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Heterosis and Combining Ability Estimate on Yield and Yield-Related Traits in a Half Diallel Crosses of Kenaf (*Hibiscus Cannabinus* L.) in Malaysia

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ABSTRACT

Understanding heterosis and combining ability among distinct kenaf (*Hibiscus cannabinus* L.) genetic resources is crucial for developing hybrid kenaf. An investigation was conducted on 36 F₁ combinations produced from nine parental genotypes of kenaf in a diallelic scheme using Griffing diallel analysis technique 2, model I. Highly significant F-test values revealed the presence of variability for all the 15 quantitative traits for general combining ability (GCA) and specific combining ability (SCA) except days to 1st flowering. The magnitude of GCA variance was considerably higher than that of SCA variance for plant height, stem middle diameter, stem top diameter, days to flowering, number of pods, number of seeds and 1000 seeds weight, showing the predominates of additive gene for these traits. Narrow-sense heritability of 50.93% in the combined environments showed that seed number was the most heritable trait, whereas days to 1st flowering and 1000 seed weight had moderate heritability. Parents P₁, P₃ and P₄ had the most dominant alleles for most traits studied. Considering SCA and heterosis values, the hybrids H3, H4, H9, H11, H23, H29 and H35 had high heterotic for fiber and seed yield.

摘要



了解不同红麻(*Hibiscus cannabinus* L.)遗传资源之间的杂种优势和配合力对于发展杂交红麻至关重要。使用Griffing双列杂交分析技术2, 模型I, 以双列杂交方案对9种红麻亲本基因型产生的36个F₁组合进行了研究。高度显著的F检验值显示, 除第一次开花的天数外, 所有15个数量性状的一般配合力(GCA)和特异配合力(SCA)都存在变异。在株高、茎中直径、茎顶直径、开花天数、荚数、种子数和1000粒种子重量方面, GCA方差显著高于SCA方差, 表明这些性状以加性基因为主。组合环境中50.93%的狭义遗传力表明, 种子数量是最具遗传性的性状, 而第一次开花天数和1000粒种子重量具有中等的遗传力。在所研究的大多数性状中, 亲本P₁、P₃和P₄具有最多的显性等位基因。考虑到SCA和杂种优势值, 杂交种H3、H4、H9、H11、H23、H29和H35在纤维和种子产量方面具有较高的杂种优势。


KEYWORDS

Kenaf; combining ability; hybrid development; diallel analysis; Griffing approach; Hayman's approach

关键词

红麻; 配合力; 混合发展; 二烯丙基分析; 欺诈方法; 欺诈方法

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Introduction

Kenaf is a significant crop primarily used for a range of pulp and paper products. Recently, it has been recognized as a valuable dual-purpose crop for seeds and stem fibers, with several bioactive components including phytosterols, tannins, tocopherols, saponins, phospholipids, polyphenols, fatty acids, and alkaloids and has long been used in medicine to treat fever, bruising, and bilious disorders (Alexopoulou et al. 2015). The combination of high market demand with comparatively low production costs and excellent yields has sparked significant interest among farmers in kenaf cultivation. Even though the current cultivars can produce high biomass yields, there is a desire further to improve productivity and fiber quality through breeding activities. This is because genetic gains can be exploited without a consequent increase in the cost of crop production, which is an attractive prospect.

The concept of heterosis or hybrid vigor was discovered by Darwin (1876) and described as hybrid F1 offspring showing phenotypic superiority over both parents. As established by rice (Ab Halim et al. 2021), eggplant (Datta et al. 2021), and pumpkin (Hosen et al. 2022), heterosis in plants can be linked to the interaction between many loci, depending on hybrids and characteristics. Therefore, the utilization of heterosis is crucial for agricultural production. The breeding process suggests that the parents' performance is inconsistent with the performance of the hybrid. Not all outstanding hybrid types are developed from outstanding parents. Therefore, breeders should evaluate a parental line based on its potential to create superior hybrids rather than solely on its performance. To discover parental lines with high hybridization potential, combining ability has been estimated and used to select desirable parents and, consequently, their hybrids. Specific combining ability (SCA) and general combining ability (GCA) are two types of genetic parameters that may be predominantly caused by non-additive and additive gene actions, respectively (Zhang et al. 2015). SCA for a certain cross or hybrid is the deviation of the hybrid performance from what can be predicted by the parental GCA (Mühleisen et al. 2013). GCA evaluation is typically conducted during early generations or breeding stages to save time and money. Depending on characteristics and hybrids, the proportional contribution of GCA and SCA impacts to hybrid performance varies, with GCA effects being more significant than SCA effects (Fujimoto et al. 2018; Zhang et al. 2013). Evaluating GCA is undoubtedly a laborious and time-consuming operation, which has become one of the most significant limitations in hybrid breeding programmes.

To breed ideal hybrids with high fiber yield, heterosis and combining ability of available germplasm with few parental lines have been investigated. Combining ability and Heterosis are typically estimated by populations derived from special genetic designs, such as diallel (Griffing method) and the NCD II (North Carolina design II), which are two of the most powerful genetic designs for analyzing combining ability and have been widely applied. However, additional research is necessary due to the great genetic diversity present in kenaf germplasm, which could contribute to further genetic improvement. Consequently, a large-scale analysis of heterosis and combining ability using diverse germplasm resources will significantly improve our understanding of hybrid performance, thereby contributing to an increase in genetic gain in kenaf hybrid breeding. This work aimed to use diallel analysis to quantify morpho-physiological parameter genetic variation and determine whether different kenaf mutants in tropical climates have different patterns of morpho-physiological parameter combining abilities. The primary goal of this study was to identify genotypes (parents and offspring) with good combining abilities that could assist future kenaf improvement with high yield.

Materials and methods

Experimental location

The field experiment was conducted in two seasons in a humid tropical climate between latitude 2°59' N and longitude 101°42' E, at 48 m above sea level at Serdang, Selangor, in Malaysia. The first season lasted from June to September 2020, while the second lasted from March to June 2021. The maximum and minimum mean monthly temperatures (°C), total rainfall (mm), and relative humidity for the experimental periods are shown in Table 1.

Table 1. Daily solar radiation, humidity, Maximum and minimum temperatures, and average precipitation of the 2020/2021 season from planting to physiological maturity.

Planting season	Duration	Daily solar radiation (MJ/m ² /d)	Relative humidity (%)	Temperature (°C)		Average precipitation (mm)
				Maximum	Minimum	
First season	June – September'2020	17.83	86.21	28.78	23.19	225.30
Second season	March – June'2021	18.10	83.50	30.15	23.55	171.19

Source: Agrobiodiversity & Environment Research Center, MARDI, Selangor, Malaysia (2021).

Breeding materials

Nine genotypes were selected as parental materials (Table 2) and mated in a diallel design, avoiding the reciprocal crosses. The nine genotypes were crossed in a diallel mating scheme, yielding 36 one-way F_1 hybrids. H1 is referred to as the first cross in half diallel, i.e., H1 ($P_1 \times P_2$) until H36 ($P_8 \times P_9$), as presented in Table 3. F_1 seeds were gathered using typical emasculation and pollination techniques.

Plant Husbandry

Kenaf seeds from 45 entries were planted in peat moss soil in germination trays, consisting of nine parents and 36 F_1 generations. The field was mechanically plowed and laddered for cultivation. There were 135 plots, each measuring $60 \times 80 \text{ cm}^2$ with a distance of $10 \times 40 \text{ cm}^2$ inter and intra-row spacing, and the entire plots measured $59 \times 9 \text{ m}^2$. NPK Green (15:15:15) and NPK Blue (12:12:17) fertilizers were applied at a rate of 450 kg per hectare shortly after seeding and 40 days after planting, following Wong et al. (2008). All recommended cultural practices for raising a healthy crop were followed. Data was collected on fifteen traits from a random ten plants for each genotype per replication.

Statistical analysis

Analysis of variance (ANOVA) was performed using the PROC GLM of the SAS version 9.4 to establish the significance of variation among genotypes and blocks. In addition, a separate ANOVA from 9×9 diallel (F_1 and parents) was performed for each environment, eliminating reciprocals as indicated by Steel and Torrie (1980). Finally, the Least Significant Difference (LSD) was used to compare the mean performances among hybrids and paternal lines.

Table 2. Origin of nine selected kenaf genotypes used as parents for diallel cross.

Genotype code	Accession/variety	State	Mutagenesis source (GY)	Origin
P ₁	ML5	Mutant line (M ₇)	Acute (300)	MNA
P ₂	ML9	Mutant line (M ₇)	Acute (300)	MNA
P ₃	ML36–10	Mutant line (M ₆)	Acute (300)	MNA
P ₄	ML36–24	Mutant line (M ₆)	Acute (1300)	MNA
P ₅	ML36–25	Mutant line (M ₆)	Acute (1300)	MNA
P ₆	ML36–27	Mutant line (M ₆)	Acute (1300)	MNA
P ₇	BJRI KENAF4	Release variety	Conventional method	BJRI
P ₈	MLRing4 P2	Mutant line (M ₆)	chronic	MNA
P ₉	ML36–21(2)	Mutant line (M ₆)	Acute (800)	MNA

Legend: MNA, Malaysian Nuclear Agency; BJRI, Bangladesh Jute Research Institute.

