniform	Blackish
$P_1 \times P_3$	Reddish	Palmate	Green	Green	Ovoid	Triangular	Blackish
$P_1 \times P_4$	Reddish	Palmate	Green	Green	Ovoid	Triangular	Ash gray
$P_1 \times P_5$	RaGb	Palmate	Green	Green	Ovoid	Triangular	Brownish
$P_1 \times P_6$	RaGb	Palmate	Green	Green	Elongated	Sub-reniform	Blackish
$P_1 \times P_7$	Purple	Palmate	Deep green	UrLg	Globular	Triangular	Ash gray
$P_1 \times P_8$	RaGb	Palmate	Green	Green	Globular	Triangular	Ash gray
$P_1 \times P_9$	RaGb	Palmate	Green	Green	Globular	Triangular	Ash gray
$P_2 \times P_3$	Grp	Cordate	Deep green	Reddish	Globular	Sub-reniform	Blackish
$P_2 \times P_4$	Grp	Cordate	Green	Green	Ovoid	Sub-reniform	Ash gray
$P_2 \times P_5$	Grp	Cordate	Green	Green	Elongated	Triangular	Blackish
$P_2 \times P_6$	Grp	Cordate	Green	Green	Ovoid	Triangular	Blackish
$P_2 \times P_7$	Purple	Palmate	Deep green	UrLg	Globular	Triangular	Ash gray
$P_2 \times P_8$	Grp	Cordate	Green	Green	Globular	Sub-reniform	Ash gray
$P_2 \times P_9$	Green	Palmate	Deep green	Green	Ovoid	Triangular	Ash gray
$P_3 \times P_4$	Green	Cordate	Green	Green	Globular	Triangular	Blackish
$P_3 \times P_5$	Green	Cordate	Green	Green	Globular	Triangular	Blackish
$P_3 \times P_6$	Grp	Cordate	Green	Green	Globular	Triangular	Ash gray
$P_3 \times P_7$	Reddish	Palmate	Green	UrLg	Globular	Triangular	Bfb
$P_3 \times P_8$	Grp	Cordate	Green	Green	Globular	Triangular	Ash gray
$P_3 \times P_9$	Green	Palmate	Green	Green	Globular	Triangular	Blackish
$P_4 \times P_5$	Green	Cordate	Deep green	Green	Globular	Triangular	Ash gray
$P_4 \times P_6$	Green	Cordate	Deep green	Green	Globular	Triangular	Ash gray
$P_4 \times P_7$	Purple	Palmate	Deep green	UrLg	Ovoid	Sub-reniform	Brownish
$P_4 \times P_8$	Grp	Cordate	Green	Green	Ovoid	Triangular	Ash gray

Legend: **Grp** Green with reddish patches, **RaGb** Reddish above greenish below, **UrLg** Upper surface light reddish but lower surface green, **Bfb** Black with few brownish

Parents/Hybrids	Stem color	Leaf shape	Leaf color (Lamina)	Petiole color	Pod shape	Seed shape	Seed coat color
$P_4 \times P_9$	Grp	Palmate	Green	Green	Ovoid	Triangular	Blackish
$P_5 \times P_6$	Grp	Cordate	Green	UrLg	Ovoid	Triangular	Brownish
$P_5 \times P_7$	Red	Palmate	Deep green	UrLg	Globular	Triangular	Brownish
$P_5 \times P_8$	Grp	Cordate	Green	Green	Ovoid	Triangular	Blackish
$P_5 \times P_9$	Grp	Palmate	Pale green	Green	Ovoid	Triangular	Blackish
$P_6 \times P_7$	Reddish	Palmate	Green	UrLg	Globular	Triangular	Ash gray
$P_6 \times P_8$	Grp	Cordate	Deep green	Green	Globular	Triangular	Blackish
$P_6 \times P_9$	Grp	Palmate	Green	Green	Globular	Triangular	Blackish
$P_7 \times P_8$	Red	Cordate	Green	Purple	Ovoid	Triangular	Bfb
$P_7 \times P_9$	Red	Palmate	Green	UrLg	Globular	Triangular	Brownish
$P_8 \times P_9$	GRp	Palmate	Green	Green	Ovoid	Sub-reniform	Blackish

Legend: **Grp** Green with reddish patches, **RaGb** Reddish above greenish below, **UrLg** Upper surface light reddish but lower surface green, **Bfb** Black with few brownish

Parents. The selected parents' stem, leaf form, leaf color (lamina), and petiole color varied greatly. Two of the nine parents, P_1 and P_2, were green stem types with green petioles. Parent P_7 had a light reddish upper surface but a green petiole on the lower surface with a purple stem. Otherwise, five parents (P_3, P_4, P_5, P_6, and P_8) had stems green with reddish patches and petioles had cordate leaves. Parents P_1, P_7, and P_9 had palmate leaf morphologies with green leaf color (Table 3). P_2, P_4, P_6, and P_8 had deep green leaves, whereas P_3 had pale green leaves. The genotypes are further divided into three groups depending on pod shape: globular (round), elongated (pointed), and oval (egg-shaped). Seed shape and seed coat color were different amongst genotypes. P_4 seeds were brownish, while P_6 seeds were black with a few brownish and the rest were ash grey.

F_1 generation. The stem color showed a lot of variances (Figure 4a). The color variance for the green with reddish patches, green, reddish above greenish below, reddish, purple, and red stem colors was 41.67%, 16.67%, 13.89%, 11.11%, 8.33%, and 8.33%, respectively (Figure 4a), from the 36 described kenaf F_1 hybrids. Palmate leaves were found in 55.56% of F_1 hybrids, whereas cordate leaves were found in 44.44% (Figure 4b). The 36 F_1 hybrids' leaf color (lamina) was diverse, falling into three categories: green, deep green, and pale green, which accounted for 72.22%, 25%, and 2.78% genotypes, respectively (Figure 4c).

Petiole color varied greatly among the hybrids investigated, with 72.22%, 22.22%, 2.78%, and 2.78% for green, upper surface light reddish but lower green, reddish, and purple, respectively (Figure 4d). The form of the kenaf pod also showed a wide range of variation. The genotypes are divided into three groups based on pod shape: globular (round) 52.78%; ovoid (egg-shaped) 41.67%; and elongated (pointed) 5.55% (Figure 4e). Seed shape and seed coat color differed across the 36 F_1 hybrids. Triangular seed shape was found in 80.56% of F_1 hybrids, whereas sub-reniform seed shape was found in 19.44% (Figure 4f). Blackish seeds were found in up to 41.67% of hybrids, ash grey seeds in 38.89%, brownish seeds in 13.89%, and black color seeds in 5.56% (Figure 4g).

Variation among all genotypes for quantitative traits in pooled environments. Across the two environments, the combined analysis of variance for the 15 quantitative features among the nine parents and 36 crosses revealed significant differences (Table 4). Except for middle diameter and top diameter, there were very significant variations ($p \leq 0.01$) in environments and genotypes (parents and offspring) for all the variables studied. There were significant variations ($p \leq 0.01$ or 0.05) for genotype by environment (G x E) except for plant height and seeds number per pod. Base diameter, core diameter, middle diameter, top diameter, number of nodes, days to 50% flowering, fresh stem weight with leaves and pod, fresh stem weight without leaves and pod, dry stick weight, dry fibre weight, number of pods per plant, and 1000 seed weight were all shown to be highly significant differences ($p \leq 0.01$). The CV% for yield and yield-related components ranges 9.40 (days to 1st flowering) to 69.05 (nodes number), showing that the traits evaluated have a wide range of variability.

Table 4
Combined analysis of variance was performed for 15 quantitative attributes of nine parents and their crosses over two environments

Traits	Environment (E)	Rep (Env)	Genotypes (G)	G × E	Error	CV(%)
DF	1	4	44	44	176	
Plant height	47672.79**	1315.93	1814.32**	769.20	644.07	12.02
Base diameter	2644.69**	53.89**	45.51**	28.09**	7.80	20.39
Core diameter	2715.94**	60.42**	42.50**	30.47**	7.73	23.81
Middle diameter	3.95	128.33**	7.08**	4.75**	2.18	19.19
Top diameter	534.35**	42.75**	1.24	1.59**	0.92	44.68
Number of nodes	5677.58**	2.27	10.16**	9.65**	2.28	69.05
Days to 1st flowering	258.13**	76.69	54.04**	19.53*	12.34	9.40
Days to 50% flowering	1946.76**	122.47**	85.63**	59.30**	33.12	12.55
Fresh stem weight with leaves and pod	18630484**	4918.52	466506**	488942**	65920.86	42.00
Fresh stem weight without leaves and pod	471711.4**	42044.66**	19213.8**	10701.5**	4361.16	30.88
Dry stick weight	18465.42**	3601.17**	2344.92**	3071.60**	877.24	36.86
Dry fibre weight	5968.42**	4.60	126.22**	102.29**	17.80	33.59
Number of pods per plant	80067.95**	3921.87**	6548.05**	5281.90**	646.90	43.81
Number of seeds per pod	1966.38**	12.62**	77.45**	49.12	3.60	23.48
1000 seeds weight	2595.63**	0.97	23.57**	20.64**	1.46	13.52

Legend: **Highly significant at P ≤ 0.01 level, *Significant at P ≤ 0.05 level, **CV** coefficient of variation, **DF** degrees of freedom.

Variation among all genotypes due to combining ability effects in pooled environments. Table 5 shows the results of the mean squares analysis of variance for the effects of combining ability. Significant differences (p ≤ 0.01 or 0.05) were observed for all studied traits for GCA except for top diameter and SCA except for plant height and top diameter, indicating the presence of both additive and non-additive gene action for the inheritance of the concerned characters. Using combining ability investigations, Mostofa et al. (2013) and Youcai et al. (1998) found similar results in *Hibiscus cannabinus*, Sobhan (1993) in *Hibiscus sabdariffa*, and Khatun (2007) in *Corchorus capsularis*. Except for plant height, and fresh stem weight without leaves and pod, significant differences (p ≤ 0.01 or 0.05) were reported for the interaction between GCA and environment. Except for plant height, top diameter, and days to first flowering, all traits showed significant variations (p ≤ 0.01 or 0.05) when SCA and environment interacted. Thus, the effects of non- additive genes in the traits interacted more with the environment. GCA and SCA ratios ranged from 0.54 (nodes number) to 8.29 (days to first flowering). For top diameter, nodes number, and fresh stem weight with leaves and pod, the ratio of GCA and SCA variances was found to be smaller than unity, indicating that non-additive gene action predominated. The estimated GCA/SCA was greater than unity for the other characters, indicating that additive gene effects predominated in their expression. In kenaf, Jianmin et al. (2005) and Heliyanto et al. (1998) found similar results.

Table 5
Mean squares of analysis of variance for combining ability of the 15 traits in pooled environments

Traits	GCA	SCA	GCA*ENV	SCA*ENV	GCA/SCA
Plant height	5893.40**	835.22	800.55	766.61	7.06
Base diameter	64.04**	40.46**	19.28*	29.96**	1.58
Core diameter	53.48**	39.65**	22.09**	32.30**	1.35
Middle diameter	15.73**	5.19**	8.07**	4.01**	3.03
Top diameter	1.14	1.31	2.50**	1.40*	0.87
Number of nodes	5.94*	11.11**	8.55**	10.30**	0.53
Days to 1st flowering	188.16**	23.08**	36.03**	14.90	8.15
Days to 50% flowering	240.02**	49.77*	63.39	56.44*	4.82
Fresh stem weight with leaves and pod	470219.89**	468542.91**	576405.65**	463451.47**	0.99
Fresh stem weight without leaves and pod	45353.95**	13576.78**	4757.88	12033.75**	3.34
Dry stick weight	5584.33**	1730.88**	2809.31**	2782.49**	3.23
Dry fibre weight	240.33**	104.98**	55.59**	111.88**	2.29
Number of pods per plant	9185.14**	5590.47**	4864.76**	5587.88**	1.64
Number of seeds per pod	51.31**	17.65**	47.78**	14.09**	2.91
1000 seeds weight	240.64**	41.05**	24.73**	55.12**	5.86

Legend: *Significant at 0.05 probability level, **highly significant at 0.01 probability level, **GCA** General combining ability, **SCA** Specific combining ability, **GCA* ENV** Interaction of GCA and environment, **SCA*ENV** Interaction of SCA and environment.

Mean performance of genotypes over two environments. The mean comparison for all genotypes (parents and offspring) was presented in Table 6. Plant heights ranged from 219.58 to 297.85 cm, with hybrid $P_3 \times P_7$ recording the greatest mean value and $P_2 \times P_9$ recording the lowest. The base diameter ranged from 19.95 mm ($P_2 \times P_9$) to 31.68 mm ($P_2 \times P_3$), but the base diameters of $P_1 \times P_9$ and $P_7 \times P_8$ were comparable. The $P_2 \times P_3$ had the largest core diameter (28.43 mm), while $P_2 \times P_9$ had the smallest (16.83 mm). The middle diameter was 9.69 mm (P_2) to 15.74 mm ($P_5 \times P_8$), with the maximum and lowest top diameters of $P_6 \times P_7$ and $P_1 \times P_7$, respectively. The hybrid $P_6 \times P_9$ had the most nodes (9.68), while P_2 had the least (4.15). Days to first flowering ranged from 43 to 56.33 days in $P_7 \times P_9$ and $P_2 \times P_5$, respectively. Days to 50% flowering ranged from 51 to 69.17 days. The hybrid $P_7 \times P_9$ was the first to mature, while parent P_2 was the last to mature (Table 6). Golam et al. (2011) found that 50% flowering and days to maturity, in addition to other morpho-agronomic features, may be the two most important variables in classifying kenaf accessions.

Table 6
Mean performance of nine parents and their hybrids for 15 yield and yield contributing characters in kenaf

Parents/Crosses	PH	BD	CD	MD	TD	NN	DTFF
P_1	247.41 i-l	25.74 g-l	21.77 j-n	12.17 c-j	4.31 b-h	6.91 h-l	52.00 b-i
P_2	230.44 g-k	21.44 e-k	17.89 e-m	9.69 f-k	4.47 gh	4.15 e-l	54.17 a-h
P_3	276.91 a-i	24.70 a-e	21.10 a-f	12.49 b-f	4.06 a-f	4.80 abc	48.33 d-l
P_4	280.59 c-i	25.47 a-f	21.88 b-h	12.29 b-f	4.31 d-h	5.10 a-i	52.67 e-l
P_5	265.45 jkl	24.61 i-m	20.99 k-n	12.23 ijk	4.36 b-h	7.38 a-f	49.17 a-d
P_6	255.22 e-k	20.88 g-m	17.15 g-m	10.95 d-j	4.15 a-h	5.10 a-i	51.83 b-j
P_7	278.07 a-d	22.36 c-i	19.06 b-j	10.85 d-j	4.10 h	6.16 a-i	45.17 c-l
P_8	258.23 b-h	21.40 e-k	18.14 d-m	11.57 c-j	4.33 fgh	6.82 b-l	52.00 b-k
P_9	271.53 g-k	23.33 k-p	19.53 m-r	10.73 jk	3.77 d-h	6.86 k-o	49.50 a-f
$\bar{x}$ Parents	262.65	23.33	19.72	11.44	4.21	5.92	50.54
P_1 x P_2	252.56 kl	26.28 n-q	22.35 pqr	11.22 k	3.66 a-h	7.17 p	52.67 a-d
P_1 x P_3	272.47 i-l	29.22 a	25.32 a	12.65 b-g	4.87 a-g	9.23 ab	50.17 a-d
P_1 x P_4	264.25 a-g	29.06 b-g	25.09 c-k	12.76 b-g	4.06 d-h	8.48 a-h	50.00 ab
P_1 x P_5	234.13 g-k	24.96 d-i	21.40 c-l	10.70 f-k	4.19 h	8.71 a-d	53.83 a
P_1 x P_6	255.62 d-j	25.47 g-l	22.07 g-m	11.64 f-k	4.51 gh	8.53 a-k	51.83 b-k
P_1 x P_7	285.13 a-i	27.89 g-l	24.65 h-m	11.57 f-k	3.45 gh	8.53 h-l	50.33 l-o
P_1 x P_8	268.35 d-j	26.35 j-o	22.59 l-p	12.09 d-j	3.82 a-h	7.78 d-l	51.50 e-l
P_1 x P_9	251.86 l	23.45 q	19.72 r	10.62 k	4.12 b-h	6.35 nop	53.67 a-h
P_2 x P_3	244.52 a-h	31.68 j-m	28.43 l-o	12.58 b-h	4.72 e-h	9.36 op	54.00 i-n
P_2 x P_4	277.81 abc	28.21 a-e	24.48 a-d	12.57 bcd	4.10 c-h	8.57 a-g	55.33 c-k
P_2 x P_5	252.45 a-d	26.88 e-l	23.73 d-m	11.35 b-j	3.46 b-h	8.98 g-l	56.33 h-n
P_2 x P_6	260.21 a-e	25.79 f-l	22.13 f-n	11.17 b-j	3.78 e-h	8.01 e-l	51.33 g-l
P_2 x P_7	269.95 a	25.86 j-o	22.02 l-p	11.09 c-j	3.68 a-h	6.88 j-n	46.33 no
P_2 x P_8	259.92 a-g	24.48 d-i	20.89 d-m	11.51 b-i	4.39 b-h	7.47 a-e	50.00 c-k
P_2 x P_9	219.58 a-i	19.95 j-o	16.83 l-p	9.74 e-k	4.26 a-g	4.89 j-o	52.67 c-k
P_3 x P_4	291.87 a-g	29.25 g-m	25.41 i-n	13.09 b-j	4.14 b-h	8.67 m-p	50.67 a-h
P_3 x P_5	285.98 a-i	26.11 a-f	22.62 b-i	12.28 b	4.24 a-h	6.99 a-k	48.67 h-n
P_3 x P_6	284.50 a-i	25.99 abc	22.20 abc	12.24 b-f	4.05 c-h	7.24 a-i	49.33 k-n
P_3 x P_7	297.85 a-f	24.56 g-m	20.78 j-n	12.14 b-f	4.36 a	6.56 h-l	45.00 k-n
P_3 x P_8	280.28 a-e	27.01 a-d	22.69 a-d	12.31 bcd	4.22 a	8.87 a-i	50.67 abc
P_3 x P_9	270.78 a-h	24.11 a-d	20.67 abc	11.37 c-j	4.60 a-e	6.45 j-n	50.67 f-l
P_4 x P_5	272.93 c-i	29.16 j-m	24.95 l-p	13.88 b-j	4.49 a-h	7.99 d-l	48.67 g-m
P_4 x P_6	272.75 a-g	30.28 k-p	26.48 m-p	12.69 d-j	4.15 e-h	8.35 f-l	47.50 h-n

Legend: **PH** Plant height (cm), **BD** Base diameter (mm), **CD** Core diameter (mm), **MD** Middle diameter (mm), **TD** Top diameter (mm), **NN** Number of nodes, **DTFF** Days to 1st flowering, **EMS** error means square, **LSD** least significant difference.

Cont'd. (Table 6**)**

Parents/Crosses	PH	BD	CD	MD	TD	NN	DTFF
P_4 x P_7	281.60 a-g	25.54 i-m	21.68 k-n	12.73 b-f	5.27 b-h	6.87 f-l	47.50 no
P_4 x P_8	284.18 ab	29.90 ab	25.75 ab	13.19 a	5.23 a-d	8.35 a-j	54.33 b-k
P_4 x P_9	276.71 h-k	29.86 l-q	25.86 m-r	12.06 d-j	4.91 gh	6.60 c-l	49.67 j-n
P_5 x P_6	278.45 f-k	23.65 pq	20.41 q-r	11.85 g-k	4.06 c-h	7.11 nop	48.67 b-j
P_5 x P_7	280.43 a-i	24.93 i-m	21.37 j-n	12.75 b-i	4.30 a	7.10 e-l	45.00 k-n
P_5 x P_8	294.45 c-i	31.15 h-m	27.80 k-n	15.74 h-k	5.15 a-h	8.13 h-l	51.50 a-g
P_5 x P_9	248.78 d-j	23.03 e-l	19.82 e-m	11.56 d-j	3.77 a-f	7.63 a	47.83 i-n
P_6 x P_7	271.49 a-g	24.85 m-q	21.62 n-r	12.33 h-k	5.44 d-h	7.18 l-o	47.67 mno
P_6 x P_8	263.88 a-d	25.21 k-p	21.37 m-q	10.82 f-k	4.53 d-h	6.91 l-o	52.83 mno
P_6 x P_9	260.09 ab	26.13 a-g	22.40 b-g	11.89 b-e	4.91 b-h	9.68 d-l	48.50 b-i
P_7 x P_8	286.03 d-k	23.45 opq	20.08 o-r	11.28 d-j	4.09 b-h	6.09 i-m	45.17 i-n
P_7 x P_9	296.17 d-j	28.52 i-m	25.20 j-n	13.03 bc	4.28 b-h	7.47 a-d	43.00 g-l
P_8 x P_9	261.70 a-i	24.88 k-p	21.53 m-r	13.67 ijk	4.31 gh	9.09 h-l	48.33 o
$\bar{x}$ Crosses	269.71	26.47	22.84	12.11	4.32	7.73	50.03
Overall Mean	268.30	25.85	22.22	11.98	4.30	7.37	50.13
Std Dev	32.26	5.27	5.29	2.30	1.92	5.09	4.71
Std Error	1.96	0.32	0.32	0.14	0.12	0.31	0.29
EMS	644.08	7.80	7.73	2.18	0.92	2.28	12.34
LSD (5%)	28.917	3.1825	3.1673	1.6839	1.0906	1.7196	4.002

Legend: **PH** Plant height (cm), **BD** Base diameter (mm), **CD** Core diameter (mm), **MD** Middle diameter (mm), **TD** Top diameter (mm), **NN** Number of nodes, **DTFF** Days to 1st flowering, **EMS** error means square, **LSD** least significant difference.

Cont'd. (Table 6**)**

Legend: **D50%F** Days to 50% flowering, **FW1** Fresh stem weight with leaves and pod (g), **FW2** Fresh stem weight without leaves and pod (g), **DSW** Dry stick weight (g), **DFW** Dry fibre weight (g), **NF** Number of pods per plant, **NS** Number of seeds per pod, **SW** 1000 seeds weight (g), **OA** Mean Overall Mean, **EMS** Error means square, **LSD** Least significant difference**.**

Fresh stem weight with leaves and pods ranged from 584.31 g (P_2 × P_9) to 1786.48 g (P_4 × P_6), with the highest and lowest fresh stem weight without leaves and pods being 449.96 g (P_4 × P_9) and 222.41 g (P_6), respectively. The dry stick weight ranged from 71.35 to 152.93 g, with P_1 × P_4 having the highest mean value (152.93 g), followed by P_4 × P_9 (147.69 g), and P_6 having the lowest mean value (71.35 g). The hybrid P_2 × P_3 yielded its most dry fibre weight per plant (38.74 g), whereas P_7 yielded the least (16.3 g). Aside from that, the hybrid P_7 × P_9 produced the most pods per plant (216.15), whereas P_2 had the least (50.82). The number of seeds per pod ranged from 15.08 to 28.76. Parent P_5 had the most seeds per pod, while P_1 × P_2 and P_2 × P_8 contained the fewest. The weight of 1000 seeds varied from 26.20 to 35.05 g. The hybrid P_2 × P_8 had the highest 1000 seed weight (35.05 g), while hybrid P_1 × P_5 had the lowest 1000 seed weight (26.20 g) (Table 6).

Plant height, base diameter, core diameter, middle diameter, top diameter, number of nodes, fresh stem weight with leaves and pod, fresh stem weight without leaves and pod, dry stick weight, dry fibre weight, and pods number per plant are all higher than parental mean. In comparison to the hybrid mean, the parental mean has somewhat longer days to first flowering and days to 50% flowering. Similarly, the parental mean had more seeds per pod and 1000 seed weight than the hybrid means. The fact that the hybrid mean has a lower weight per 1000 seeds than the parental mean is advantageous because it allows for smaller seed sizes. The largest standard deviation (SD) value was observed for fresh stem weight with leaves and pod (518.40) with standard error (Sem, ±31.55), while the lowest was for top diameter (SD, 1.92; Sem, ±0.12) (Table 6). The standard error (SE) indicates of consistency of the average values, lower SE values suggest that the sample mean is a more precise depiction of the true population mean.

Combining ability effects on genotypes (parents and offspring)

General combining ability effects on genotypes (parents and offspring) in pooled environment. For a taller stature combination, a positive GCA effect is desired for plant height. The parent P_7 had the most considerable plant height and number of pods per plant, with GCA values of 11.99 and 17.57, respectively. Parent P_7, on the other hand, had the lowest GCA effect for days to first flowering and days to 50% flowering, with -3.74 and -3.71, respectively (Table 7). Whereas, for base diameter (2.32), core diameter (2.12), middle diameter (0.8), top diameter (0.24), fresh stem weight with leaves and pod (176.17), fresh stem

Parents/Crosses	D50%F	FW1	FW2	DSW	DFW	NF	NS	SW
P_1	60.67 b-j	1127.22 k-r	328.89 a	93.78 g-o	26.71 e-i	86.83 o-t	26.08 b-f	34.18 ab
P_2	69.17 c-k	670.50 f-o	225.00 ab	74.56 f-o	17.55 f-i	50.82 i-o	20.08 s	33.78 abc
P_3	57.67 c-k	962.03 a-d	331.94 ab	123.24 a-i	22.82 bcd	70.83 d-j	26.65 b-f	31.92 c-i
P_4	63.83 d-n	1118.01 b-g	351.42 abc	90.62 a	24.78 b-e	67.56 b-f	26.02 b-f	30.50 b-f
P_5	58.00 b-i	818.14 l-r	247.97 abc	79.60 d-o	19.49 i-n	92.84 m-t	28.76 h-k	30.33 x
P_6	64.00 b-j	929.25 c-l	222.41 abc	71.35 c-n	17.64 g-k	97.54 g-m	25.73 mno	33.79 m-r
P_7	55.67 f-n	937.78 b-h	258.77 a-d	96.26 c-m	16.30 c-h	121.94 bcd	20.59 k-n	32.65 g-o
P_8	60.50 c-m	911.30 f-o	287.22 a-e	95.06 c-m	23.59 d-h	83.87 b-g	27.36 b-g	33.04 c-i
P_9	55.83 a-f	1102.31 m-s	255.87 a-e	81.46 i-o	19.17 g-k	106.78 b-h	27.79 e-h	32.47 j-q
Parents	60.59	952.95	278.83	89.55	20.89	86.56	25.45	32.52
P_1 x P_2	59.83 a	1214.51 tu	328.52 a-f	97.78 no	25.96 no	115.30 u	15.08 l-o	33.90 a-d
P_1 x P_3	59.83 b-j	1526.75 a-e	379.58 b-g	122.30 c-m	31.54 a	136.92 q-u	25.95 qrs	32.79 b-h
P_1 x P_4	57.50 abc	1490.28 e-n	410.69 b-h	152.93 a-i	31.34 b-e	156.96 j-p	25.85 opq	33.36 d-j
P_1 x P_5	61.50 ab	1112.78 h-p	272.33 b-i	103.16 c-o	21.11 b-g	95.92 m-r	22.57 l-o	26.20 h-p
P_1 x P_6	61.00 c-l	1362.22 l-s	316.11 b-i	108.05 h-o	25.12 f-i	123.14 m-s	20.03 c-g	30.70 f-m
P_1 x P_7	56.83 mn	1483.89 d-m	350.83 b-i	111.67 c-n	27.42 f-i	162.83 e-l	20.69 l-o	31.83 l-q
P_1 x P_8	58.83 c-l	1211.11 g-p	323.43 c-j	109.12 g-o	27.25 f-j	151.15 d-i	25.79 rs	32.65 a
P_1 x P_9	62.83 c-k	1044.78 u	312.56 d-k	84.37 mno	24.62 mno	144.50 p-t	24.54 pqr	31.13 b-e
P_2 x P_3	61.33 c-m	1521.67 n-t	414.45 d-k	110.00 a-h	38.74 h-m	75.88 stu	16.45 a-e	32.91 g-m
P_2 x P_4	64.17 c-m	1230.00 a-d	386.11 d-l	121.12 a-e	31.46 b-f	109.50 m-s	18.42 b-g	32.44 r-u
P_2 x P_5	66.50 c-l	1192.92 b-h	322.08 d-l	104.17 a-f	29.03 f-j	101.67 g-m	20.25 b-e	31.57 i-p
P_2 x P_6	59.00 c-l	1071.88 l-s	331.67 e-l	90.58 b-k	26.04 h-m	96.58 d-j	24.96 f-i	32.00 k-q
P_2 x P_7	52.33 n	1301.58 k-r	318.10 e-l	107.78 a-g	26.00 g-k	131.35 l-p	20.39 k-n	30.85 g-p
P_2 x P_8	59.33 c-m	1198.18 b-k	303.06 e-m	95.69 a-f	25.91 g-k	140.24 d-k	15.74 g-j	35.05 uv
P_2 x P_9	59.83 c-m	584.31 q-t	229.22 e-m	78.82 c-n	18.94 i-n	83.91 k-p	17.81 a-d	33.67 q-t
P_3 x P_4	57.67 a-e	1573.89 l-r	415.19 e-m	133.33 h-o	29.92 g-k	98.61 tu	25.67 b-f	29.40 n-s
P_3 x P_5	59.50 c-l	1478.81 ab	383.70 e-m	130.00 b-j	25.89 b-g	123.69 h-n	26.56 a-e	31.49 tuv
P_3 x P_6	59.00 i-n	1101.85 a	305.56 e-m	114.54 a-d	22.86 b-g	136.07 b	24.18 c-g	30.98 f-l
P_3 x P_7	51.00 c-m	1137.01 i-q	353.02 f-m	126.30 c-l	24.88 h-m	105.17 r-u	20.95 nop	31.69 vw
P_3 x P_8	58.17 b-j	1413.89 c-l	343.33 f-m	130.00 a-d	24.78 b-g	134.39 m-t	23.68 abc	28.35 q-t
P_3 x P_9	58.33 f-n	887.92 abc	290.00 g-n	105.31 ab	22.29 bc	106.08 m-r	26.72 ab	29.90 e-k
P_4 x P_5	59.33 c-m	1660.39 stu	367.50 g-n	116.79 l-o	28.75 mno	120.28 n-t	26.68 a	28.72 p-s
P_4 x P_6	55.67 c-m	1786.48 r-u	419.35 g-o	134.46 g-o	28.87 i-n	172.30 l-q	24.98 b-e	32.11 s-u
P_4 x P_7	58.67 lmn	1174.26 f-o	303.52 g-o	112.92 h-o	23.47 l-o	75.45 b-e	19.26 a-d	27.55 m-r
P_4 x P_8	60.50 g-n	1360.67 ab	403.78 h-o	134.09 abc	29.05 b	96.00 d-k	26.86 i-l	29.78 w
P_4 x P_9	56.33 h-n	1627.02 g-o	449.96 h-o	147.69 d-o	32.11 f-k	100.78 f-l	27.30 d-h	32.31 p-s
P_5 x P_6	57.67 a-d	850.86 o-t	266.85 i-o	95.37 o	22.29 no	104.46 m-s	26.47 b-g	29.18 a-d