Table 3. Represents the 36 cross or hybrid combinations that resulted from the half diallel mating design.

	P ₂	P ₃	P ₄	P ₅	P ₆	P ₇	P ₈	P ₉
P ₁	H1	H2	H3	H4	H5	H6	H7	H8
P ₂		H9	H10	H11	H12	H13	H14	H15
P ₃			H16	H17	H18	H19	H20	H21
P ₄				H22	H23	H24	H25	H26
P ₅					H27	H28	H29	H30
P ₆						H31	H32	H33
P ₇							H34	H35
P ₈								H36

Estimation of heterosis

The relative heterosis (MP) and heterobeltiosis (BP) forms of heterosis were determined and expressed as percentages (Mather and Jinks 1971). The difference between the mean of F₁ hybrids and the mid-parental value for a given trait was used to calculate heterosis (Rai 1979).

Combining ability analysis

First, the combining ability ratio was calculated according to Baker (1978). Modified Hayman ANOVA was computed according to Hayman (1954) following Jones (1965) modification. All analyses were performed using the “AGD-R” (Rodriguez et al. 2018) and “R software” (R Core Team 2020). The genetic system influencing important kenaf features, general and specific combining ability has been studied.

Diallel analysis by Griffing’s method

The GCA of parents and SCA of hybrids were determined by Griffing’s method 2 model 1 (fixed effects) (Griffing 1956). According to Zhang and Kang (2003), the linear model for data from each kenaf attribute in each environment were studied.

Diallel analysis - Hayman’s approach

The main features of Hayman’s approach: are (i) Hayman’s ANOVA; (ii) Vr, Wr analysis with graphical representation; and (iii) Components of variation and genetic parameters.

Hayman’s ANOVA and Morley Jones modification

Using the same model as Hayman, the determination of the sums of squares corresponding to additive effects (a), and on the assumption of no epistasis to mean dominance (b₁), to additional dominance effects that can be accounted for by genes with one allele present in only one line (b₂) (the remaining *n*-1 lines being assumed to carry the same alternative allele), and to residual dominance effects (b₃), is in essence a straightforward application of fitting constants by least squares. Hayman (1954) and Jinks (1954) were used to determining the genetic and environmental components of variation and allied or related genetic factors in F₁.

Results

Combining ability analysis of kenaf hybrids for yield and yield components

Combining ability effects by Griffing’s method

For all analyzed qualities in the F₁ individually (Table 4) for both environments, ANOVA was used for combining ability using Griffing’s (1956) technique. Highly significant mean squares influenced the

Table 4. Half diallel analyses on the analyzed features in two environments using Griffing’s Method 2.

S.O.V	GCA		SCA		Error		GCA/SCA	
	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2
DF	8		36		88			
PH	4271.90**	2604.07	1214.27**	415.38	320.23	967.92	3.52	6.27
SBD	54.24**	35.15	62.60**	7.49	6.94	8.66	0.87	4.69
CD	48.31**	31.10	63.98**	7.56	7.17	8.29	0.76	4.11
SMD	13.61**	10.59	7.22**	1.86	1.52	2.85	1.89	5.69
STD	1.35**	2.35	1.11**	1.53	0.17	1.66	1.22	1.54
NN	11.08**	2.42	19.68**	1.54	2.82	1.73	0.56	1.57
DTFF	126.12**	106.23**	25.87	12.41**	16.52	8.15	4.88	8.56
D50%F	97.58**	221.51	58.34**	47.89	16.75	49.49	1.67	4.63
FW1	632640.81**	418094.2	828108.02**	106164.9	24335.52	107506.2	0.76	3.94
FW2	21635.6**	28799.3	22257.7**	3097.7	1854.3	6868.01	0.97	9.30
NF	12075.56**	2145.52*	10297.52**	1001.08	395.88	897.93	1.17	2.14
NS	89.14**	178.02**	65.30**	30.04**	1.26	5.93	1.37	5.93
SW	60.10**	39.21**	17.08**	14.89**	0.78	2.14	3.52	2.63
DSW	1562.64**	7773.80	2651.59**	1893.84	141.55	1612.93	0.59	4.10
DFW	178.16**	108.70	198.39**	17.16	11.86	23.73	0.90	6.33

inheritance of the analyzed traits for GCA in all studied traits in the 1st environment. However, fewer traits showed significant mean squares in the 2nd environment, indicating that additive gene activity is essential and displayed differently in various environments. In 1st environment, SCA effects were significant for all traits except for days to 1st flowering. Meanwhile, in 2nd environment, SCA effects were highly significant for days to 1st flowering, seeds number and 1000 seed weight measured. For seeds number, and 1000 seed weight, the additive and non-additive effects are significant, indicating that the traits were affected by both dominant and additive gene actions. The ratio of GCA and SCA changes was less than unity for stem base diameter, core diameter, nodes number, stem weight with leaves and pod, fresh stem weight, dry stick weight and dry fiber weight in the 1st environment, indicating that non-additive gene action predominated. The GCA/SCA estimates for the other characters in the 1st environment and all characters in the 2nd environment were both more than one, indicating that additive gene effects dominated their expression.

General combining ability (GCA) of kenaf genotypes for yield and yield components

The GCA influences of individual parental genotypes in the F₁ generation were statistically significant or highly significant for most variables. In both environments (Table 5), parent P₄ was discovered to be the best general combiners, with highly significant values for stem base diameter, stem middle diameter, fresh stem weight, seeds per pod, dry stick weight and dry fiber weight, all of which are more suitable for desired kenaf features such as fiber and stick production. The parents P₅ and P₉ were demonstrated to be positive and significant general combiners for seed number per pod in the 1st and 2nd environments, respectively. In the 1st and 2nd environments, Parent P₂ exhibited the most favorably significant GCA effect for days to 1st flowering (2.01 and 2.66) and for days to 50% flowering (1.86 and 4.13). Parent P₇ showed the lowest negatively significant effect for days to 1st flowering (−4.54 and −2.92) and days to 50% flowering (−3.90 and −3.87), respectively. Parent P₃ also had a positive and highly significant GCA effect on plant height (12.03) and seeds number (1.27) during the 1st environment, as well as stem middle diameter (0.97) and dry stick weight (25.76) during the 2nd environment.

Except for the number of nodes and 1000 seed weight, where the opposite situation is desirable, i.e., significant negative values would be advantageous from a breeder’s perspective, substantial positive GCA impacts would be favorable for all examined variables. In this regard, P₂ and P₇ in the 1st environment functioned as a highly significant negative general combiner for a number of nodes, whereas P₅ and P₇ in the 1st environment, also P₆ and P₈ in the 2nd environment had the highest

Table 5. Effects of nine parental kenaf genotypes on general combining ability in two separate environments.

Traits	Env	P ₁	P ₂	P ₃	P ₄	P ₅	P ₆	P ₇	P ₈	P ₉	LSD (gi-gj)		
											5%	1%	%
PH	Env1	-12.74**	-20.18**	12.03**	5.89	0.81	3.77	15.44**	0.72	-5.73	5.84	7.75	
	Env2	-6.14	-13.48*	5.98	12.34*	-1.63	-8.42	10.34	5.14	-4.14	10.16	13.47	
	Env2	-0.34	-0.81	0.27	3.10**	0.63	-0.94	3.10**	-0.27	-0.78	0.86	1.14	
SBD	Env2	1.38*	-0.36	1.34*	1.22*	-0.52	-0.76	-0.62	-0.32	-1.37*	0.96	1.27	
	Env1	-0.56	-0.74	0.20	2.86**	0.88	-0.89	-0.62	-0.36	-0.75	0.87	1.16	
	Env2	1.38*	-0.27	1.28*	1.01	-0.53	-0.79	-0.60	-0.22	-1.26*	0.94	1.25	
SMD	Env1	-0.53*	-0.92**	-0.27	0.71**	0.94**	-0.53*	0.08	0.64*	-0.13	0.40	0.64*	
	Env2	0.13	-0.75*	0.97**	0.70*	-0.07	-0.07	0.07	0.07	-0.68*	0.55	0.73	
	Env1	-0.04	-0.18*	-0.32**	0.22*	0.01	-0.14	0.08	0.34**	0.13	0.13	0.18	
STD	Env2	-0.27	-0.18	0.38	0.14	-0.12	0.28	-0.06	0.23	-0.39	0.42	0.56	
	Env1	0.53	-0.71*	-0.34	0.11	0.58	0.41	-0.67*	0.68	-0.60	0.55	0.73	
	Env2	0.37	-0.03	0.22	-0.04	0.09	-0.50	-0.18	-0.20	0.27	0.43	0.57	
DTFF	Env1	0.98	2.01*	-0.49	0.69	1.04	1.05	-4.54**	-0.16	-1.37*	1.33	1.76	
	Env2	2.05**	2.66**	-0.49	0.71	-1.49*	1.05	-2.92**	0.93	-1.37*	0.93	1.24	
	Env1	0.07	1.86*	-0.84	1.31	1.43	-0.05	-3.90**	0.56	-0.44	1.34	1.77	
D50%F	Env2	2.07	4.13**	-0.54	0.46	-1.78	2.79*	-3.87*	-1.08	-2.18	2.30	3.05	
	Env1	-105.14**	-222.56**	-119.51**	230.97**	-25.88	82.85*	1.07	129.60**	28.60	50.92	67.54	
	Env2	170.36*	-83.98	160.20*	95.75	-35.67	-141.59*	-50.03	-55.70	-59.35	107.03	141.96	
FW2	Env1	4.55	-4.93	17.95*	55.62**	2.51	-26.40**	-25.76**	-3.38	-20.15*	14.06	18.64	
	Env2	12.33	-27.03	34.73*	53.46**	-25.17	-28.78	-2.27	5.83	-23.10	27.05	35.88	
	Env1	4.56	-30.30**	-16.43**	-16.53**	-7.46	22.23**	27.60**	8.60*	7.73*	6.50	8.61	
NF	Env2	8.41	-12.06*	-7.31	-6.03	1.62	-1.79	2.46	0.50	14.21*	9.78	12.97	
	Env1	-0.26	-3.37**	1.27**	0.64**	1.67**	-0.14	-1.76**	0.58*	1.38**	0.37	0.49	
	Env2	-0.24	-5.02**	0.19	1.47**	1.66**	2.19**	-2.33**	0.57	1.53**	0.80	1.05	
SW	Env1	-0.01	1.59**	-0.82**	-0.37*	-2.44**	1.77**	-1.07**	0.88**	0.48*	0.29	0.38	
	Env2	1.56**	1.60**	0.63*	-0.67*	-0.56*	-0.99**	0.25	-1.49**	-0.33	0.48	0.63	
	Env1	-7.19**	-6.12*	-0.43	12.45**	2.83	-6.94**	1.48	-3.90	7.82**	3.88	5.15	
DSW	Env2	6.82	-16.41*	25.76**	15.84*	-9.47	-13.71	-2.34	9.99	6.82*	13.11	17.39	
	Env1	0.84	0.59	1.57*	3.99**	0.61	-1.96**	-4.31**	-0.47	-0.84	1.12	1.49	
	Env2	2.15*	0.48	1.19	2.05*	-1.99*	-2.37*	-1.01	1.36	-1.85*	1.59	2.11	

Legend: *Significant at 0.05 probability level; **highly significant at 0.01 probability level; ENV, Environment; LSD, Least significant difference; gi, GCA effects of the ith parent; gj, GCA effects of the jth parent; PH, Plant height; SBD, Stem base diameter; CD, Core diameter; SMD, Stem middle diameter; STD, Stem top diameter; NN, Number of nodes; DTFF, Days to first flowering; D50%F, Days to 50% flowering; FW1, Stem weight with leaves and pod; FW2, Fresh stem weight; NF, Number of pods per plant; NS, Number of seeds per pod; SW, 1000 seeds weight; DSW, Dry stick weight and DFW, Dry fiber weight.

negative GCA effect for 1000 seeds weight (Table 5), indicating that these parents had more decreasing alleles toward quality fiber and smaller seed size. Plant height (P_2), days to 1st flowering (P_7), days to 50% flowering (P_7), seeds number (P_2 and P_7), dry stick weight (P_2) and dry fiber weight (P_6) had the lowest negative and significant GCA effect in both environments. This information could be used in future breeding efforts.

Specific combining ability (SCA) of kenaf genotypes for yield and yield components

The SCA effects on hybrids in various contexts show in Table 6. The best combinations for SCA effects with high significance in the 1st environment were H4 for 1000 seed weight (−5.54); H9 for stem base diameter (9.81), core diameter (10.87), stem middle diameter (2.58), stem top diameter (1.19), stem weight with leaves and pods (945.18), fresh stem weight (169.29), dry stick weight (46.92), and dry fiber weight (22.48) and H11 for dry stick weight (23.66), and dry fiber weight (10.20). Furthermore, the best cross combinations with highly significant in the 1st environment were H23 and H32 for pods number (104.76 and 60.38 respectively); H29 for plant height (29.88), stem base diameter (8.72), core diameter (9.13), stem middle diameter (3.99), stem weight with leaves and pods (890.73), fresh stem weight (183.01), 1000 seed weight (−3.75), dry stick weight (62.01) and dry fiber weight (15.09); H35 for plant height (29.54), stem base diameter (7.17), core diameter (7.32), stem middle diameter (3.02), stem weight with leaves and pods (822.79), fresh stem weight (81.99), pods number (144.17), dry stick weight (36.98) and dry fiber weight (6.87).

Regarding the performance of all genotypes (Table 6), the strongest cross combinations for SCA impacts with significance at 2nd environment were H3 for dry stick weight (49.23); H4 and H20 for 1000 seed weight (−3.09 and −2.55); H12 and H28 for seeds number (12.51 and 4.77); H14 for pods number (35.54); H15 and H19 for dry fiber weight (5.24 and 5.23); H17 for pods number (38.17) and dry stick weight (44.21); H25 for stem base diameter (3.96), core diameter (3.99), seeds number (3.55) and dry stick weight (44.67); H29 for stem middle diameter (1.95) and H31 for stem top diameter (1.98).

Estimation of kenaf hybrid heterosis effect for yield and yield components

Relative heterosis and heterobeltiosis response in each location

First environment estimates of mid-parent and better parent heterosis for traits measured ranged from −56.18% to 283.35% and −67.88% to 182.88%, respectively, 2nd environment estimates ranged from −42.86% to 133.18% and −52.94% to 102.61%, respectively (Table 7). For dry fiber weight in the 1st environment, hybrid H9 had the highest mid-parent and better parent heterosis (140.43% and 77%, respectively), followed by H13 (121.05% and 110.59%, respectively), indicating that these hybrids had good additive genes for this trait transmitted from their parental lines. For dry stick weight, H26 had the highest mid-parent and better parent heterosis (137.35% and 136.99%, respectively) in 1st environment, followed by H10 (137.30% and 75.78%, respectively). Hybrid H19 had the highest mid and better parent heterosis estimates for dry fiber weight (41.23% and 28.81%, respectively), followed by H25 (29.55% and 27.46%, respectively) in 2nd environment. Hybrid H3 had the highest estimates of dry stick weight (79.10% and 70.96%, respectively), followed by H25 (72.31% and 60%, respectively) in 2nd environment.

Analysis of variance and genetic component estimate by Hayman's method

Hayman's analysis of variances (ANOVA)

The Hayman's ANOVA results for 15 yield and yield components for each environment were presented in Table 8 following Jones (1965) modification. Except for days to 1st flowering, both additive and dominance genetic effects (a) were significant in the 1st environment for all characteristics. In the 2nd environment, however, most of the traits were significant. Furthermore, the Baker

Table 6. Specific combining ability effects of thirty-six kenaf F₁ hybrids separately in two environments.