weight without leaves and pod (59.86), dry stick weight (16.57), and dry fibre weight (16.57), Parent P_4 had the highest positively significant GCA effect (3.53).

P_5 x P_7	53.17 e-n	1209.44 l-s	329.35 i-o	92.22 i-o	19.73 k-o	160.25 b-h	26.78 h-k	30.72 g-n
P_5 x P_8	56.17 a-g	1655.33 b-j	419.49 i-o	137.78 h-o	32.81 i-n	134.25 b-f	22.22 b-f	26.95 g-o
P_5 x P_9	56.00 b-h	1206.69 b-i	277.08 k-o	103.78 e-o	25.14 g-l	130.72 bc	24.67 b-g	30.43 o-s
P_6 x P_7	57.33 i-n	1088.89 n-t	270.83 k-o	88.89 f-o	20.36 o	144.31 h-m	22.63 k-n	31.87 c-i
P_6 x P_8	62.67 k-n	1435.15 j-q	294.83 l-o	90.72 c-m	22.16 i-n	158.92 i-o	26.28 nop	31.82 vw
P_6 x P_9	62.50 n	1463.17 abc	305.50 mno	100.12 a-e	24.51 f-j	170.63 a	25.70 j-m	30.46 q-t
P_7 x P_8	53.33 b-j	1149.64 p-t	313.34 no	109.30 g-o	22.05 h-m	113.99 p-t	19.18 ab	28.03 b-g
P_7 x P_9	51.00 j-n	1652.45 a-f	348.28 o	132.68 b-j	25.56 g-k	217.15 c-i	21.82 ab	30.07 p-s
P_8 x P_9	54.83 i-n	1501.94 l-s	296.76 o	115.65 k-o	25.03 mno	142.44 k-p	27.27 ab	30.33 d-j
Crosses	58.32	1304.52	337.67	112.49	26.19	126.99	23.07	30.92
OA Mean	58.77	1234.20	325.90	107.90	25.13	118.91	23.54	31.24
Std Dev	7.38	518.40	100.62	39.78	8.44	52.10	5.53	4.23
Std Error	0.45	31.55	6.12	2.42	0.51	3.17	0.34	0.26
EMS	33.12	65920.85	4361.17	877.24	17.80	646.90	3.60	1.46
LSD (5%)	6.5575	292.55	75.246	33.748	4.8066	28.98	2.1605	1.3767

Table 7
Estimates of general combining ability effect for 15 morphological characters of kenaf

Traits	**P_1**	**P_2**	**P_3**	**P_4**	**P_5**	**P_6**	**P_7**	**P_8**	**P_9**	**LSD (gi-gj)**	
										5%	**1%**
PH	-10.34^{**}	-17.73^{**}	8.11^{*}	8.22^{**}	-1.31	-3.22	11.99^{**}	2.03	2.24	4.11	5.43
BD	0.68	-0.43	0.96^{**}	2.32^{**}	0.22	-0.69^{*}	-0.58	-0.14	-2.34^{*}	0.45	0.60
CD	0.60	-0.32	0.92^{**}	2.12^{**}	0.36	-0.65	-0.42	-0.11	-2.49^{*}	0.45	0.59
MD	-0.11	-0.74^{**}	0.44^{*}	0.80^{**}	0.53^{**}	-0.21	-0.01	0.45^{*}	-1.15^{*}	0.24	0.32
TD	-0.10	-0.13	0.09	0.24^{*}	0.00	0.12	0.06	0.18	-0.46	0.16	0.20
NN	0.49^{**}	-0.33	-0.03	0.07	0.38^{*}	-0.01	-0.39^{*}	0.28	-0.47	0.24	0.32
DTFF	1.50^{**}	2.32^{**}	-0.51	0.69	-0.24	-0.01	-3.74^{**}	0.63	-0.64	0.57	0.75
D50%F	1.25	3.17^{**}	-0.51	1.07	0.01	1.55^{*}	-3.71^{**}	-0.09	-2.74	0.93	1.23
FW1	45.42	-140.47^{**}	33.15	176.17^{**}	-17.97	-16.56	-11.68	49.76	-117.80	41.59	54.89
FW2	13.76	-10.66	31.66^{**}	59.86^{**}	-6.01	-22.27^{**}	-8.70	6.54	-64.18^{**}	10.70	14.12
DSW	2.24	-8.84^{*}	15.09^{**}	16.57^{**}	-0.89	-7.89^{*}	2.00	5.47	-23.76^{*}	4.80	6.33
DFW	2.00^{**}	1.04^{*}	1.89^{**}	3.53^{**}	-0.19	-1.66^{**}	-2.15^{**}	0.95	-5.41^{**}	0.68	0.90
NF	9.02^{**}	-18.64^{**}	-9.33^{**}	-8.74^{**}	-0.38	12.76^{**}	17.57^{**}	7.09^{*}	-9.34	4.12	5.44
NS	-0.56^{*}	-4.50^{**}	0.42	0.75^{**}	1.36^{**}	0.72^{**}	-2.36^{**}	0.27	3.91^{**}	0.31	0.41
SW	0.65^{**}	1.47^{**}	-0.22	-0.65^{**}	-1.63^{**}	0.26	-0.54^{**}	-0.43^{**}	1.09^{*}	0.20	0.26

Legend: ***, **** Significant at P≤0.05 and P≤0.01 respectively, **PH** Plant height, **BD** Base diameter, **CD** Core diameter, **MD** Middle diameter, **TD** Top diameter, **NN** Number of nodes, **DTFF** Days to 1st flowering, **D50%F** Days to 50% flowering, **FW1** Fresh stem weight with leaves and pod, **FW2** Fresh stem weight without leaves and pod, **DSW** Dry stick weight, **DFW** Dry fibre weight, **NF** Number of pods per plant, **NS** Number of seeds per pod, **SW** 1000 seeds weight.

Parent P4, for example, had the highest positively significant GCA values for the trait's base diameter, core diameter, middle diameter, top diameter, fresh stem weight with leaves and pod, fresh stem weight without leaves and pod, dry stick weight, and dry fibre weight, all of which are favorable traits, and it contributed positively to the hybrid for these traits. Besides the P_4, parent P_1 (2), P_3 (1.89), and P_2 (1.04) were also shown to be positive and significant general combiners for dry fibre weight, and parent P_3 also showed a positive and very significant GCA effect for dry stick weight (15.09). Seed yield, a crucial feature that determines the number of pods per plant, was favorable and considerably a good general combiner for the parent P_6 (12.76), P_1 (9.02), and P_8 (7.09).

With values of 2.32 and 3.17 for days to 1st flowering and days to 50% flowering, respectively, the Parent P_2 had the most positively significant GCA effect. Plant height, fresh stem weight with leaves and pod, number of pods per plant, and number of seeds per pod, on the other hand, revealed the lowest GCA effect with values of -17.73, -140.47, -18.64, and -4.5, respectively, for the parent P_2. The parent P_9 had the highest positive GCA value for number of seeds per pod (-2.34) and the lowest negative GCA values for base diameter (-2.49), core diameter (-1.15), middle diameter (-1.15), top diameter (-0.46), number of nodes (-0.47), fresh stem weight (-64.18), dry stick weight (-23.76), and dry fibre weight (-5.41). To produce a smaller seed size combination, a negative GCA effect is desired for 1000 seeds weight. P_5 had the smallest (-1.63) and most significant negative GCA effect, followed by P_4 (-0.65) and P_7 (-0.54), indicating that they were good general combiners for reduced seed sizes and would be beneficial in future breeding programs. To increase the number of nodes, a negative GCA effect is desired. P_9 had the smallest (-0.47) and most significant negative GCA effect, followed by P_7 (-0.39) and P_2 (-0.33), indicating that they were good general combiners for fibre output and might be used in future breeding efforts.

Specific combining ability effects on hybrids across the environment. The SCA effects on hybrids in various contexts shows in Table 8. *Hibiscus cannabinus* has a major fibre yield component in the form of plant height and base diameter. SCA effects were found in all 36 hybrids studied, with 19 combinations showing positive (desire direction) SCA impacts for plant height. The cross $P_5 \times P_8$ (24.44), which were rated good combiners for tallness, had the best hybrids with significant and positive SCA effects. Conversely, as evidenced by the considerable negative SCA effects for plant height, the hybrids $P_2 \times P_9$ (-37.62) and $P_1 \times P_5$ (-23.51) were identified as poor specific combiners for this trait. When it came to base diameter, the SCA effects ranged from -6.33 to 5.47. These 5 cross combinations ($P_2 \times P_3$, $P_5 \times P_8$, $P_7 \times P_9$, $P_4 \times P_6$, and $P_1 \times P_7$) were found as good specific combiners for this characteristic. A total of 16 crosses had positive but negligible SCA scores, indicating that they may be considered average combiners. Other crosses had negative SCA effects, with one ($P_2 \times P_9$) having a highly significant SCA value of -6.33 and another ($P_3 \times P_9$) having a substantial SCA value of -3.08, respectively. As a result, this cross combination is regarded as the poorest specific combiner for base diameter. Only 5 crosses demonstrated significant positive SCA values for core diameter in kenaf, indicating heterotic performance over the mean of their parents, out of 36 cross combinations. Except for one, all the remaining cross pairings had negligible SCA effects ($P_2 \times P_9$). The $P_2 \times P_3$ cross had the most significant positive SCA effect, indicating that it was the best specific combiner for the trait. $P_2 \times P_9$ had the most negative SCA effect and was considered the worst specific combiner for core diameter.