Hybrids	PH		SBD		CD		SMD		STD	
	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2
H1	2.25	18.80	-1.45	2.45	-1.73	2.18	-0.11	0.66	-0.35	-0.25
H2	22.12*	-12.93	2.59	1.51	2.39	1.50	0.47	0.58	0.19	1.20
H3	1.43	-8.89	-0.03	1.11	0.36	0.69	0.13	0.43	-0.65**	0.12
H4	-32.99**	-15.65	-3.43*	0.50	-3.43*	0.63	-2.34**	-0.69	0.19	0.02
H5	-12.62	10.79	1.05	-1.15	1.58	-1.03	-0.04	0.36	0.54*	0.05
H6	12.71	14.05	3.06*	1.47	3.59*	1.67	-0.07	-0.14	-0.60**	-0.81
H7	4.98	8.13	1.14	-0.58	1.03	-0.52	0.18	-0.28	-0.99**	0.07
H8	11.88	-16.03	-1.35	-2.32	-1.66	-2.14	-0.71	-0.81	0.07	-0.07
H9	-17.43	-14.48	9.81**	1.41	10.87**	1.07	2.58**	-0.41	1.19**	-0.04
H10	37.04**	-2.60	3.47*	-1.90	3.40*	-1.72	1.84**	-0.39	-0.20	-0.20
H11	7.79	-5.01	4.45**	-1.32	4.96**	-1.27	0.21	-0.68	-0.97**	-0.24
H12	15.16	6.96	2.27	0.48	2.41	0.09	1.01	-0.37	-0.69**	-0.13
H13	15.49	-4.30	4.53**	-1.85	3.97**	-2.15	0.57	-0.46	-0.62**	-0.26
H14	13.81	-2.77	-0.19	-0.78	-0.63	-0.44	-0.45	0.47	-0.24	0.53
H15	-61.28**	7.37	-9.71**	1.24	-9.33**	1.58	-2.86**	0.85	-0.49*	0.83
H16	3.44	7.46	1.88	-1.00*	2.27	-1.22	0.14	-0.02	-0.20	-0.54
H17	7.47	10.70	-0.89	-0.31	-0.81	-0.21	-1.21	0.25	-0.08	0.01
H18	10.12	8.92	-0.30	0.67	-0.74	0.89	0.08	0.34	-0.65**	-0.04
H19	-3.50	18.80	-4.05**	1.35	-5.02**	1.89	-0.39	0.23	-0.19	0.23
H20	-3.51	3.60	1.84	-0.54*	1.00	-0.95*	-1.03	0.27	-0.76**	0.29
H21	-1.21	-1.98	-3.41*	0.49	-3.25*	0.69	-1.46*	0.34	0.34	0.26
H22	-1.34	-6.81	1.49	0.71	1.33	-0.08	1.45*	0.07	0.00	0.14
H23	-4.21	-0.48	4.36**	1.88	4.20**	2.14	0.09	0.52	-0.79**	-0.01
H24	-24.59*	7.18	-3.69*	0.24	-3.96**	0.22	-0.36	0.66	0.44	1.13
H25	-4.04	11.71	0.42	3.96	-0.21	3.99	-1.01	1.31	0.64**	0.60
H26	1.59	6.87	5.10**	0.78	4.69**	0.74	-1.08	0.62	0.43	0.49
H27	9.06	16.70	-3.56*	0.75	-3.32*	1.04	0.42	-0.95	0.26	-0.76
H28	7.55	-8.26	0.04	-0.51	-0.18	-0.64	0.38	0.50	-0.59*	0.68
H29	29.88**	17.38	8.72**	2.37	9.13**	2.26	3.99**	1.95*	0.19	1.37
H30	-13.90	-14.45	-3.74*	0.16	-3.33*	0.20	-1.31	0.41	-0.62**	-0.28
H31	-1.35	-13.40	0.27	0.92	0.75	0.94	0.07	1.44	0.15	1.98**
H32	8.37	-18.41	1.12	-0.11	0.80	-0.23	-1.71*	-0.73	0.17	-0.09
H33	8.16	-10.06	5.63**	-1.21	5.36**	-1.31	1.56*	-0.35	0.74**	0.39
H34	20.95*	-17.12	-1.28	-1.45	-0.97	-1.52	-0.83	-1.08	0.30	-1.00
H35	29.54**	10.29	7.17**	1.82	7.32**	1.88	3.02**	0.10	-0.20	0.20
H36	-20.08*	10.88	0.99	-0.18	1.25	-0.02	3.19**	0.27	-0.08	-0.10
LSD (sij-slk)5%	18.79	32.67	2.77	3.09	2.81	3.02	1.29	1.77	0.43	1.35
LSD (sij-slk)1%	24.93	43.33	3.67	4.10	3.73	4.01	1.72	2.35	0.57	1.80
LSD (sij-skl)5%	16.63	28.90	2.45	2.73	2.49	2.67	1.15	1.57	0.38	1.20
LSD (sij-skl)1%	22.05	38.34	3.25	3.63	3.30	3.55	1.52	2.08	0.51	1.59

Hybrids	NN		DTFF		D50%F		FW1		FW2	
	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2
H1	-0.36	-0.19	-1.15	-1.48	-4.02	-1.99	-156.84	358.77*	-30.27	50.60
H2	2.70**	0.27	-1.96	0.00	-3.99	5.35	450.43**	28.75	58.14*	-20.33
H3	0.49	0.76	-4.51*	-0.18	-7.47**	1.01	-47.72	167.93	-6.76	50.38
H4	-0.17	1.29	4.49*	0.33	2.41	1.25	-333.64**	87.12	-86.75**	-14.60
H5	1.11	0.41	0.92	-0.55	4.22	-4.65	225.40**	24.15	14.15	4.57
H6	2.19*	0.10	1.73	3.09*	-0.26	2.01	301.63**	181.49	51.85*	9.17
H7	-0.83	0.27	-1.57	0.00	-2.72	1.22	-268.58**	83.26	-2.57	-21.70
H8	-2.22*	-0.40	2.28	3.21*	3.62	4.98	-193.01*	-220.31	40.24	-40.55
H9	3.77**	1.08	0.34	3.73*	-2.78	3.28	945.18**	-104.41	169.29**	-12.91
H10	3.98**	-0.91	0.46	3.88*	-2.59	5.62	64.70	-93.29	76.62**	-33.31
H11	3.17**	0.11	4.79*	3.39*	1.28	8.53*	351.56**	-66.04	64.73**	-17.74
H12	2.35**	-0.23	0.55	-2.82	-3.56	-4.72	44.92	-4.29	83.63**	15.04
H13	1.09	-0.48	-3.30	-1.52	-5.05*	-6.05	602.77**	-112.50	89.66**	-45.28
H14	0.28	0.18	-3.93	-2.27	-0.17	-4.17	155.76	4.83	6.17	-22.34
H15	-3.37**	-0.51	3.25	-1.39	1.83	-3.08	-886.53**	-75.97	-137.50**	19.36
H16	3.10**	-0.43	-1.02	1.70	-0.23	-2.38	452.76**	-140.81	39.11	-22.29
H17	-0.75	-0.55	-1.36	-0.12	4.65*	-1.47	-121.86	631.94**	35.93	49.67
H18	0.46	-0.50	-1.93	1.33	-4.20	3.28	-250.97**	4.30	-31.47	-6.72
H19	-1.22	0.59	-0.45	-1.36	-1.68	-4.72	-274.43**	88.31	-27.17	56.77

(Continued)

Table 6. (Continued).

H20	2.71**	-0.06	0.25	0.55	-1.14	1.83	137.46	107.31	-42.27	22.01	
H21	-1.01	-0.36	5.10*	-1.58	2.86	0.25	-530.97**	-171.54	-55.49*	-25.73	
H22	-1.00	1.50*	-2.24	-1.64	-1.84	1.53	562.69**	24.50	5.29	-8.50	
H23	1.42	0.55	-2.81	-3.85*	-6.35**	-4.38	761.14**	75.42	84.56**	48.44	
H24	-1.06	0.84	1.34	-0.55	8.16**	-2.38	-443.74**	46.09	-107.19**	-18.62	
H25	1.09	0.32	7.70**	-1.97	6.04**	-3.84	-346.13**	198.43	-25.72	69.95	
H26	-1.13	-0.16	-1.12	0.24	0.38	-4.41	541.88**	-52.21	179.61**	2.68	
H27	-1.73	0.62	-1.81	-0.67	-1.81	-2.81	-575.46**	-70.94	-33.43	-6.82	
H28	0.19	-0.56	-2.99	0.64	-2.29	-0.81	200.15*	-139.16	32.60	25.01	
H29	0.78	-0.41	1.04	0.88	-1.41	-2.93	890.73**	-60.82	183.01**	24.39	
H30	0.75	-0.57	-0.12	-2.58	1.59	-4.17	-228.72**	265.99	-56.72*	25.00	
H31	0.19	0.36	0.76	1.76	-4.47*	6.62	-103.03	-79.90	-23.87	-3.05	
H32	-1.21	-0.11	2.46	1.67	-0.26	5.83	459.84**	-73.13	3.41	-12.81	
H33	5.18**	-0.14	-1.36	-0.45	5.07*	2.25	539.67**	7.75	56.52*	1.11	
H34	-1.30	-0.89	-2.05	-1.70	-1.75	-0.84	-52.56	-141.50	19.40	-18.94	
H35	1.98*	-0.59	-4.21	-1.15	-6.08**	0.92	822.79**	93.42	81.99**	34.05	
H36	2.24*	1.05	-3.84	0.42	-5.53*	0.80	450.47**	41.86	-21.76	4.29	
LSD (sij-slk)5%	1.76	1.38	4.27	3.00	4.30	7.39	163.83	344.34	45.22	87.03	
LSD (sij-slk)1%	2.34	1.83	5.66	3.98	5.70	9.80	217.29	456.70	59.98	115.43	
LSD (sij-skl)5%	1.56	1.22	3.78	2.65	3.80	6.54	144.93	304.62	40.01	76.99	
LSD (sij-skl)1%	2.07	1.62	5.01	3.52	5.04	8.67	192.22	404.02	53.06	102.12	
		NF	NS		SW		DSW		DFW		
Hybrids		Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2
H1		-15.79	37.97*	-5.88**	-2.14	-1.61	2.19**	-10.77	13.43	-3.51	1.11
H2		47.91**	-1.11	3.04**	0.81	-0.07	1.81*	17.59**	-13.74	7.52**	-0.47
H3		55.10**	30.61	1.80**	1.20	2.11**	1.62*	12.92*	49.23*	1.83	1.55
H4		-43.39**	-9.71	-5.00**	0.23	-5.54**	-3.09**	-25.61**	23.15	-9.21**	-0.44
H5		-30.14**	5.20	-9.38**	0.81	-1.98	-1.43	14.49*	6.83	0.72	0.59
H6		25.77**	19.06	1.01	-2.11	3.34**	-2.89**	16.08*	-7.31	4.33*	2.57
H7		42.68**	-0.26	2.72**	1.13	1.26	0.63	-2.24	-1.03	-1.86	2.22
H8		33.71**	-17.44	-1.67**	1.25	0.49	-2.42**	-7.08	-30.95	1.99	-3.32
H9		11.11	-31.06	-5.24**	-2.02	1.88	-1.54	46.92**	-45.51*	22.48**	0.91
H10		43.03**	3.08	-6.45**	2.48	0.15	0.10	36.83**	-16.15	6.60**	-1.05
H11		41.64**	-27.91	2.73**	-4.26**	-1.26	1.73*	23.66**	-1.95	10.20**	-2.09
H12		-9.06	-13.67	-3.33**	12.51**	-1.72	-0.72	7.93	0.62	5.91**	-0.83
H13		47.28**	-10.08	6.90**	-0.71	-3.25**	0.10	40.56**	-17.41	7.71**	-1.71
H14		40.39**	35.54*	-3.92**	-4.45**	2.11**	2.93**	5.11	-13.08	-0.44	0.04
H15		-52.08**	2.50	-3.95**	-2.02	-0.16	1.67*	-53.69**	26.73	-16.01**	5.24*
H16		20.39	-14.67	-1.26*	1.93	-0.04	-2.41**	15.02*	-17.76	1.58	-0.80
H17		0.99	38.17*	0.67	0.58	0.64	3.05**	-18.69**	44.21*	-3.47	3.60
H18		42.71**	-5.08	-1.00	-1.23	-0.88	-0.22	-4.85	13.45	-3.34	0.36
H19		-27.29*	-6.49	-3.23**	0.68	-1.82	3.73**	-8.08	20.41	-3.17	5.23*
H20		48.15**	-2.54	1.17	-3.50**	-2.42**	-2.55**	-1.96	14.75	-2.69	-1.68
H21		-26.76*	2.91	-0.66	2.65*	-1.31	-1.32	-1.40	-20.45	-4.10*	-1.65
H22		46.09**	-14.94	-0.95	1.80	-2.06**	1.06	-0.21	-3.65	2.57	0.02
H23		104.76**	4.14	0.45	-1.74	1.49	0.50	7.12	38.37	3.77*	2.01
H24		-85.47**	-8.94	-5.86**	-0.71	-3.33**	-2.19**	-31.06**	13.66	-4.49*	0.45
H25		-37.20**	4.84	-0.17	3.55**	-0.54	-0.72	-26.67**	44.67*	-3.35	4.26
H26		-34.11**	-1.53	0.96	1.54	-0.84	3.87**	72.62**	-12.67	12.08**	-1.46
H27		-63.30**	19.82	2.04**	-1.56	-0.18	-1.73*	-11.44	13.67	-2.82	2.85
H28		47.90**	10.57	2.47**	4.77**	4.21**	-1.44	0.51	-24.36	-1.10	-3.01
H29		50.07**	-22.64	-8.59**	1.48	-3.75**	-1.22	62.01**	-1.69	15.09**	0.76
H30		16.71	-9.18	-1.71**	-2.26	2.42**	-1.20	1.95	5.11	2.80	1.28
H31		10.99	-10.68	1.66**	-1.43	-2.29**	3.59**	0.26	-16.79	0.85	-0.74
H32		60.38**	-9.90	2.95**	-0.66	0.56	0.42	6.21	-26.01	0.60	-3.09
H33		33.50**	27.56	0.81	-1.46	0.00	-2.49**	23.07**	-9.31	7.33**	-1.56
H34		-50.77**	1.77	-3.97**	-1.80	-3.15**	-1.84*	-1.78	-0.64	-0.71	-1.02
H35		144.17**	0.31	-5.15**	2.90*	0.33	-2.02*	36.98**	22.09	6.87**	2.00
H36		11.60	4.43	4.07**	-0.67	-0.15	-1.20	-3.92	21.99	-0.55	2.15