Table 8
Estimates of specific combining ability (SCA) effects for 15 different morphological characters of kenaf

Hybrids	PH	BD	CD	MD	TD	NN	DTFF	D50%F	FW1	FW2	DSW	DFW	NF	NS
P_1 x P_2	11.33	0.36	0.06	0.20	-0.35	-0.31	-1.31	-3.16	89.44	5.37	-0.85	-1.66	8.80	-3.73**
P_1 x P_3	5.4	1.91	1.78	0.44	0.64	1.45*	-0.97	0.52	228.07*	14.12	-0.26	3.07	21.11*	2.20**
P_1 x P_4	-2.92	0.40	0.36	0.20	-0.32	0.59	-2.34	-3.39	48.58	17.03	28.89*	1.23	40.57**	1.78*
P_1 x P_5	-23.51*	-1.61	-1.57	-1.60**	0.05	0.52	2.42	1.67	-134.78	-55.46*	-3.42	-5.28**	-28.84**	-2.11**
P_1 x P_6	-0.11	-0.19	0.11	0.08	0.24	0.73	0.19	-0.38	113.25	4.57	8.48	0.20	-14.76	-4.01**
P_1 x P_7	14.19	2.12*	2.46*	-0.19	-0.75*	1.11	2.42	0.71	230.03*	25.72	2.20	2.99	20.13*	-0.28
P_1 x P_8	7.36	0.14	0.09	-0.14	-0.51	-0.31	-0.78	-0.91	-104.18	-16.92	-3.82	-0.28	18.92*	2.20**
P_1 x P_9	-10.54	-1.84	-1.84	0.50	0.72	-2.38**	1.51	5.34	-286.68	24.25	-15.27	1.58	-18.62	0.63
P_2 x P_3	-15.15	5.47**	5.81**	1.00	0.52	2.39**	2.04	0.09	408.87**	73.40**	-1.48	11.24**	-12.26	-3.35**
P_2 x P_4	18.03	0.65	0.67	0.64	-0.25	1.50**	2.18	1.35	-25.82	16.87	8.16	2.32	20.77*	-1.71*
P_2 x P_5	2.20	1.42	1.68	-0.32	-0.66	1.60**	4.10**	4.74*	131.24	18.71	8.67	3.60*	4.58	-0.49
P_2 x P_6	11.87	1.23	1.09	0.24	-0.46	1.02	-1.12	-4.30*	8.79	44.55	2.09	2.08	-13.65	4.87**
P_2 x P_7	6.40	1.20	0.75	-0.03	-0.49	0.27	-2.40	-5.71**	233.61*	17.41	9.39	2.54	16.32	3.37**
P_2 x P_8	6.33	-0.63	-0.70	-0.07	0.10	0.19	-3.09*	-2.33	68.77	-12.87	-6.17	-0.66	35.68**	-3.91**
P_2 x P_9	-37.62**	-6.33**	-5.86**	-0.95	1.10*	-4.15**	0.22	5.07	-646.22**	-89.71*	-6.81	-10.37**	-32.23*	-0.26
P_3 x P_4	6.26	0.30	0.36	-0.03	-0.42	1.30*	0.35	-1.47	144.45	3.62	-3.56	-0.07	0.57	0.61
P_3 x P_5	9.89	-0.74	-0.67	-0.57	-0.08	-0.68	-0.73	1.43	243.52*	38.01	10.57	-0.39	17.30	0.90
P_3 x P_6	10.33	0.04	-0.09	0.12	-0.39	-0.06	-0.29	-0.62	-134.86	-23.88	2.12	-1.95	16.53	-0.84
P_3 x P_7	8.46	-1.49	-1.73	-0.17	-0.03	-0.35	-0.90	-3.36	-104.58	10.01	3.98	0.57	-19.18	-0.99
P_3 x P_8	0.85	0.51	-0.14	-0.46	-0.28	1.29*	0.41	0.18	110.86	-14.92	4.21	-2.64	20.52*	-0.89
P_3 x P_9	-17.46	-3.08*	-2.54	-0.07	0.39	-2.86**	0.89	3.12	-571.94**	-48.94	-3.41	-4.30	-17.98	0.43
P_4 x P_5	-3.27	0.96	0.46	0.68	0.02	0.22	-1.93	-0.32	282.07**	-6.40	-4.12	0.84	13.29	0.70
P_4 x P_6	-1.54	2.98**	3.00**	0.22	-0.45	0.95	-3.32*	-5.53*	406.76**	61.71*	20.56	2.43	52.16**	-0.37
P_4 x P_7	-7.90	-1.87	-2.03	0.07	0.73*	-0.15	0.41	2.73	-210.35*	-67.69**	-10.88	-2.48	-49.49**	-3.01**
P_4 x P_8	4.64	2.05	1.73	0.07	0.57	0.67	2.88*	0.94	-85.37	17.33	6.81	0.00	-18.46	1.96**
P_4 x P_9	-8.17	-0.62	-0.16	-0.65	0.50	-2.71**	0.63	2.56	-105.89	45.89	1.89	2.57	-28.33*	-0.60
P_5 x P_6	13.69	-1.55	-1.31	-0.35	-0.30	-0.59	-1.23	-2.47	-334.72**	-24.91	-1.07	-0.44	-24.03*	0.52
P_5 x P_7	0.46	-0.38	-0.58	0.36**	0.00	-0.22	-1.17	-1.71	18.98	24.01	-14.12	-2.51	26.95**	3.90**
P_5 x P_8	24.44*	5.40**	5.53**	2.88	0.73*	0.15	0.97	-2.33	403.43**	98.91**	27.97*	7.47**	11.43	-3.28**
P_5 x P_9	-22.66	-2.01	-1.80	-0.39	0.12	-0.30	-1.93	-0.43	-243.69	-32.82	-0.65	1.43	1.82	-2.31*
P_6 x P_7	-6.57	0.45	0.68	0.67	1.01**	0.24	1.27	0.91	-102.99	-18.25	-10.45	-0.41	-2.13	0.39
P_6 x P_8	-4.22	0.36	0.12	-1.31*	-0.01	-0.69	2.07	2.62	181.83	-9.49	-12.09	-1.70	22.96*	1.42*
P_6 x P_9	-15.84	0.08	-0.04	0.85	0.68	0.61	0.72	7.44*	119.67	18.80	8.46	3.39	7.00	-2.39*
P_7 x P_8	2.72	-1.51	-1.41	-1.04	-0.40	-1.13*	-1.87	-1.45	-108.55	-4.56	-3.40	-1.32	-26.78**	-2.61**

Legend: *Significant at 0.05 probability level, **highly significant at 0.01 probability level, **PH** Plant height, **BD** Base diameter, **CD** Core diameter, **MD** Middle diameter, **TD** Top diameter, **NN** Number of nodes, **DTFF** Days to 1st flowering, **D50%F** Days to 50% flowering, **FW1** Fresh stem weight with leaves and pod, **FW** Fresh stem weight without leaves and pod, **DSW** Dry stick weight, **DFW** Dry fibre weight, **NF** Number of pods per plant, **NS** Number of seeds per pod, **SW** 1000 seeds weight.

Hybrids	PH	BD	CD	MD	TD	NN	DTFF	D50%F	FW1	FW2	DSW	DFW	NF	NS	S
P_7 x P_9	-2.56	3.62*	3.98*	1.32	0.18	0.62	-0.27	3.38	302.83*	57.22	36.25*	4.57	63.49**	-2.19*	(
P_8 x P_9	-27.00	-2.32	-1.55	1.28	0.08	0.89	-1.19	1.18	-58.46	-11.56	7.59	2.02	-17.84	2.17	(
LSD (sij-slk)5%	18.70	2.06	2.05	1.09	0.71	1.11	2.59	4.24	189.23	48.7	21.83	3.11	18.75	1.40	(
LSD (sij-slk)1%	24.68	2.72	2.70	1.44	0.93	1.47	3.42	5.60	249.71	64.2	28.81	4.10	24.74	1.84	1
LSD (sij-skl)5%	16.55	1.82	1.81	0.96	0.62	0.98	2.29	3.75	167.40	43.1	19.31	2.75	16.58	1.24	(
LSD (sij-skl)1%	21.84	2.40	2.39	1.27	0.82	1.30	3.02	4.95	220.91	56.8	25.48	3.63	21.88	1.63	1

Legend: *Significant at 0.05 probability level, **highly significant at 0.01 probability level, **PH** Plant height, **BD** Base diameter, **CD** Core diameter, **MD** Middle diameter, **TD** Top diameter, **NN** Number of nodes, **DTFF** Days to 1st flowering, **D50%F** Days to 50% flowering, **FW1** Fresh stem weight with leaves and pod, **FW** Fresh stem weight without leaves and pod, **DSW** Dry stick weight, **DFW** Dry fibre weight, **NF** Number of pods per plant, **NS** Number of seeds per pod, **SW** 1000 seeds weight.

For stem mid-diameter, the SCA effects ranged from -1.60 to 2.88. P_5 × P_7 (0.36) were the best hybrids with significant and positive SCA effects, and they were regarded as good specific combiners for this trait. Another 18 crosses had SCA values that were positive but insignificant, indicating that they may be used as average combiners. Other crossings had negative SCA effects, with one (P_1 × P_5) being highly significant (-1.60) and another (P_6 × P_8) being significant (-1.31). As a result, this cross combination is regarded as the worst specific combiner for medium diameters (Table 8). When it came to top diameter, the SCA effects ranged from -0.75 to 1.10. P_6 × P_7, P_2 × P_9, P_4 × P_7, and P_5 × P_8 were selected as good specific combiners for this trait since three crossings showed significant positive SCA effects, one of which was highly significant (P_6 × P_7, P_2 × P_9, P_4 × P_7, and P_5 × P_8) Another 14 crosses had SCA values that were positive but not significant, thus they may be considered average combiners. Conversely, had negative SCA impacts, with one (P_1 × P_7) having a large SCA value (-0.75). As a result, this cross combination is regarded as the worst specific combiner for top diameter. For the given number of nodes, SCA impacts ranged from -4.15 to 2.39. P_2 × P_9 (-4.15) had the highest negative and highly significant SCA estimate, followed by P_3 × P_9 (-2.86), P_4 × P_9 (-2.71), and P_1 × P_9 (-2.38), with one negative significant P_7 × P_8 (-1.13), indicating that these hybrids had good SCA for lower branch stem and better fibre yield. On the other hand, three of the 21 positive SCA effects were found to be highly significant (P_2 × P_3, P_2 × P_5, and P_2 × P_4), and three were determined to be significant (P_1 × P_3, P_3 × P_4 and P_3 × P_8). As a result, they were classified as poor combiners. The average combiners for the number of nodes characteristic were found as negative but insignificant SCA impacts in the other ten crossovers.

For days to first flowering, the SCA effects varied from -3.32 to 4.10. (Table 8). The crosses P_2 × P_5 (4.10) and P_4 × P_8 (2.88) showed the largest significant and positive SCA effects, showing that these hybrids had good SCA for this trait. On the other hand, the offspring P_4 × P_6 (-3.32) had the greatest negative and significant SCA estimate, followed by P_2 × P_8 (-3.09), both of which were judged poor specific combiners for the days to 1st flowering trait. For days to 50% flowering, SCA impacts varied from -5.71 to 7.44. The most significant SCA effects were identified in P_6 × P_9 (7.44) and P_2 × P_5 (4.74), showing that these hybrids exhibited good specific combining capacity for this trait. On the other hand, the hybrid P_2 × P_7 (-5.71) had the greatest negative and significant SCA estimate, followed by P_4 × P_6 (-5.53) and P_2 × P_6 (-4.30), both of which were judged poor specific combiners for days to 50% flowering. Four crosses viz. P_2 × P_3 (408.87), P_4 × P_6 (406.76), P_5 × P_8 (403.43) and P_4 × P_5 (282.07) showed highly significant positive SCA effects for fresh stem weight with leaves and pod trait, but the other five crosses viz. P_7 × P_9 (302.83), P_3 × P_5 (243.52), P_2 × P_7 (233.61), P_1 × P_7 (230.03) and P_1 × P_3 (228.07) exhibited significant positive SCA effects. Eleven more crossings had favorable but negligible SCA effects, thus they may be considered average specific combiners (Table 8). The remaining sixteen crosses had negative SCA effects, with four of them showing significant SCA values: P_4 × P_7 (-210.35), P_5 × P_6 (-334.72), P_3 × P_9 (-571.94), and P_2 × P_9 (-646.22). As a result, they were considered poor specific combiners for the fresh stem weight with leaves and pod characteristic.

Two crosses, P_5 × P_8 (98.91) and P_2 × P_3 (73.40), showed highly significant favorable SCA effects, with one cross, P_4 × P_6 (61.71), showing these hybrids had good SCA for fresh stem weight without leaves and pod trait. Another eighteen crossings had positive but insignificant SCA effects and may be considered average specific combiners (Table 8). The remaining 15 crosses had negative SCA effects, with three of them having significant SCA values: P_1 × P_5 (-55.46), P_4 × P_7 (-67.69), and P_2 × P_9 (-89.71). As a result, they were considered as poor specific combiners for fresh stem weight without leaves and the pod characteristic. For dry stick weight per plant in kenaf, 18 cross combinations showed positive SCA effects, while the remaining 18 cross combinations showed negative SCA values, showing heterotic performance over the mean of their parents. The cross P_7 × P_9 had the highest significant positive SCA effect (36.25), followed by P_1 × P_4 (28.89) and P_5 × P_8 (27.97), showing that it was the best specific combiner for the stick weight per plant trait. Only three of the 36 crosses had significant positive SCA effects for dry fibre weight per plant, whereas the remaining 17 had positive but negligible SCA effects. The cross P_2 × P_3 (11.24) yielded the greatest significant positive SCA value, followed by P_5 x P_8 (7.47) and P_2 x P_5 (3.60), suggesting better fibre yielding hybrids than their parents' mean and considered best specific combiners for enhanced fibre weight per plant of kenaf. The remaining 16 hybrids, on the other hand, showed unfavorable SCA consequences. Two of them, P_1 × P_5 (-5.28) and P_2 × P_9 (-10.37), showed highly significant negative values and were considered the lowest combiners for the trait in consideration.

For the number of pods per plant, the SCA impacts varied from -49.49 to 63.49. (Table 8). There were 21 positive SCA effects among the cross combinations, and 11 of them had significant positive SCA values for the number of pods per plant. The remaining 15 crosses had negative SCA effects, with six of them having severe negative SCA effects. As a result, the crosses $P_4 \times P_7$, $P_2 \times P_9$, $P_1 \times P_5$, $P_4 \times P_9$, $P_7 \times P_8$, and $P_5 \times P_6$ yielded the most pods per plant. The crosses $P_2 \times P_3$ (7.20), $P_3 \times P_4$ (4.70), and $P_2 \times P_4$ (3.32) revealed highly significant positive SCA effects, whereas $P_4 \times P_6$ (-3.43), $P_1 \times P_3$ (-2.18), and $P_1 \times P_5$ (-1.05) showed highly significant negative SCA effects. The hybrids with non-significant positive or negative SCA values were considered average specific combiners for the number of pods per plant. For the number of seeds per pod, SCA impacts varied from -4.01 to 4.87 (Table 8). Sixteen of the cross combinations had positive SCA effects, with nine of them having significant positive SCA values for the number of seeds per pod. The remaining 20 crosses had negative SCA effects, with 12 of them having significant negative SCA effects. As a result, the crosses $P_2 \times P_6$, $P_5 \times P_7$, $P_2 \times P_7$, $P_1 \times P_3$, $P_1 \times P_8$, $P_8 \times P_9$, $P_4 \times P_8$, $P_1 \times P_4$, and $P_6 \times P_8$ yielded the most seeds per pod.