(Continued)

Table 6. (Continued).

LSD (sij-sk)5%	20.90	31.47	1.18	2.56	0.93	1.54	12.49	42.18	3.62	5.12
LSD (sij-sk)1%	27.71	41.74	1.56	3.39	1.23	2.04	16.57	55.94	4.80	6.79
LSD (sij-sk)5%	18.49	27.84	1.04	2.26	0.82	1.36	11.05	37.31	3.20	4.53
LSD (sij-sk)1%	24.52	36.92	1.38	3.00	1.09	1.80	14.66	49.49	4.24	6.00

Legend: *Significant at 0.05 probability level; **highly significant at 0.01 probability level; ENV, Environment; LSD, Least significant difference; gi, GCA effects of the ith parent; gj, GCA effects of the jth parent; PH, Plant height; SBD, Stem base diameter; CD, Core diameter; SMD, Stem middle diameter; STD, Stem top diameter.

Legend: *Significant at 0.05 probability level; **highly significant at 0.01 probability level; ENV, Environment; LSD, Least significant difference; NN, Number of nodes; DTF, Days to first flowering; D50%F, Days to 50% flowering; FW1, Stem weight with leaves and pod; FW2, Fresh stem weight.

Legend: *Significant at 0.05 probability level; **highly significant at 0.01 probability level; ENV, Environment; LSD, Least significant difference; NF, Number of pods per plant; NS, Number of seeds per pod; SW, 1000 seeds weight; DSW, Dry stick weight; DFW, Dry fiber weight.

ratio for the examined traits was altered from 0.53 to 0.95, indicating that the additive effect plays a more significant role in determining the traits.

Vr -Wr regression analysis

In the absence of non-allelic interaction and regardless of the genes between the parents, Hayman (1958) demonstrated that the linear regression of W_r on V_r would have a unit slope, and the W_r , V_r , array point would lie along the lines. Furthermore, the regression line's magnitude and a sign of the intercept cutoff revealed the dominance level (Supplementary figure 1). The regression coefficient b was not statistically significant compared to zero (Table 9). The deviation from unity for all the 15 characters except for stem top diameter (1st env.), days to 50% flowering (1st env.), and 1000 seeds weight (1st env.) indicated the validity of the hypothesis proposed by Hayman (1958). The non-significant t^2 values of the plant height (2nd env.), core diameter (2nd env.), stem top diameter (1st env.), nodes number (2nd env.), days to 1st flowering (2nd env.), days to 50% flowering (both env.), fresh stem weight (2nd env.), seeds number (both env.), 1000 seeds weight (both env.), dry stick weight (2nd env.) and dry fiber weight (2nd env.) characters also showed that the concept of additive dominance with independent gene distribution among the parents is valid for this diallel cross for the characters.

Components of variation and genetic parameters

Hayman (1954) and Jinks (1954) were used to determine the genetic and environmental components of variation and allied or related genetic factors in F_1 . Data indicated that the additive genetic component (D) was negative for all attributes except for the number of seeds and 1000 seeds weight (Table 10). The magnitude of dominance (H_1 and H_2) for seven traits, including fiber yield, was greater than that of additive components (D), indicating that these qualities were over-dominant. The value of H_1 was greater than H_2 for nine traits out of 15, indicating that the frequency of gene distribution in the parents was unequal, and that was also supported by the ratio of $H_2/4H_1$ (<0.25), which showed asymmetrical gene distribution at the loci in the parents showing dominance for all these traits. The F value was negative for all attributes suggesting the presence of dominant, recessive genes in the parents influencing these traits. Except for plant height, stem top diameter, and days to 1st flowering, the overall dominance effects of heterozygous loci (h^2) were positive for all variables, indicating that most of the dominant genes had favorable one's effects.

The average degree of dominance over all loci, as estimated by $(H_1/D)^{0.5}$ ratio, was found to be more than unity for all traits except stem base diameter, core diameter, nodes number, stem weight with leaves and pod, dry fiber weight and pods number, indicating the role of over dominance gene effects in the inheritance of most studied traits, as was also observed in the V_r - W_r graph. The h^2/H_2 values for the trait's stem base diameter, core diameter, nodes number, stem weight with leaves and

Table 7. Estimates of relative heterosis and heterobeltiosis of crosses in kenaf in two growth environments for 15 characteristics.