The SCA impacts for the character 1000 seeds weight ranged from -4.20 to 2.64. (Table 8). $P_1 \times P_5$, $P_4 \times P_7$, $P_7 \times P_8$, $P_3 \times P_8$, $P_5 \times P_8$, $P_1 \times P_6$, and $P_2 \times P_7$ had extremely significant negative SCA effects, whereas $P_3 \times P_9$, $P_3 \times P_4$, and $P_2 \times P_6$ had significant negative SCA effects, showing that these hybrids had good SCA for lower seed size. Seven more crossings had negative but small SCA effects, thus they may be considered average specific combiners (Table 8). The crosses $P_2 \times P_8$, $P_1 \times P_4$, $P_3 \times P_5$, $P_5 \times P_9$, $P_5 \times P_7$, $P_4 \times P_6$, $P_3 \times P_7$, $P_1 \times P_8$, and $P_1 \times P_3$ were among the remaining nineteen crosses that indicated positive SCA effects. As a result, they were judged to be poor specific combiners for the 1000 seed weight trait.

Estimation of heterosis effect of kenaf hybrids for yield and yield components and morphological traits. The relative performance of the hybrids of the mid-parent (MPH) and better parent (BPH) values was used to estimate heterosis. In hybrid development, better parent heterosis is preferred over mid parent heterosis. High positive heterosis values are preferred for yield production traits, but negative values are preferred for node number and 1000 seed weight.

Relative heterosis response in pooled environments. Percentage heterosis relative to mid-parents (MPs) was significantly positive in 13 of the 36 crosses in dry fibre weight (25.74 to 91.94), five crosses in dry stick weight (8.95 to 42.54), and 20 crosses in number of pods per plant (49.22 to 108.72). However, mid-parents of eighteen fresh stem weights with leaves and pod crosses (32.75 to 91.43) and five fresh stem weights without leaves and pod crosses (46.16 to 56.76) were significantly positive (Table 9). For 1000 seed weight, 29 hybrids out of 36 had negative heterosis (in the desired direction). This indicates that they had smaller-sized seeds. Over dominance was observed in cross P_5 x P_8 for plant height, base diameter, core diameter, middle diameter, fresh stem weight with leaves and pods, and fresh stem weight without leaves and pods, as well as cross $P_4 \times P_6$ for base diameter, core diameter, fresh stem weight with leaves and pods, fresh stem weight without leaves and pods, and pods number per plant and the cross $P_2 \times P_3$ for base diameter and core diameter, with a high potency's ratio. Furthermore, the crosses $P_2 \times P_3$ and $P_2 \times P_5$ for fibre yield and the crosses $P_1 \times P_4$ and $P_4 \times P_9$ for stick yield, cross $P_6 \times P_7$ for top diameter, and cross $P_2 \times P_5$ for 1st flowering and days to 50% flowering features in late maturity cultivars had the highest mid parent heterosis. Due to the existence of over dominance, hybrid $P_7 \times P_9$ was chosen for pods number per plant and $P_2 \times P_6$ for seeds number per pod for seed yield. Negative heterosis estimates for the nodes number and 1000 seed weight are desirable, where small values for these traits indicate good fiber quality and smaller seed size, therefore negative magnitude implies high heterosis. Cross $P_2 \times P_9$ had the lowest negative nodes number value (-11.02) for quality fibre yield, and cross $P_1 \times P_5$ with the lowest negative heterosis for 1000 seed weight would produce well where smaller seed size kenaf accessions perform well.

Table 9

Estimates of mid-parent and better parent heterosis for 15 characteristics of 36 crosses in kenaf over two environments

Hybrids	PH		BD		CD		MD		TD		NN		DTFF		D5
	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MP
P_1 x P_2	5.71	2.08	11.39	2.09	12.7	2.66	2.67	-7.8	-16.57	-18.04	29.7	3.74	-0.78	1.28	-7.8
P_1 x P_3	3.93	-1.61	15.87*	13.51*	18.12	16.3	2.62	1.32	16.36	12.9	57.74**	33.59	0	-3.53	1.1
P_1 x P_4	0.09	-5.82	13.51	12.91	14.96	14.66	4.37	3.87	-5.79	-5.86	41.09*	22.63	-4.46	-5.06	-7.6
P_1 x P_5	-8.7	-11.8	-0.87	-3.05	0.11	-1.68	-12.34	-12.56	-3.33	-3.83	21.95	18.12	6.43	3.53	3.6
P_1 x P_6	1.71	0.16	9.26	-1.06	13.44	1.4	0.69	-4.35	6.47	4.48	42.14*	23.46	-0.16	-0.32	-2.1
P_1 x P_7	8.52	2.54	15.98	8.35	20.75*	13.24*	0.49	-4.96	-18.07	-20.06	30.53	23.46	3.6	-3.21	-2.2
P_1 x P_8	6.14	3.92	11.8	2.36	13.22	3.79	1.81	-0.7	-11.63	-11.79	13.28	12.54	-0.96	-0.96	-2.8
P_1 x P_9	-2.94	-7.25	-4.42	-8.9	-4.49	-9.4	-7.28	-12.78	1.94	-4.45	-7.82	-8.2	5.75	3.21	7.8
P_2 x P_3	-3.61	-11.7	37.32**	28.28**	45.81**	34.73**	13.45	0.73	10.74	5.6	109.27**	95.1**	5.37	-0.31	-3.2
P_2 x P_4	8.72	-0.99	20.25*	10.75*	23.12*	11.89*	14.4	2.3	-6.62	-8.34	85.24**	67.85**	3.59	2.15	-3.5
P_2 x P_5	1.82	-4.9	16.75	9.24	22.09*	13.08*	3.51	-7.26	-21.71	-22.7	55.81**	21.69	9.03	4	4.5
P_2 x P_6	7.15	1.95	21.85*	20.26*	26.3*	23.68*	8.19	1.95	-12.38	-15.5	73.4**	57.25*	-3.14	-5.23	-11
P_2 x P_7	6.17	-2.92	18.1	15.69	19.18	15.53	7.98	2.19	-14.09	-17.63	33.42	11.58	-6.71	-14.46	-16
P_2 x P_8	6.38	0.66	14.29	14.16	15.93	15.13	8.32	-0.49	-0.16	-1.76	36.18	9.47	-5.81	-7.69	-8.4
P_2 x P_9	-12.51	-19.13	-10.9	-14.5	-10.05	-13.82	-4.58	-9.21	3.38	-4.69	-11.02	-28.61	1.61	-2.77	-4.2
P_3 x P_4	4.71	4.71	16.61*	16.61*	18.26	18.26	5.67	5.67	-0.97	-0.97	75.25**	75.25**	0.33	0.33	-5.0
P_3 x P_5	5.46	3.27	5.92	5.74	7.5	7.22	-0.65	-1.67	0.77	-2.72	14.87	-5.22	-0.17	-1.02	2.8
P_3 x P_6	6.93	2.74	14.04	5.24	16.07	5.2	4.4	-2.03	-1.29	-2.44	46.34*	42.03	-1.5	-4.82	-3.0
P_3 x P_7	7.34	7.11	4.41	-0.54	3.51	-1.5	4.01	-2.8	6.84	6.23	19.76	6.47	-3.74	-6.9	-10
P_3 x P_8	4.75	1.22	17.19	9.36	15.64	7.54	2.32	-1.44	0.74	-2.43	52.65**	29.98	1	-2.56	-1.5
P_3 x P_9	-1.26	-2.22	0.42	-2.36	1.75	-2.03	-2.04	-8.94	17.55	13.44	10.73	-5.91	3.58	2.36	2.7
P_4 x P_5	-0.03	-2.73	16.46*	14.5*	16.41	14.03	13.2	12.94	3.75	3.13	28.09	8.37	-4.42	-7.59	-2.6
P_4 x P_6	1.81	-2.79	30.64**	18.88**	35.71**	21.02**	9.21	3.26	-1.94	-3.69	63.65**	63.5*	-9.09	-9.81	-12
P_4 x P_7	0.81	0.36	6.8	0.27	5.9	-0.93	9.99	3.56	25.34	22.38	21.89	11.42	-2.9	-9.81	-1.8
P_4 x P_8	5.49	1.28	27.6**	17.4**	28.69**	17.7**	10.59	7.36	21.08	20.78	40.04*	22.4	3.82	3.16	-2.6
P_4 x P_9	0.24	-1.38	22.4**	17.26**	24.89*	18.18*	4.76	-1.89	21.65	14.12	10.29	-3.79	-2.77	-5.7	-5.8
P_5 x P_6	6.96	4.9	3.97	-3.91	7.05	-2.75	2.24	-3.12	-4.66	-6.92	14.03	-3.59	-3.63	-6.11	-5.4
P_5 x P_7	3.19	0.85	6.14	1.28	6.74	1.83	10.42	4.19	1.55	-1.42	4.82	-3.8	-4.59	-8.47	-6.4
P_5 x P_8	12.46	10.92	35.43**	26.59**	42.06**	32.43**	32.25**	28.67**	18.55	18.14	14.58	10.28	1.81	-0.96	-5.2
P_5 x P_9	-7.34	-8.38	-3.91	-6.41	-2.16	-5.56	0.68	-5.5	-7.32	-13.54	7.23	3.45	-3.04	-3.37	-1.6
P_6 x P_7	1.82	-2.37	14.96	11.18	19.42	13.43	13.07	12.56	31.71	30.93	27.51	16.46	-1.72	-8.04	-4.1
P_6 x P_8	2.79	2.19	19.25*	17.82*	21.13	17.8	-3.95	-6.52	6.92	4.75	15.89	1.22	1.77	1.6	0.6
P_6 x P_9	-1.25	-4.21	18.21*	12.01*	22.15*	14.69*	9.64	8.53	23.82	18.16	62.02**	41.22*	-4.28	-6.43	4.3

Legend: ******Highly significant at P ≤ 0.01 level, *****Significant at P ≤ 0.05 level, **LSD** least significant difference, **PH** Plant height, **BD** Base diameter, **CD** Core diar Middle diameter, **TD** Top diameter, **NN** Number of nodes, **DTFF** Days to 1st flowering, **D50%F** Days to 50% flowering.

Cont'd. (Table 9**)**

Hybrids	PH		BD		CD		MD		TD		NN		DTFF		D5
	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MP
P_7 x P_8	6.67	2.86	7.18	4.88	7.94	5.35	0.59	-2.53	-3.01	-5.53	-6.2	-10.73	-7.03	-13.14	-8.1
P_7 x P_9	7.78	6.51	24.86**	22.25**	30.62**	29.04**	20.77*	20.08	8.65	4.28	14.82	9.02	-9.15	-13.13	-8.5
P_8 x P_9	-1.2	-3.62	11.24	6.64	14.33	10.27	22.6*	18.13	6.39	-0.44	32.91*	32.59	-4.76	-7.05	-5.7
Mean	2.69	-0.93	13.61	8.47	15.97	10.07	5.95	1.13	2.91	0.13	32.84	19.56	-1.03	-3.80	-3.6
LSD5%	35.42	40.90	3.90	4.50	3.88	4.48	2.06	2.38	1.34	1.55	2.11	2.43	4.90	5.66	8.0
LSD1%	46.75	53.98	5.14	5.94	5.12	5.91	2.72	3.14	1.77	2.04	2.78	3.21	6.47	7.47	10.

Legend: **Highly significant at P ≤ 0.01 level, *Significant at P ≤ 0.05 level, **LSD** least significant difference, **PH** Plant height, **BD** Base diameter, **CD** Core diar Middle diameter, **TD** Top diameter, **NN** Number of nodes, **DTFF** Days to 1st flowering, **D50%F** Days to 50% flowering.