Hybrids	Plant height						Stem base diameter						Core diameter					
	MPH		BPH		BPH		MPH		BPH		MPH		MPH		BPH			
	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2		
H1	3.25	8.25	-0.12	4.35	9.29	13.59	-4.11	9.20	11.34	14.09	-3.71	9.94						
H2	10.56*	-3.33	2.06	-5.84	18.22*	13.23	14.55	12.33	20.16	15.78	18.12	14.22						
H3	2.30**	-2.21**	-4.34**	-7.39**	12.89**	14.27**	10.59**	10.19**	16.16**	13.47**	11.86**	8.93**						
H4	-10.30**	-7.00**	-14.39**	-8.98**	-8.07**	8.22**	-9.99**	4.04**	-7.53	9.97	-10.77	1.02						
H5	-0.76**	4.41**	-4.68**	3.14**	16.92**	0.70**	4.55**	-7.48**	23.60**	1.94**	9.95**	-8.38**						
H6	10.97**	5.99**	4.55**	0.44**	19.22**	12.21**	12.12**	4.03**	24.60**	16.12**	19.74**	5.81**						
H7	7.87**	4.40**	6.48**	1.37**	19.06**	3.75**	7.27**	-3.27**	20.89**	4.62**	9.83**	-3.12**						
H8	1.10**	-7.38**	-6.07**	-8.62**	-2.88**	-6.35**	-3.64**	-14.94**	-3.74**	-5.45**	-4.03**	-16.19**						
H9	-6.02**	-3.50**	-9.30**	-8.30**	47.80**	9.80**	14.18**	6.98**	60.73**	9.47**	29.88**	6.90**						
H10	16.26**	0.81**	5.41**	-7.78**	40.55**	-2.34**	21.16**	-2.65**	47.09**	-3.72**	23.24**	-4.10**						
H11	5.62**	-2.23**	-2.33**	-7.69**	34.45**	-3.79**	15.85**	-7.29**	45.47**	-5.25**	22.09**	-9.85**						
H12	10.46**	3.54**	2.77**	1.01**	39.03**	4.59**	36.08**	-0.24**	49.39**	3.22**	44.66**	-4.00**						
H13	12.68**	-0.60**	2.91**	-9.00**	41.54**	-0.82**	31.42**	-10.11**	46.02**	10.60**	30.79**	-14.90**						
H14	12.02**	0.65**	7.02**	-5.68**	29.41**	6.57**	25.61**	-3.93**	31.75**	0.22**	24.70**	-3.84**						
H15	-26.31**	2.77**	-33.61**	-2.20**	-26.13**	6.57**	-34.75**	0.44**	-27.74**	10.60**	-37.67**	1.38**						
H16	3.47**	6.08**	2.04**	3.06**	25.69**	5.84**	19.38**	2.85**	29.31**	4.61**	22.49**	1.75**						
H17	5.31**	5.62**	1.68**	5.11**	6.43**	5.29**	1.03**	1.38**	8.26**	6.53**	2.75**	-0.91**						
H18	7.96**	5.74**	3.57**	1.78**	18.04**	9.69**	8.63**	1.53**	18.26**	13.60**	6.82**	3.36**						
H19	5.19**	9.69**	2.92**	6.64**	-2.69**	12.46**	-5.65**	5.04**	-9.01**	18.54**	-11.07**	9.36**						
H20	4.85**	4.64**	-2.04**	4.31**	28.81**	4.65**	19.48**	-1.69**	26.68**	3.32**	16.92**	-3.10**						
H21	-2.77**	0.50**	-3.44**	-0.80**	-5.21**	7.31**	-7.46**	-1.82**	-5.72**	11.40**	-7.60**	-0.07**						
H22	1.55**	-1.73**	-0.61**	-4.98**	19.21**	12.77**	19.14**	8.34**	21.72**	8.96**	21.46**	4.07**						
H23	2.24**	1.33**	-0.58**	-5.14**	41.03**	18.30**	23.84**	12.50**	46.22**	22.70**	25.86**	14.54**						
H24	-2.81**	4.63**	-3.59**	4.55**	4.07**	10.17**	-4.00**	5.76**	1.84**	11.23**	-5.61**	5.33**						
H25	3.98**	7.03**	-1.57**	4.31**	27.06**	28.23**	12.40**	23.83**	25.68**	32.38**	10.39**	27.50**						
H26	-2.55**	3.33**	-3.23**	-0.87**	30.56**	11.53**	26.94**	4.80**	32.91**	13.60**	28.37**	4.51**						
H27	7.51**	6.34**	6.79**	2.83**	-0.31**	9.28**	-12.50**	8.12**	2.44**	13.03**	-11.67**	10.35**						
H28	8.97**	-2.96**	7.50**	-6.10**	8.76**	2.76**	0.28**	2.68**	9.83**	2.48**	2.00**	1.57**						
H29	17.16**	7.55**	13.22**	6.69**	49.96**	17.55**	32.60**	16.92**	59.47**	19.78**	40.32**	18.73**						
H30	-7.68**	-6.96**	-4.95**	-7.72**	-10.06**	4.65**	-12.61**	2.26**	-8.18**	6.74**	-11.13**	2.63**						
H31	7.55**	-4.45**	5.41**	-10.49**	19.57**	9.74**	13.29**	8.67**	24.72**	13.06**	15.05**	11.35**						
H32	10.98**	-5.97**	7.94**	-9.77**	32.11**	5.47**	30.99**	3.81**	34.56**	6.28**	31.43**	2.87**						
H33	1.77**	-4.74**	-1.71**	-7.14**	34.92**	-2.33**	21.48**	-3.55**	40.47**	-1.66**	24.63**	-3.19**						
H34	17.62**	-4.51**	12.19**	-6.87**	14.80**	-1.37**	9.66**	-1.98**	16.09**	-1.74**	9.49**	-3.47**						
H35	11.24**	3.95**	9.58**	-0.21**	34.51**	12.50**	27.43**	10.02**	39.99**	17.69**	34.14**	14.15**						
H36	-6.83**	4.89**	-12.39**	3.21**	17.68**	3.40**	6.77**	0.51**	20.59**	6.30**	9.26**	1.35**						
LSD5%	25.17	43.76	29.06	50.53	3.71	4.14	4.28	4.78	3.77	4.05	4.35	4.68						
LSD1%	33.38	58.03	38.54	67.01	4.91	5.49	5.67	6.34	4.99	5.37	5.77	6.20						

(Continued)



Table 7. (Continued).

Hybrids	Stem middle diameter				Stem top diameter				Number of nodes			
	MPH		BPH		MPH		BPH		MPH		BPH	
	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2
H1	-0.25	5.40	-14.11	-1.38	-36.52	-2.28	-37.45	-4.21	37.04*	7.32	-1.29	-8.33
H2	-2.93	7.99	-4.13	4.10	-8.39	30.00	-24.59	21.41	65.30**	32.93	28.35*	13.54
H3	-1.54	10.64**	-4.02	8.73**	-31.77	12.44	-32.84	11.34	28.84**	107.68	13.14**	71.03
H4	-20.12	-3.85	-22.85	-6.96*	-16.88	6.60	-18.12	6.38	7.15**	100.74*	3.11**	100.00*
H5	-2.58	3.82*	-10.40	1.80**	2.33	8.95	-9.97	3.60	36.94**	71.96	21.14**	35.29
H6	-0.79	1.81*	-0.79	-4.25**	-36.19	-4.13	-36.99	-9.04	32.39**	22.67	21.14**	12.20
H7	1.13	2.54*	0.92	-2.35**	-45.48	11.05	-47.65	7.75	7.25*	44.33	6.72**	42.21
H8	-10.35	-3.92	-12.57	-12.98	-7.76	9.50	-9.51	-0.80	-8.43	5.82	-16.35	-27.21
H9	35.92*	-0.84	22.73	-10.33	6.66	6.52	-3.65	1.38	53.65**	26.35	4.76**	26.35
H10	26.03	2.96*	6.22	-2.06	-24.24	5.68	-21.83	4.60	121.70**	-22.86	75.42**	-43.75
H11	11.90	-4.98	-6.41	-8.24	-52.96	1.04	-52.97	-1.15	70.54**	8.26	20.00**	-7.81
H12	21.72	-3.54	13.21	-8.05	-41.71	5.19	-49.36	1.98	100.27**	-10.07	57.48**	-36.77
H13	18.69	-2.13	6.84	-2.67	-41.62	6.93	-41.74	-0.45	58.91**	-29.66	21.63**	-34.79
H14	7.93	8.69*	-6.91	6.69	-28.94	19.05	-32.72	17.82	47.60**	1.23**	6.63**	-14.58
H15	-20.10	11.11**	-29.70	7.29	-28.72	28.24	-31.08	14.11	-0.63**	-31.73	-23.85	-39.57
H16	1.88	9.49**	-1.88	3.79	-11.07	4.44	-25.87	-1.56	95.81**	8.57	69.48**	-20.83
H17	-8.10	7.07**	-12.31	0.00	-17.41	10.99	-32.81	3.46	21.19**	-7.03	-8.43*	-20.83
H18	2.13	6.45**	-4.98	0.69	-29.99	11.56	-35.21	9.46	63.26**	-11.11	40.31**	-37.50
H19	0.02	7.90**	-3.73	-1.95	-18.46	21.70	-33.54	8.25	21.68**	14.61	1.37**	6.25
H20	-5.41	10.14**	-6.39	1.31	-35.18	19.03	-44.83	14.43	68.22**	1.23	31.08**	-14.58
H21	-13.29	9.62**	-14.39	-3.92	11.94	20.85	-6.43	3.00	25.42**	-21.12	4.64**	-30.18**
H22	16.46	9.49**	15.36	7.78	-13.45	16.03	-16.06	14.67	9.70**	133.18*	-6.79*	92.59*
H23	6.48	11.93**	-4.32	11.67	-29.94	14.43	-37.50	9.83	57.56**	102.41	56.24**	90.91
H24	4.45	15.95**	-3.03	10.87	0.83	43.69	-1.98	35.07*	12.73*	61.90	7.73**	24.39
H25	-1.06	23.57**	-3.75	19.69	10.79	27.80	8.04	25.20	37.07**	56.36	20.89**	30.30
H26	-5.59	16.64**	-10.19	7.32	11.59	29.29	11.22	16.10	12.95*	1.66	8.13**	-31.22
H27	10.08	-5.81	-1.92	-7.07	-6.70	-3.41	-18.97	-8.33	4.91*	69.01	-10.24*	33.33
H28	11.32	9.41**	2.44	6.23	-35.61	30.62	-35.77	24.17	9.15**	-14.38	-3.55**	-21.95**
H29	39.09**	24.43**	34.06	22.39	-11.67	39.17	-16.38	34.77*	16.94**	1.87	12.00**	0.74
H30	-6.64	9.32*	-11.99	2.07	-27.05	8.35	-29.47	-1.67	15.09**	-19.83	1.54**	14.07
H31	9.63	16.38**	5.82	11.53	-7.74	56.99*	-19.71	42.03*	28.64**	22.31	23.93**	-9.76**
H32	-6.80	-1.10	-14.11	1.98	-2.91	12.40	-11.40	16.39**	16.39**	12.95	3.41**	-10.15
H33	18.33	0.72	11.42	-7.13	23.35	24.13	10.36	7.49	83.71**	-11.37	77.30**	-41.81
H34	3.00	-2.01	-1.84	-3.30	-1.84	-0.78	-10.95	-8.51	1.42	-38.65	-6.79*	-44.63
H35	32.64*	7.54*	29.27	3.29	-13.30	27.03	-15.99	20.96	32.30**	-33.79	32.05**	-45.10
H36	32.30*	11.40**	29.28	5.65	-6.65	15.82	-8.67	2.13	35.98**	22.77	24.77**	-6.10
LSD5%	1.73	2.37	2.00	2.74	0.58	1.81	0.67	2.09	2.36	1.85	2.73	2.14
LSD1%	2.30	3.15	2.66	3.64	0.77	2.40	0.89	2.78	3.13	2.45	3.62	2.83