Cont'd. (Table 9**)**

Hybrids	FW1		FW2		DSW		DFW		NF		NS		SW	
	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH
P_1 x P_2	35.12	7.74	18.62	-0.11	16.17	4.26	17.29	-2.81	67.52*	32.78	-34.66	-42.18	-0.24	-0.82
P_1 x P_3	46.15*	35.44*	14.88	14.35	12.71	-0.76	27.35*	18.06	73.68**	57.68*	-1.6	-2.65	-0.79	-4.07
P_1 x P_4	32.75*	32.21*	20.74	16.87	65.88**	63.08*	21.72	17.32	103.33**	80.76**	-0.79	-0.91	3.16	-2.39
P_1 x P_5	14.4	-1.28	-5.58	-17.2	19.01	10.01	-8.6	-20.96	6.77	3.31	-17.7	-21.53	-18.76	-23.34
P_1 x P_6	32.48	20.85	14.68	-3.88	30.87	15.22	13.24	-5.98	33.57	26.24	-22.69	-23.21	-9.68	-10.19
P_1 x P_7	43.72*	31.64*	19.4	6.67	17.52	19.08	27.5	2.65	55.99**	33.54	-11.34	-20.68	-4.73	-6.87
P_1 x P_8	18.82	7.44	4.99	-1.66	15.57	14.79	8.34	2.01	77.09**	74.07**	-3.5	-5.75	-2.84	-4.46
P_1 x P_9	-6.28	-7.31	6.9	-4.97	-3.71	-10.03	7.32	-7.83	49.27*	35.33	-8.91	-11.71	-6.59	-8.93
P_2 x P_3	86.42**	58.17**	48.83**	24.85	11.22	-10.74	91.94**	69.82**	24.74	7.12	-29.6	-38.27	0.19	-2.57
P_2 x P_4	37.54	10.02	33.97	9.87	46.66	33.66	48.6**	26.93	85**	62.09*	-20.11	-29.22	0.93	-3.96
P_2 x P_5	60.27*	45.81*	36.2	29.89	35.15	30.87	56.74**	48.97**	41.54	9.51	-17.1	-29.61	-1.51	-6.54
P_2 x P_6	34.01	15.35	48.26*	47.41	24.17	21.5	47.93**	47.55*	30.2	-0.98	8.95	-3.01	-5.27	-5.29
P_2 x P_7	61.86**	38.79**	31.51	22.93	26.19	11.96	53.63**	48.13*	52.07*	7.72	0.27	-0.96	-7.12	-8.67
P_2 x P_8	51.5*	31.48*	18.33	5.51	12.84	0.67	25.93	9.83	108.24**	67.21**	-33.66	-42.48	4.92	3.76
P_2 x P_9	-34.08	-46.99	-4.66	-10.41	1.03	-3.25	3.12	-1.22	6.48	-21.42	-25.59	-35.91	1.64	-0.34
P_3 x P_4	51.33**	51.33**	21.51	21.51	24.69	24.69	25.74*	25.74*	42.51	42.51	-2.54	-2.54	-5.79	-5.79
P_3 x P_5	66.14**	53.72**	32.33	15.59	28.18	5.48	22.39	13.47	51.15*	33.23	-4.12	-7.64	1.18	-1.34
P_3 x P_6	16.52	14.53	10.24	-7.95	17.72	-7.06	12.98	0.18	61.63**	39.5	-7.67	-9.26	-5.69	-8.31
P_3 x P_7	19.7	18.19	19.53	6.35	15.07	2.48	27.25	9.07	9.11	-13.75	-11.29	-21.38	-1.83	-2.93
P_3 x P_8	50.95*	46.97*	10.9	3.43	19.1	5.49	6.79	5.05	73.74**	60.23*	-12.29	-13.43	-12.69	-14.17
P_3 x P_9	-13.98	-19.45	-1.33	-12.64	2.88	-14.55	6.2	-2.29	19.46	-0.65	-1.83	-3.84	-7.11	-7.9
P_4 x P_5	71.51**	48.51**	22.62	4.58	37.23	28.88	29.91*	16.03	49.97*	29.55	-2.58	-7.22	-5.57	-5.84
P_4 x P_6	74.52**	59.79**	46.16**	19.33	66.04*	48.39	36.11*	16.51	108.72**	76.64*	-3.47	-3.99	-0.12	-4.99
P_4 x P_7	14.24	5.03	-0.52	-13.63	20.85	17.3	14.27	-5.29	-20.37	-38.12	-17.34	-25.96	-12.74	-15.61
P_4 x P_8	34.1	21.7	26.45	14.9	44.43	41.06	20.11	17.22	26.79	14.46	0.65	-1.82	-6.26	-9.85
P_4 x P_9	46.56**	45.53**	48.19**	28.04	71.65**	62.98*	46.13**	29.58*	15.61	-5.62	1.48	-1.76	2.63	-0.48
P_5 x P_6	-2.61	-8.44	13.46	7.61	26.37	19.82	20.06	14.38	9.74	7.1	-2.84	-7.96	-9	-13.66
P_5 x P_7	37.76	28.97	29.99	27.28	4.88	-4.2	10.25	1.22	49.22**	31.42	8.53	-6.88	-2.44	-5.91
P_5 x P_8	91.43**	81.65**	56.76**	46.05*	57.78*	44.94	52.34**	39.1*	51.94*	44.6	-20.8	-22.73	-14.93	-18.41
P_5 x P_9	25.67	9.47	9.99	8.29	28.87	27.39	30.04	28.98	30.97	22.42	-12.74	-14.21	-3.09	-6.29
P_6 x P_7	16.64	16.11	12.57	4.66	6.06	-7.66	19.94	15.36	31.5	18.35	-2.28	-12.05	-4.06	-5.68
P_6 x P_8	55.95**	54.44**	15.71	2.65	9.03	-4.56	7.49	-6.05	75.2**	62.92**	-1	-3.94	-4.78	-5.84
P_6 x P_9	44.04*	32.74*	27.75	19.4	31.04	22.9	33.13*	27.83	67.02**	59.8**	-3.99	-7.54	-8.05	-9.85
P_7 x P_8	24.35	22.59	14.78	9.09	14.26	13.54	10.58	-6.51	10.77	-6.52	-19.99	-29.89	-14.65	-15.15
P_7 x P_9	62**	49.91**	35.35	34.59	49.3*	37.83	44.14*	33.33	89.89**	78.09**	-9.79	-21.48	-7.66	-7.91
P_8 x P_9	49.18**	36.25**	9.29	3.32	31.03	21.66	17.07	6.1	49.43*	33.4	-1.11	-1.88	-7.39	-8.18

Mean	37.52	26.36	21.36	10.63	26.05	16.31	25.97	14.76	47.76	29.57	-9.58	-14.87	-4.91	-7.19
LSD5%	358.38	413.82	92.18	106.44	41.34	47.74	5.89	6.80	35.50	40.99	2.65	3.06	1.69	1.95
LSD1%	472.94	546.10	121.64	140.46	54.56	63.00	7.77	8.97	46.85	54.10	3.49	4.04	2.23	2.57

Legend: **Highly significant at $P \leq 0.01$ level, *Significant at $P \leq 0.05$ level, **LSD** least significant difference**, FW1** Fresh stem weight with leaves and pod, **FW2** Fresh stem weight without leaves and pod, **DSW** Dry stick weight, **DFW** Dry fibre weight, **NF** Number of pods per plant, **NS** Number of seeds per pod, **SW** 1000 seeds weight.

Heterobeltiosis response exposed to a pooled environment. Overdominance for heterobeltiosis was seen in the most striking crosses $P_2 \times P_3$ and $P_2 \times P_5$ for fibre yield and the crosses $P_1 \times P_4$ and $P_4 \times P_9$ for stick yield, as shown in Table 9, since their heterobeltiosis values were very significant positive with high potence ratio. For 1st flowering and days to 50% flowering attributes in late maturity cultivars, the crosses $P_2 \times P_5$ and $P_1 \times P_9$ will be the best choice. Due to the presence of over dominance, the seed yield cross $P_1 \times P_4$ was chosen for pods per plant and seeds per pod. Overdominance for heterobeltiosis, as indicated by the potence ratio, was found in the promising crosses $P_2 \times P_3$ and $P_5 \times P_8$ for base diameter and core diameter, cross $P_6 \times P_7$ for top diameter, cross P_5 x P_8 for plant height, middle diameter, fresh stem weight with leaves and pods, cross $P_4 \times P_6$ for base diameter, core diameter, fresh stem weight with leaves and pods, fresh stem weight without leaves and pods, and pods number per plant, and cross $P_2 \times P_6$ for fresh stem weight without leaves and pods. In terms of node number and seed weight, negative heterosis is preferable. Meanwhile, in terms of percentage F_1 heterosis above high parent in node number and 1000 seed weight, crosses $P_2 \times P_9$ and $P_1 \times P_5$ had the lowest negative heterosis values.

Selection of best parents and offspring. The yield and yield contributing components of fifteen parents and crosses were investigated in this study. Table 10 lists the best general and specific combiners based on trait performance. It's always possible that some crosses will work better in some characters than others. To determine the most favorable, rate each on a character-by-character basis and see which ones perform better across the range. When the SCA results of 36 crosses were reviewed, the cross $P_5 \times P_8$ was shown to be the best in ranking for all the characters. $P_7 \times P_9$, $P_1 \times P_3$, $P_2 \times P_3$, $P_1 \times P_7$, $P_4 \times P_8$, and $P_2 \times P_4$ were the next crosses (Table 11). This was possibly due to their greater distance from the others. The performance of the cross $P_5 \times P_9$ was determined to be extremely low. This was because these two genotypes are the most similar. However, based on their cumulative rating, ten superior crossings were selected for inclusion in a future breeding effort. Thirty-six kenaf F_1s were arrayed in order of merit, with the rank total against the crosses indicating the lot's position.

Table 10
Best general and specific combiner for 15 traits

Sl No	Traits	General combiner	Specific combiner
1	Plant height (cm)	P_7 (BJRI Kenaf4)	P_5 (ML36-25) × P_8 (MLRing4 P2)
2	Base diameter (mm)	P_4 (ML36-24)	P_2 (ML9) × P_3 (ML36-10)
3	Core diameter (mm)	P_4 (ML36-24)	P_2 (ML9) × P_3 (ML36-10)
4	Middle diameter (mm)	P_4 (ML36-24)	P_5 (ML36-25) × P_7 (BJRI Kenaf4)
5	Top diameter (mm)	P_4 (ML36-24)	P_6 (ML36-27) × P_7 (BJRI Kenaf4)
6	Number of nodes	P_1 (ML5)	P_2 (ML9) × P_9 (ML36-21(2))
7	Days to first flowering	P_2 (ML9)	P_2 (ML9) ×x P_5 (ML36-25)
8	Days to 50% flowering	P_2 (ML9)	P_6 (ML36-27) × P_9 (ML36-21(2))
9	Fresh stem weight with leaves and pod (g)	P_4 (ML36-24)	P_2 (ML9) × P_3 (ML36-10)
10	Fresh stem weight without leaves and pod (g)	P_4 (ML36-24)	P_5 (ML36-25) × P_8 (MLRing4 P2)
11	Dry stick weight (g)	P_4 (ML36-24)	P_7 (BJRI Kenaf4) × P_9 (ML36-21(2))
12	Dry fibre weight (g)	P_4 (ML36-24)	P_2 (ML9) × P_3 (ML36-10)
13	Number of pods per plant	P_7 (BJRI Kenaf4)	P_7 (BJRI Kenaf4) × P_9 (ML36-21(2))
14	Number of seeds per pod	P_9 (ML36-21(2))	P_2 (ML9) × P_6 (ML36-27)
15	1000 seeds weight (g)	P_2 (ML9)	P_1 (ML5) × P_5 (ML36-25)

Table 11
Rank positions of the F_1·s based on 15 morpho-physiological characters

Crosses	PH	BD	CD	MD	TD	NN	DTFF	D50%F	FW1	FW2	DSW	DFW	NF	NS	SW	Cumulative Rank	Position of crosses
P_1 x P_2	6	17	19	15	27	11	29	31	16	19	21	28	17	34	22	312	26
P_1 x P_3	14	7	6	10	7	33	24	17	9	17	19	6	7	4	28	208	3
P_1 x P_4	23	15	14	14	26	22	33	33	18	15	2	16	3	8	35	277	18
P_1 x P_5	34	30	30	36	17	21	3	10	29	34	26	35	34	26	1	366	34
P_1 x P_6	20	22	17	17	12	26	18	21	14	20	8	19	25	36	6	281	20
P_1 x P_7	3	5	5	26	36	30	4	16	8	8	15	7	10	18	20	211	5
P_1 x P_8	10	19	18	24	34	10	22	24	25	28	28	22	11	5	29	309	25
P_1 x P_9	29	31	33	9	5	4	8	2	33	9	36	14	29	12	14	268	15
P_2 x P_3	30	1	1	4	9	36	7	19	1	2	23	1	23	33	19	209	4
P_2 x P_4	2	12	12	8	23	34	5	12	21	16	10	11	8	25	18	217	7
P_2 x P_5	17	8	8	27	35	35	1	4	12	12	7	4	19	20	21	230	9
P_2 x P_6	5	9	9	12	32	29	25	34	20	6	17	12	24	1	10	245	12
P_2 x P_7	11	10	10	21	33	20	34	36	7	13	6	9	14	3	7	234	10
P_2 x P_8	12	25	26	23	15	17	35	28	17	26	30	26	4	35	36	355	32
P_2 x P_9	36	36	36	33	1	1	17	3	36	36	31	36	35	17	12	366	35
P_3 x P_4	13	18	15	20	30	32	16	26	11	21	27	21	21	13	9	293	21
P_3 x P_5	8	26	25	31	22	7	21	11	6	7	5	23	12	10	34	248	13
P_3 x P_6	7	21	21	16	28	15	20	23	30	30	16	30	13	22	15	307	24
P_3 x P_7	9	27	31	25	21	9	23	32	26	18	14	18	30	24	30	337	29
P_3 x P_8	18	13	22	30	24	31	14	18	15	27	13	33	9	23	4	294	22
P_3 x P_9	32	35	35	22	11	2	11	6	35	33	25	34	27	15	8	331	28
P_4 x P_5	24	11	13	6	18	18	31	20	5	23	29	17	15	11	16	257	14
P_4 x P_6	21	4	4	13	31	28	36	35	2	3	4	10	2	19	31	243	11
P_4 x P_7	27	32	34	18	3	14	15	7	31	35	33	31	36	31	2	349	31
P_4 x P_8	15	6	7	19	8	25	2	14	23	14	12	20	28	7	13	213	6
P_4 x P_9	28	24	23	32	10	3	13	9	27	5	18	8	33	21	27	281	19
P_5 x P_6	4	29	27	28	25	8	28	30	34	31	22	25	31	14	11	347	30
P_5 x P_7	19	23	24	11	19	13	26	27	19	10	35	32	5	2	32	297	23
P_5 x P_8	1	2	2	1	4	16	10	29	3	1	3	2	16	32	5	127	1
P_5 x P_9	33	33	32	29	14	12	32	22	32	32	20	15	20	28	33	387	36
P_6 x P_7	26	14	11	7	2	19	9	15	24	29	32	24	22	16	25	275	17
P_6 x P_8	25	16	16	35	20	6	6	8	10	24	34	29	6	9	24	268	16
P_6 x P_9	31	20	20	5	6	23	12	1	13	11	9	5	18	29	17	220	8

Legend: The lowest value for each character indicates the best one, **PH** Plant height, **BD** Base diameter, **CD** Core diameter, **MD** Middle diameter, **TD** Top diameter, **NN** Number of nodes, **DTFF** Days to 1st flowering, **D50%F** Days to 50% flowering, **FW1** Fresh stem weight with leaves and pod, **FW2** Fresh stem weight without leaves and pod, **DSW** Dry stick weight, **DFW** Dry fibre weight, **NF** Number of pods per plant, **NS** Number of seeds per pod, **SW** 1000 seeds weight.

Crosses	PH	BD	CD	MD	TD	NN	DTFF	D50%F	FW1	FW2	DSW	DFW	NF	NS	SW	Cumulative Rank	Position of crosses
P_7 x P_8	16	28	28	34	29	5	30	25	28	22	24	27	32	30	3	361	33
P_7 x P_9	22	3	3	2	13	24	19	5	4	4	1	3	1	27	23	154	2
P_8 x P_9	35	34	29	3	16	27	27	13	22	25	11	13	26	6	26	313	27

Legend: The lowest value for each character indicates the best one, **PH** Plant height, **BD** Base diameter, **CD** Core diameter, **MD** Middle diameter, **TD** Top diameter, **NN** Number of nodes, **DTFF** Days to 1st flowering, **D50%F** Days to 50% flowering, **FW1** Fresh stem weight with leaves and pod, **FW2** Fresh stem weight without leaves and pod, **DSW** Dry stick weight, **DFW** Dry fibre weight, **NF** Number of pods per plant, **NS** Number of seeds per pod, **SW** 1000 seeds weight.