(Continued)

Table 7. (Continued).

Hybrids	Days to 1 st flowering				Days to 50% flowering				Stem weight with leaves and pod			
	MPH		BPH		MPH		BPH		MPH		BPH	
	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2
H1	-1.61	0.00	-3.16	-2.40	-15.40	-0.51	-19.80	7.65	13.19*	56.83	-21.99	48.08
H2	-4.35	4.29	-6.54	-0.63	-12.99	15.17	-14.92	12.02	60.11**	31.33	32.74**	24.38
H3	-9.74**	0.63**	-10.32**	0.00**	-17.36**	1.56**	-17.58**	-2.99**	26.82**	40.09**	21.36**	33.86**
H4	9.87**	2.97**	9.15**	-1.89**	1.69**	5.59**	-0.55**	3.28**	-12.90**	56.96**	-20.46**	24.74**
H5	0.33**	-0.62**	-1.96**	-2.42**	-1.09**	-3.14**	-2.16**	-7.04**	41.10**	20.29**	30.99**	7.08**
H6	-1.05**	8.11**	-7.19**	0.63**	-9.83**	5.11**	-13.81**	1.09**	49.29**	36.92**	30.57**	33.10**
H7	-2.91**	0.95**	-3.85**	0.00**	-10.74**	4.95**	-10.99**	4.37**	7.06**	34.68**	-3.47**	22.24**
H8	4.67**	6.80**	2.61**	3.77**	4.40**	11.17**	-1.66**	8.74**	-5.37**	-7.54**	-5.43**	-9.87**
H9	-2.55**	9.97**	-3.16**	2.40**	-11.89**	6.22**	-19.31**	-3.76**	48.46**	-1.74**	-10.18**	-11.84**
H10	0.32**	6.71**	-0.63**	4.79**	-11.46**	3.86**	-15.84**	0.94**	87.24**	-6.32**	32.37**	-15.24**
H11	10.68**	7.40**	8.23**	0.00**	-2.93**	11.86**	-9.90**	1.88**	104.68**	11.16**	49.20**	-7.55**
H12	0.00**	-6.02**	-3.80**	-6.59**	-15.76**	-7.28**	-19.31**	-10.33**	74.95**	-7.10**	26.11**	-12.75**
H13	-10.96**	-2.63**	-17.72**	-11.38**	-19.89**	-12.57**	-27.23**	-21.60**	156.72**	-17.30**	93.18**	-19.74**
H14	-7.01**	-4.64**	-7.59**	-7.78**	-8.85**	-8.12**	-13.37**	-15.02**	103.40**	2.66**	49.60**	-1.57**
H15	6.89**	-3.47**	3.16**	-8.38**	-1.66**	-6.70**	-11.88**	-15.02**	-53.41**	-14.44**	-67.88**	-17.19**
H16	-3.65**	4.26**	-6.45**	-1.24**	-4.79**	-5.35**	-7.14**	-11.94**	102.06**	2.52**	73.78**	1.56**
H17	-2.36**	2.08**	-3.97**	2.08**	6.36**	-0.57**	6.36**	-1.14**	27.66**	111.52**	14.66**	61.50**
H18	-6.16**	2.91**	-6.16**	10.42**	-14.53**	8.06**	-17.30**	1.01**	23.02**	9.48**	8.76**	-7.06**
H19	-6.43**	-1.07**	-10.27**	-3.47**	-11.83**	-8.19**	-13.87**	-9.25**	20.90**	18.58**	13.56**	9.35**
H20	0.00**	2.00**	-3.21**	-1.92**	-7.61**	4.52**	-9.89**	2.21**	73.40**	27.93**	57.73**	10.59**
H21	9.90**	-2.72**	9.52**	-4.67**	3.90**	1.72**	0.00**	1.14**	-18.62**	-8.93**	-32.50**	-15.81**
H22	-4.58**	-4.26**	-5.81**	-9.32**	-3.66**	-1.60**	-6.04**	-7.96**	100.55**	30.88**	90.95**	0.58**
H23	-8.31**	-9.82**	-10.97**	-10.91**	-16.62**	-9.50**	-17.30**	-9.95**	123.85**	11.44**	116.85**	-4.66**
H24	-3.11**	-2.68**	-9.68**	-9.94**	6.63**	-9.73**	1.65**	-16.92**	19.10**	8.87**	8.36**	1.27**
H25	-5.99**	-5.99**	13.46**	-7.45**	5.49**	-10.47**	5.49**	-14.93**	35.63**	32.24**	27.43**	15.24**
H26	-3.31**	-5.25**	-5.81**	-5.59**	0.58**	-5.49**	-17.41**	-1.71**	85.18**	-2.40**	77.30**	-8.98**
H27	-4.38**	-2.91**	-5.96**	-9.09**	-6.70**	-4.28**	-9.73**	-10.05**	-10.41**	10.39**	-12.00**	-3.12**
H28	-10.18**	1.07**	-15.23**	-1.39**	-8.88**	-4.07**	-10.98**	-5.71**	63.57**	1.78**	55.93**	-17.34**
H29	2.93**	0.67**	1.28**	-3.21**	-4.23**	-6.18**	-6.59**	-7.73**	135.59**	21.93**	132.32**	5.04**
H30	0.67**	-6.80**	-0.66**	-4.86**	5.71**	-8.57**	1.73**	-8.57**	7.31**	55.21**	18.51**	102.61**
H31	-5.00**	1.32**	-8.90**	-7.27**	-18.29**	9.24**	-22.70**	1.01**	41.82**	-15.15**	32.91**	-22.51**
H32	3.31**	0.31**	0.00**	-2.42**	-7.90**	8.95**	-8.65**	4.02**	101.37**	-8.15**	95.10**	-10.11**
H33	-4.44**	-4.13**	-4.76**	-8.48**	5.51**	3.21**	-1.62**	-3.02**	78.40**	-5.94**	65.70**	-14.31**
H34	-8.97**	-5.12**	-15.38**	-10.90**	-11.82**	-4.57**	-15.93**	-7.73**	56.34**	-13.95**	51.07**	-19.82**
H35	-13.88**	-4.53**	-17.69**	-8.67**	-15.69**	-1.74**	-16.97**	-3.43**	107.13**	5.49**	81.23**	5.20**
H36	-7.59**	-1.96**	-10.26**	-3.85**	-11.11**	-0.56**	-16.48**	-2.21**	80.05**	6.42**	62.43**	-1.10**
LSD5%	5.72	4.02	6.60	4.64	5.76	9.89	6.65	11.42	219.40	461.14	253.34	532.48
LSD1%	7.58	5.33	8.75	6.15	7.63	13.12	8.82	15.15	290.991	611.61	336.01	706.23

(Continued)



Table 7. (Continued).