Discussion

Segregation was seen in 36 crosses for stem color, leaf form, leaf color (lamina), petiole color, pod shape, seed shape, and seed coat color in the F_1 generation. In addition, some of the crosses indicated significant differences in leaf shape and pigmentation pattern on the stem and petiole (Table 3). The parents had green, green with reddish patches, and purple stem color, however the cross combinations had green, green with reddish patches, purple, reddish above greenish below, reddish, and red stem color. When the upper surface light reddish but lower surface green pigmented parent P_7 was crossed with the rest of the green parents, the F_1 showed various pigmentation patterns on the petiole, including green, upper surface light reddish but lower green, reddish, and purple. When the ash grey, brownish, and black with few brownish seed coat color parents crossed, offspring with blackish, ash grey, brownish, and black with few brownish seeds in F_1 were produced. In addition, the leaf form, leaf color (lamina), pod shape, and seed shape of selected parents and their F_1 hybrids showed a wide range of diversity.

Table 4 shows that except for plant height and seeds number per pod, genotypes and environment interaction were highly significant in the pooled quantitative data showed that the environment significantly impacted both parents and offspring for all attributes. We employed nine kenaf genotypes with a range of morpho-physiological and yield features. The mean squares of GCA were bigger than the mean squares of SCA for all traits except top diameter, nodes number, and fresh stem weight with leaves and pods in our investigation indicating that the parental materials studied had a lot of genetic variability. Due to the presence of large additive gene effects, this result usually favors the selection strategy of breeding (Sarker et al., 2003; Sarker and Mian, 2002a). Days to first flowering, fibre weight per plant, and 1000-seed weight were found to indicate the prevalence of additive gene effects in the development of the features by Mostofa et al. (2011). Days to first flowering and plant height were controlled by one dominant gene pair, while raw fibre yield was controlled by three (Thombre and Patil, 1985). For seed yield per plant and number of pods per plant in kenaf, Mukewar et al. (1997) found that additive gene action predominated. For yield components such as plant height, fresh and dry weight of bark, and usable stick in kenaf, Pace et al. (1998) found additive gene action was more relevant. When both general and specific combining ability effects are essential, Comstock et al. (1949) suggested using a reciprocal recurrent selection strategy to generate high yielding varieties. All the examined parameters (excluding plant height, days to 50% flowering, fresh stem weight without leaves and pod) showed a very significant effect on GCA environments, indicating that environmental variation influenced additive gene action. Furthermore, environments had a big influence on how these characters changed (Abu et al., 2017).

The findings revealed that environmental influences controlled the expression of kenaf genetic features. The mean of hybrids is higher than the parental mean for plant height, base diameter, core diameter, middle diameter, top diameter, fresh stem weight with leaves and pod, fresh stem weight without leaves and pod, dry stick weight, dry fibre weight, and number of pods per plant. In comparison to their parents, hybrids have higher fibre and stick yields and a higher seed yield. Days to first flowering and days to 50% flowering of hybrids, on the other hand, were lower than the parental mean, indicating that potential combines with a photo-insensitive variety with high fibre yield. However, the mean hybrid of 1000 seeds weight had a lower mean value than the parental mean, indicating that smaller seed size hybrids were preferable to parents, but that when the number of nodes was larger than the parental mean, the fibre production per plant was reduced. P_1 generated the meanest fibre weight per plant (26.71 g) among the parental lines, followed by P_4 (24.78 g), and P_8 (23.59 g). Similarly, the hybrids $P_2 \times P_3$, $P_4 \times P_6$, and $P_5 \times P_8$ had much greater bast fibre (38.74 g, 28.87 g, and 32.81 g, respectively) than their parents. Parent P_3 produced the meanest stick weight per plant (123.24 g), followed by P_7 (96.26 g), and P_8 (95.06 g). $P_1 \times P_4$, $P_5 \times P_8$, and $P_7 \times P_9$ generated the highest mean stick weight per plant, which was significantly higher than both parents (152.93 g, 137.78 g, and 132.68 g, respectively). The cross combinations $P_1 \times P_4$, $P_4 \times P_6$, and $P_7 \times P_9$ produced the most fruits per plant, 157, 172, and 217, respectively, far exceeding any of the parents, demonstrating the presence of transgressive segregation in the cross.

The results of combining ability analysis are used to select parents and crosses. However, the nature of gene action revealed that both additive and non-additive gene effects were crucial in governing the diverse characters of kenaf in this investigation, but non-additive gene action was shown to control most of the characters. Gupta and Singh (1986) state that non-additive gene activity affects plant height, basal stem diameter, fibre weight per plant, and stick weight per plant (*H. sabdariffa*). Non-additive gene action predominated for all other parameters except days to first flowering, dry fibre weight, and 1000 seed weight. Through pedigree and single seed descent methods of breeding, it is possible to improve traits with a predominance of additive genetic effects. When non-additive gene effects predominated, however, bi-parental mating and a recurrent selective breeding system would be an effective way to obtain hybrid diversity.

Parents' breeding potential is usually linked to their GCA effects. Parents having high GCA effects for certain qualities could be employed as donor parents in hybridization programs to increase these features. A low or negative combining ability effect reflects a plant's inability to pass on its genetic superiority to hybrids (Cruz and Regazzi, 1994). Positive values with the highest magnitudes have the most impact. On the other hand, the greatest negative values have the least impact (Tenkouano et al., 1998). The GCA component is largely caused by additive genetic variance. Therefore, the GCA variation with each parent has a significant influence on the parents' choices. A parent with a higher positive significant GCA effect is an excellent general combiner (Quamruzzaman et al., 2007). GCA's high value for the traits of interest was dispersed across genotypes in this study, indicating that none of the genotypes employed had the best combination of GCA values for the various characters of interest.

Parent P_4 (ML36-24) was the best parental line in terms of base diameter, core diameter, middle diameter, top diameter, fresh stem weight with leaves and pod, fresh stem weight without leaves and pod, dry stick weight, and dry fibre weight content. The major goal of this breeding effort is to create high-yielding hybrids with high potential fibre yield as compared to existing cultivars or on equal with existing cultivars. As a result, for fibre yield per plant, parent P_4 might be well combined. Furthermore, the parent P_3 (ML36-10) had positive effects on plant height, fresh stem weight without leaves and pods, dry stick weight, and dry fibre weight, and the parent P_1 (ML5) was the best general combiner for days to first flowering, dry fibre weight, and number of pods per plant. Other parents are specialised in one or two characteristics. To put it briefly, the parental lines P_1 (ML5), P_3 (ML36-10), and P_4 (ML36-24) were determined to be outstanding general combiners for fibre (bast fibre) yield and yield-related parameters. Parents P_3 (ML36-10) and P_4 (ML36-24) were good general combiners in terms of stick (core fibre) yield. The parents P_1 (ML5), P_6 (ML36-27), and P_7 (BJRI Kenaf4), on the other hand, were good general combiners for seed yield (pods number per plant). In contrast, parent P_2 (ML9) was chosen as a good general combiner for the first flowering and days to 50% flowering features, which are important for late maturity cultivars.

Parents with a high GCA for a certain trait and high adaptability indicate additive gene action. Because additive variance may be fixed, selecting for qualities regulated by additive variance is a very effective strategy (Singh and Narayanan, 1993). The parents P_3 and P_4 were found to be the finest general combiners, with extremely significant values for fresh stem weight without leaves and pod, dry stick weight, and dry fibre weight, all of which are more suitable for desired kenaf features such as bast fibre and core fibre production. The parents with the highest GCA values (strong GCA effects) could be used to improve the kenaf population in Malaysia through varietal development based on desirable features.

Crosses with high x low general combiners for yield components perform better in general. High specific combiners involved high × high, high × low, high × average, average × average, average × low, and low × low combining parents, according to an analysis of combining ability effects. Jinks (1956) described strong SCA effects because of over-dominance and epistasis in crosses with high x low and low x low general combiners. Crosses involving high x low general combiners for yield components with negative SCA effects were caused by mutual cancellation of heterosis components, namely dominance and its interaction (Hayman, 1958). Crossing two parents with low × low general combiners produces high performance, attributed to complementary gene action (Mohndiratta, 1968). SCA effects were found to be significant for most yield characteristics in this study. For base diameter, core diameter, fresh stem weight with leaves and pod, and fresh stem weight without leaves and pod, the best crossings suggested by SCA effects (Table 8) were $P_2 \times P_3$, $P_4 \times P_6$, and $P_5 \times P_8$.

In contrast, the hybrids P_2 (ML9) × P_3 (ML36-10) and P_5 (ML36-25) × P_8 (MLRing4 P2) were shown to be the best specific combiners for fibre (bast fibre) yield, with high base diameter, core diameter, fresh stem weight with leaves and pod, and fresh stem weight without leaves and pod features. Furthermore, for stick (core fibre) yield and seed yield (plant number of pods), the hybrids P_1 (ML5) × P_4 (ML36-24) and P_7 (BJRI Kenaf4) × P_9 (ML36-21(2)) were chosen as the best specific combiners. The hybrid P_2 (ML9) × P_5 (ML36-25) will be the best choice for 1st flowering and days to 50% flowering attributes in late maturity cultivars. In terms of another feature, the rest of the hybrids performed better. The strongest positive estimations of mid-parent and better-parent heterosis for the qualities examined, indicating the accumulation of favourable genes inherited from their parental inbred lines. Among the hybrids produced, P_2 (ML9) × P_3 (ML36-10), P_5 (ML36-25) × P_8 (MLRing4 P2), P_4 (ML36-24) × P_6 (ML36-27), P_1 (ML5) × P_4 (ML36-24), P_7 (BJRI Kenaf4) × P_9 (ML36-21(2)), P_2 (ML9) × P_5 (ML36-25), P_2 (ML9) × P_9 (ML36-21(2)) and P_1 (ML5) × P_5 (ML36-25) had higher yield and yield component qualities indicated by hybrids evaluated based on pooled data from the two environments.

For dry stick weight and number of pods per plant, hybrids $P_1 \times P_4$ and $P_7 \times P_9$ were chosen as the best specific combiners. Days to first flowering and days to 50% flowering were also chosen as unique combiners for the hybrid $P_2 \times P_5$. In addition to their good SCA effects, the hybrids $P_4 \times P_9$ and $P_6 \times P_9$ were considered for days to 1st flowering and days to 50% flowering. The hybrids $P_1 \times P_3$ and $P_4 \times P_5$ hybrids were chosen as the best specific combiners for fresh stem weight with leaves and pod, while $P_1 \times P_3$ was also chosen for number of seeds per pod trait. The hybrids $P_1 \times P_8$, $P_2 \times P_6$, $P_2 \times P_7$, and $P_5 \times P_7$ were chosen as good specific combiners for number of pods per plant and number of seeds per pod, respectively. The hybrids $P_1 \times P_5$, $P_3 \times P_8$, $P_4 \times P_7$, and $P_7 \times P_8$ were chosen as good specific combiners for another desired characteristic 1000 seed weight (smaller seed size). The GCA effects of parents were not related to the SCA impacts of their crosses, which had the highest significant positive magnitude, according to the findings. It's possible that these crossovers' high SCA effects are due to complementary gene effects. According to Moll and Stuber (1974), any combination of parents can result in hybrid vigour, which could be due to dominant, over-dominant, or epistatic gene action.

Table 9 shows estimates of mid-parent and better-parent heterosis for yield and yield component qualities indicated by hybrids evaluated based on pooled data from the two environments. Liu (2005) noticed a lot of heterosis in yield characteristics based on the mid-parent and better-parent. Heterosis estimates based on midparental values were generally high, with stalk dry weight and bast percentage ranging from 10–55% (Behmaram et al., 2014). The strongest positive estimations of mid-parent and better-parent heterosis for the qualities examined were derived from $P_4 \times P_6$ based on the combined data of the two environments (108.72% and 76.64%, respectively for the pods number per plant). $P_2 \times P_3$ showed the greatest mid-parent and better-parent heterosis for 5 of the 15 phenotypic parameters measured, including base diameter, core diameter, nodes number, fresh stem weight with leaves and pods, and dry fibre weight, based on the combined data from the two environments.

In addition, $P_5 \times P_8$ had the second highest mid-parent and better-parent heterosis for base diameter, core diameter, middle diameter, fresh stem weight with leaves and pods, fresh stem weight without leaves and pods, and dry fibre weight, as well as $P_4 \times P_6$ for base diameter, core diameter, fresh stem weight with leaves and pods, fresh stem weight without leaves and pods, and pods number per plant. In terms of the features indicated, these hybrids outperformed their inbred parents. Furthermore, the hybrids $P_1 \times P_4$ and $P_7 \times P_9$ were chosen as the best combiners for stick yield and seed yield (pods number per plant). In late maturity cultivars, the hybrid $P_2 \times P_5$ will be the best choice for 1st flowering and days to 50% flowering features.

In contrast, $P_2 \times P_9$ for Plant height, base diameter, core diameter, and fresh stem weight with leaves and pods showed low mid-parent and better-parent heterosis estimates, followed by $P_1 \times P_5$ for middle diameter, fresh stem weight without leaves and pods, and dry fibre weight, where the high values were unfavourable. Higher heterosis values compared to the better parent and the mid-parent suggested the absence of epistasis and the frequency of partial or total dominance of genes for fibre and seed yield. Crosses that produce superior transgressive segregants with higher fibre production could be found by looking at the percent F_1 heterosis over the high parent.

The strongest positive estimations of mid-parent and better-parent heterosis for the qualities examined, indicating the accumulation of favorable genes inherited from their parental inbred lines. Among the hybrids produced, P_2 (ML9) × P_3 (ML36-10), P_5 (ML36-25) × P_8 (MLRing4 P2), P_4 (ML36-24) × P_6 (ML36-27), P_1 (ML5) × P_4 (ML36-24), P_7 (BJRI Kenaf4) × P_9 (ML36-21(2)), P_2 (ML9) × P_5 (ML36-25), P_2 (ML9) × P_9 (ML36-21(2)) and P_1 (ML5) × P_5 (ML36-25) had higher yield and yield component qualities indicated by hybrids evaluated based on pooled data from the two environments. Both additive and non-additive genetic components were essential in the control of many morphological and yield-related characters, with non-additive gene activities predominating for most of the characters.

Conclusion

In this study, additive and non-additive variations had a role in the genetic control of all variables, including fibre yield and yield-related characteristics. New high-yielding kenaf hybrid types could be released via diallel selective mating or mass selection with simultaneous random mating. GCA effects were higher than SCA effects, except for top diameter and number of nodes, as demonstrated by mean squares, showing that additive gene action predominates for these traits. Fiber yield (bast fibre and core fibre) and seed yield (number of pods per plant) are two important characteristics of kenaf production. Parent P_4 (ML36-24) was the best general combiner for fibre yield (bast fibre) based on GCA performance, followed by P_1 (ML5) and P_3 (ML36-10). Conversely, P_4 (ML36-24) was the best general combiner for stick yield (core fibre), followed by P_3 (ML36-10). For the number of pods per plant (seed yield), P_7 (BJRI Kenaf4) was shown to be the best general combiner, followed by P_6 (ML36-27) and P_1 (ML5). For days to 1st flowering and days to 50% flowering qualities, P_2 (ML9) was chosen as an excellent general combiner. In a breeding programme, the hybrids P_2 (ML9) × P_3 (ML36-10), P_4 (ML36-24) × P_6 (ML36-27), and P_5 (ML36-25) × P_8 (MLRing4 P2) will be the best for bast fibre and P_1 (ML5) × P_4 (ML36-24), P_5 (ML36-25) × P_8 (MLRing4 P2), and P_7 (BJRI Kenaf4) × P_9 (ML36-21(2)) will be the best for core fibre if fibre yield is the most significant selection factor. If seed yield is important in the breeding programme, the hybrids P_1 (ML5) × P_4 (ML36-24), P_4 (ML36-24) × P_6 (ML36-27), and P_7 (BJRI Kenaf4) × P_9 (ML36-21(2)) will be the best choices for number of pods per plant, and the hybrid P_2 (ML9) × P_5 (ML36-25) will be the best choice for days to first flowering and days to 50% flowering traits for late maturity cultivars. The strongest positive estimations of mid-parent and better-parent heterosis for the qualities examined, indicating the accumulation of favorable genes inherited from their parental inbred lines. Among the crosses, P_1 (ML5) × P_4 (ML36-24), P_2 (ML9) × P_3 (ML36-10), P_2 (ML9) × P_5 (ML36-25), P_4 (ML36-24) × P_6 (ML36-27), P_5 (ML36-25) × P_8 (MLRing4 P2), and P_7 (BJRI Kenaf4) × P_9 (ML36-21(2)) hybrids were found to be promising for their heterotic response and could be useful by adopting proper strategies for future improvement in kenaf breeding programmes.

Declarations

Acknowledgements

The authors would like to express their heartfelt gratitude to the Bangladesh Agriculture Research Council (BARC) and Universiti Putra Malaysia (UPM) for allowing them to conduct this research. The authors are also grateful to the Bangladesh Jute Research Institute (BJRI) and the Ministry of Agriculture of the People's Republic of Bangladesh for referring the lead author to UPM for a PhD programme.

Author’s Contributions

Conceptualization, Md Al-Mamun and Mohd Y. Rafii; Data curation, Md Al-Mamun and Md Mahmudul Hasan Khan; Formal analysis, Md Al-Mamun; Funding acquisition, Md Al-Mamun, Mohd Y. Rafii and Md Mahmudul Hasan Khan; Investigation, Mohd Y. Rafii, Zulkarami Berahim, Azizah Misran and Zaiton Ahmad; Supervision, Mohd Y. Rafii; Writing – original draft, Md Al-Mamun; Writing – review & editing, Zulkarami Berahim, Md Mahmudul Hasan Khan and Yusuff Oladosu. All authors have read and agreed to the published version of the manuscript.

Conflicts of Interest

The authors announce no conflict of benefits.

Funding

This work was supported by the Bangladesh Agriculture Research Council, Ministry of Agriculture, Bangladesh [PIU-BARC, NATP-2], and Universiti Putra Malaysia under the research grant vote number 6282507.

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Figures

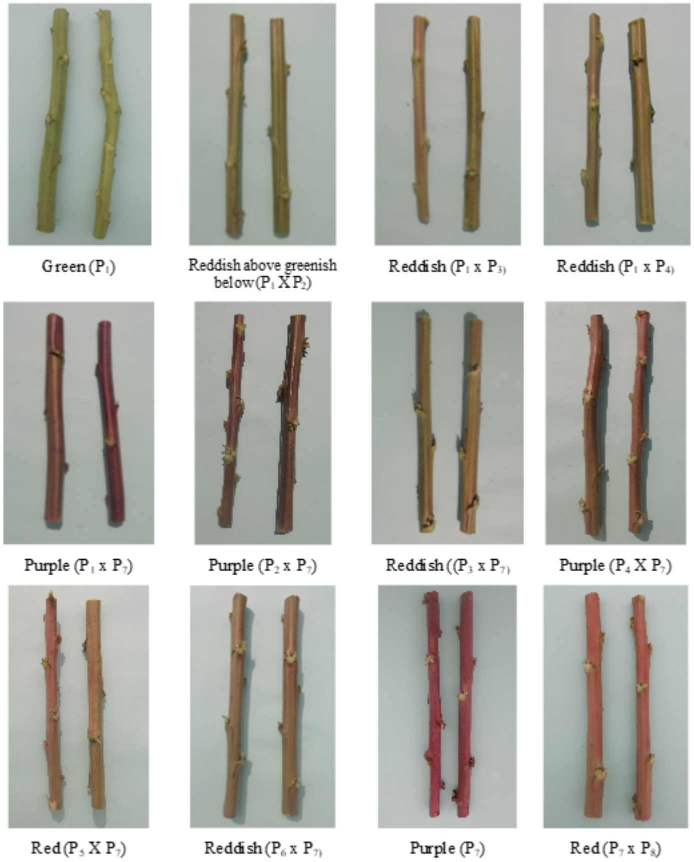

Figure 1

Photographs of the parents' and F_1 pop's stem coloration (70 DAS)

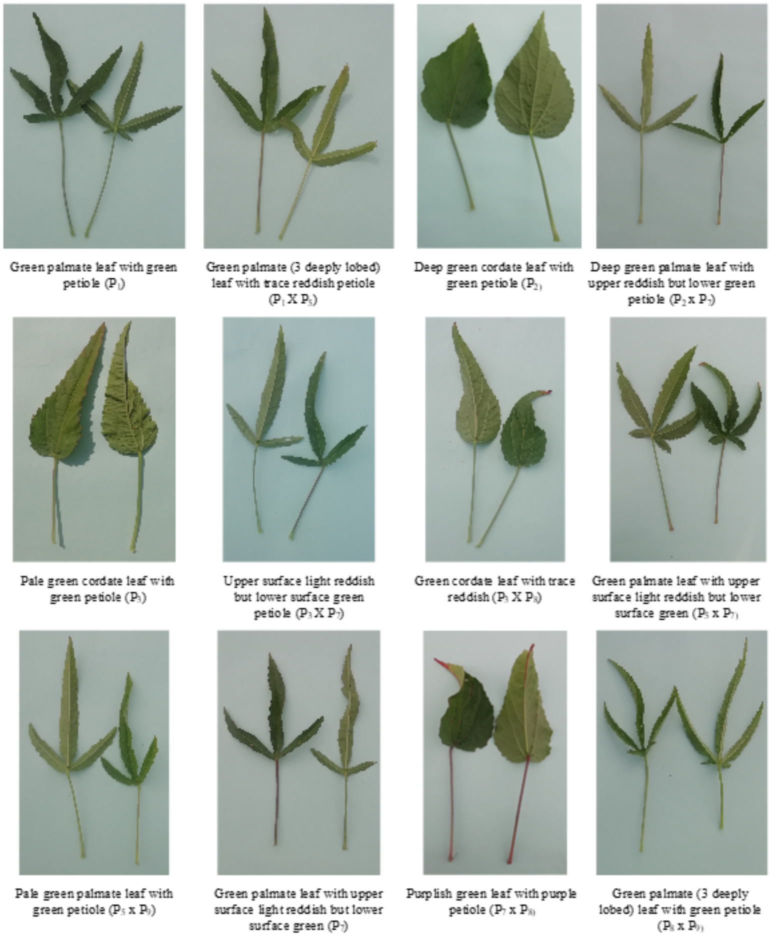

Figure 2

Photographs of the parents' and F_1 pop's leaf shapes and coloration

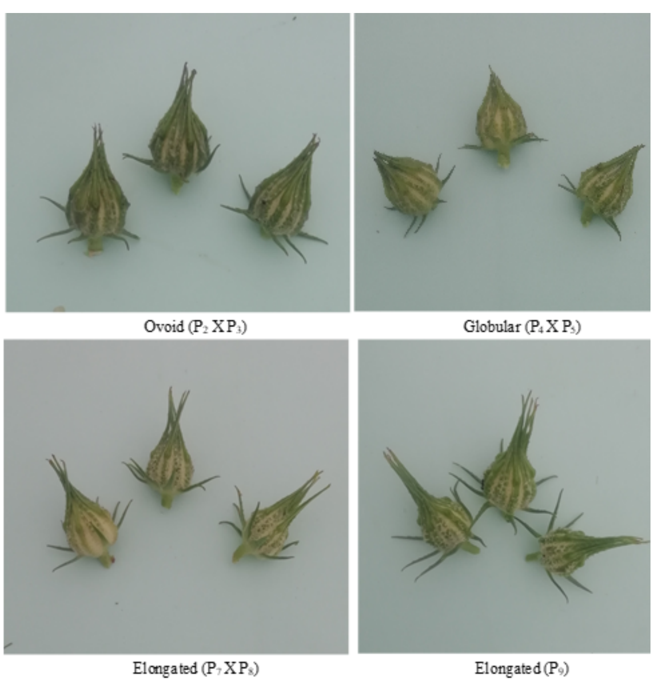

Figure 3

Photographs depicting the color of various kenaf accessions' pods

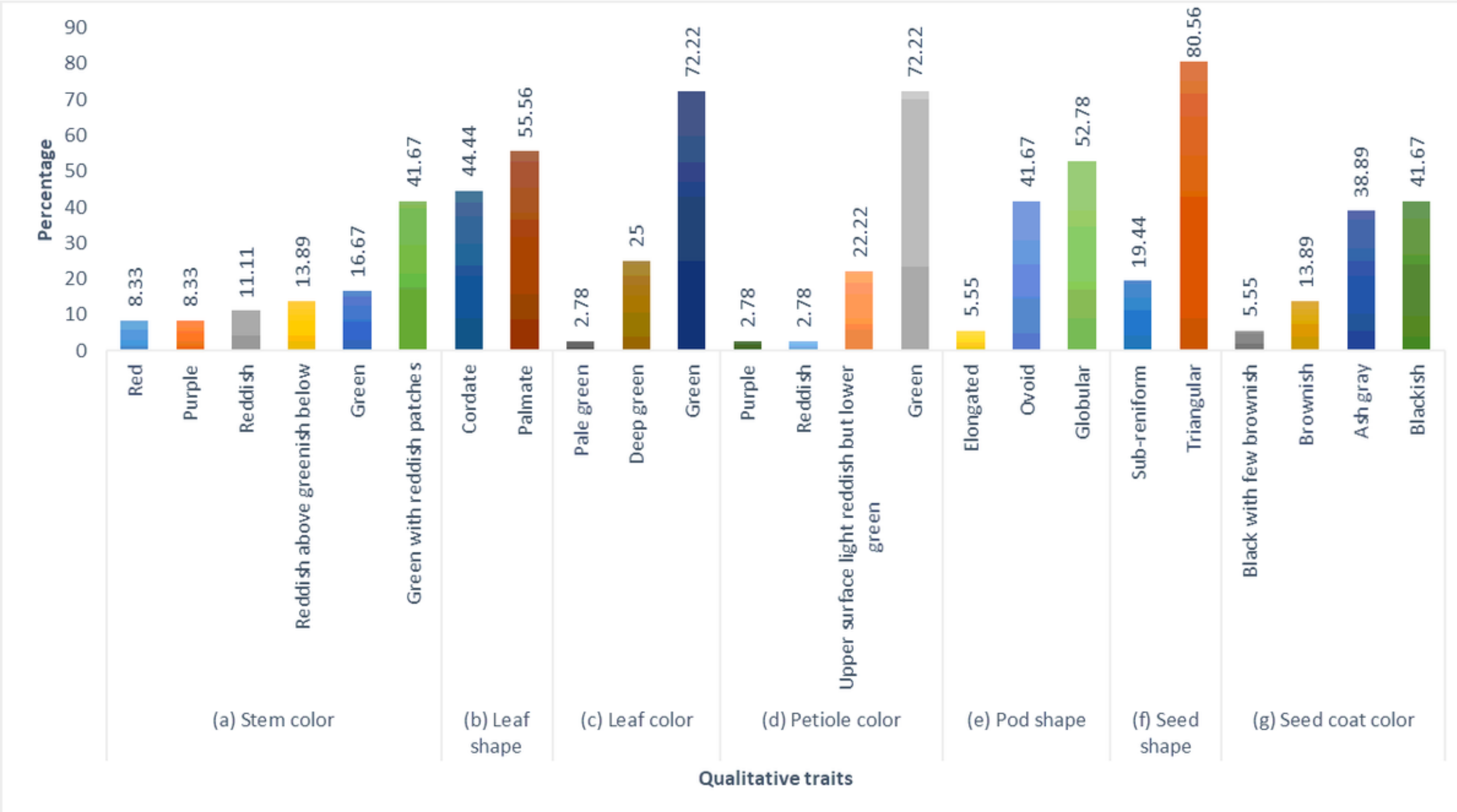

Figure 4

Some qualitative characters' variation (a) Stem color (b) Leaf shape (c) Leaf color (lamina) (d) Petiole color (e) Pod shape (f) Seed shape and (g) Seed coat color.

Supplementary Files

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