Hybrids	Fresh stem weight				Number of pods per plant				Number of seeds per pod			
	MPH		BPH		MPH		BPH		MPH		BPH	
	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2
H1	21.58	15.66	-5.80	6.67	72.62**	64.14*	8.31	57.53*	-55.26	-9.62	-58.02	-25.18
H2	30.27**	-1.84	25.31*	-6.75	160.86**	10.91	97.14**	4.81	-7.18	4.18	-7.81	1.25
H3	17.97**	23.80**	17.70**	15.46**	167.32**	54.20**	105.26**	52.45**	-16.08	16.22**	-17.39	13.91**
H4	-12.48**	3.59**	-19.50**	-14.44**	12.16**	2.43**	2.86**	-9.60**	-37.67	2.64**	-39.15	-4.40**
H5	20.82**	7.46**	0.62**	-9.26**	37.59**	29.16**	25.66**	26.93**	-56.18	9.09**	-59.05	3.57**
H6	29.47**	8.33**	11.34**	1.11**	74.53**	34.87**	43.71**	20.93**	-16.36	6.18**	-26.58	-14.36**
H7	11.19**	-2.13**	2.38**	-6.48**	142.99**	20.31**	119.80**	13.66**	-7.95	0.70**	-11.57	-7.18**
H8	22.27**	-11.79**	9.66**	-22.41**	107.49**	0.98**	106.45**	-14.73**	-25.20	7.60**	-25.54	1.59**
H9	94.81**	-4.92**	49.46**	-16.33**	-24.79**	-41.89**	-58.98**	-47.16**	-43.59	-10.16**	-44.24	-27.29**
H10	79.07**	-7.59**	38.98**	-20.03**	283.35**	3.35**	182.88**	-1.89**	-54.72	23.77**	-58.14	4.14**
H11	73.02**	-4.58**	43.15**	-15.46**	194.39**	-34.10**	92.18**	-43.87**	-15.89	-18.49**	-22.83	-36.19**
H12	93.19**	5.80**	76.36**	-3.95**	86.04**	-12.12**	12.62**	-17.05**	-40.59	61.42**	-40.85	28.27**
H13	87.88**	-18.37**	65.67**	-19.41**	129.76	-12.86**	33.82**	-24.66**	2.62	-2.52**	-4.46	-12.56**
H14	46.88**	-8.65**	21.40**	-11.99**	233.20**	42.44**	119.09**	29.45**	-41.77	-25.17**	-43.19	-41.89*
H15	-14.65**	5.31**	-27.77**	0.00**	11.30**	3.89**	-30.31**	-15.16**	-41.46	-7.56**	-45.31	-26.86*
H16	39.90**	2.94**	34.87**	0.96**	170.22**	-20.50**	164.12**	-24.05**	-21.11	17.36**	-22.86	11.86**
H17	34.43**	29.83**	28.29**	3.00**	92.69**	27.88**	55.42**	18.91**	-11.03	0.21**	-13.72	-1.73**
H18	15.27**	4.94**	-0.84**	-15.00**	145.64**	-6.12**	74.74**	-9.79**	-16.26	2.68**	-21.24	-2.18**
H19	13.15**	25.84**	0.65**	12.00**	33.55**	-12.23**	-11.13**	-17.00**	-27.17	4.45**	-35.69	-7.08**
H20	7.65**	14.29**	2.86**	4.00**	205.98**	-4.85**	149.70**	-4.89**	-7.33	-16.82**	-10.39	-21.24**
H21	0.89**	-3.76**	-6.22**	-19.00**	51.50**	0.30**	14.10**	-11.04**	-15.25	11.32**	-16.21	8.05
H22	31.32**	12.09**	21.04**	-12.34**	164.52**	-18.14**	117.19**	-27.03**	-21.02	16.87**	-21.69	6.84**
H23	62.03**	29.12**	35.18**	3.05**	223.51**	10.27**	133.37**	9.60**	-15.11	7.99**	-21.82**	0.60**
H24	-5.37**	4.40**	-18.48**	-8.65**	-32.10**	-9.55**	-54.29**	-18.07**	-42.59	9.77**	-50.28	2.08**
H25	19.95**	33.33**	10.68**	19.23**	54.97**	8.95**	28.78**	4.04**	-17.00	17.88**	-21.46	6.68**
H26	82.08**	10.42**	63.62**	-8.52**	38.10**	1.40**	5.67**	-13.56**	-13.55	17.25**	-14.51	8.64**
H27	15.27**	11.05**	3.33**	8.06**	-1.87**	19.98**	-17.11**	7.53**	-5.76	-0.20**	-13.87	-2.21**
H28	35.16**	23.66**	25.52**	8.33**	96.42**	4.96**	51.19**	3.10**	-4.72	21.47**	-18.08	4.00**
H29	82.82**	23.33**	82.60**	5.79**	161.07**	-22.67**	157.15**	-28.06**	-45.52	1.50**	-48.85	0.37**
H30	0.40**	23.23**	-2.35**	33.38**	90.11**	-9.03**	110.17**	-3.99**	-20.22	-5.51**	-21.76	-6.87**
H31	17.68**	7.14**	13.25**	-3.85**	63.64**	-7.52**	45.84**	-15.77**	-6.08	1.13**	-12.22	-11.90**
H32	26.59**	3.47**	13.36**	-9.15**	157.85**	-2.95**	115.14**	-6.77**	0.23	-2.02**	-2.61	-5.04**
H33	44.67**	7.42**	33.00**	2.44**	105.88**	31.94**	88.89**	13.03**	-9.73	1.19**	-16.00	0.60**
H34	28.15**	0.77**	18.88**	-1.69**	18.19**	3.36**	-9.98**	-2.22**	-30.69	-10.42**	-36.93	-24.02**
H35	49.14**	20.04**	42.20**	12.61**	182.75**	1.35**	133.74**	-5.32**	-35.75	15.40**	-43.83	0.02**
H36	10.21**	8.20**	7.07**	-0.81**	106.51**	8.66**	85.95**	-3.59**	3.08	-4.87**	-1.41	-7.27**
LSD5%	60.56	116.56	69.93	134.59	27.98	42.14	32.31	48.66	1.58	3.42	1.82	3.95
LSD1%	80.325	154.59	92.75	178.50	37.114	55.90	42.86	64.54	2.094	4.54	2.42	5.25

(Continued)

Table 7. (Continued).

Hybrids	1000 seeds weight				Dry stick weight				Dry fiber weight			
	MPH		BPH		MPH		BPH		MPH		BPH	
	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2	Env1	Env2
H1	-9.86	7.92**	-15.47	1.13	29.52*	9.09	-2.58	9.09	22.96*	11.39	-9.31	5.90
H2	-5.46	2.82	-6.45	-2.31	42.30**	-3.57	41.32**	-20.59	41.61**	8.68	29.96**	2.10
H3	2.94	3.34*	2.60	-6.09**	48.39**	79.10**	45.03**	70.96**	25.59**	16.70**	19.26**	18.75**
H4	-26.90	-12.69	-30.78	-17.82	-16.45**	51.85**	-21.90**	24.24**	-19.18**	6.69**	-27.88**	-11.69**
H5	-11.79	-7.84	-18.32	-14.68	40.92**	23.30*	28.93**	5.55**	17.72**	7.46**	-3.82**	-8.87**
H6	4.67	-11.96	4.43	-15.25	43.40**	0.00**	41.83**	-2.86**	31.57**	22.68**	0.30**	5.78**
H7	-2.43	-3.18	-8.10	-10.72*	14.29**	16.42**	11.27**	13.09**	0.40**	18.50**	-7.41**	14.64**
H8	0.66	-12.15	-0.02	-15.53	17.55**	-21.27**	15.06**	-31.31**	18.87**	-8.86**	4.00**	-23.69**
H9	-4.67	0.61	-7.40	-0.85**	94.29**	-42.86**	33.33**	-52.94**	140.43**	13.25**	77.00**	11.85**
H10	-5.07	6.55**	-11.25	3.10**	137.30**	-5.29**	75.78**	-9.60**	95.01**	2.81**	49.02**	-0.64**
H11	-12.18	7.66**	-21.72	7.15**	87.06**	-1.85**	34.54**	-19.70**	113.89**	-5.26**	71.69**	-18.18**
H12	-11.67	1.09	-12.86	-0.22**	82.65**	-7.96**	46.82**	-21.21**	102.51**	-2.88**	77.13**	-13.94**
H13	-18.31	2.75*	-23.56	-0.09**	135.80**	-29.41**	78.69**	-31.43**	121.05**	-1.97**	110.59**	-11.59**
H14	-1.12	10.85**	-0.65	12.81**	68.30**	-14.71**	28.96**	-17.14**	46.14**	6.47**	14.18**	4.56**
H15	-2.97	5.69**	-8.72	2.89**	-20.68**	14.62**	-41.19**	0.00**	-27.59**	35.14**	-40.86**	18.13**
H16	-6.28	-5.37	-6.96	-9.72*	60.63**	3.70**	55.93**	-17.65**	39.30**	8.64**	34.37**	3.75**
H17	-6.42	7.09**	-10.49	6.04**	0.60**	47.22**	-6.57**	3.92*	15.15**	32.65**	11.65**	15.79**
H18	-10.00	-1.76	-4.42**	4.42**	24.12**	14.09**	14.29**	-16.67**	16.09**	9.09**	2.09**	-2.26**
H19	-15.00	8.74**	-15.70	7.26**	21.56**	11.63**	21.07**	-5.88**	14.95**	41.23**	-6.42**	28.81**
H20	-16.10	-9.63	-21.75	-12.44	24.50**	16.28**	22.04**	-1.96**	9.89**	2.95**	9.31**	-0.12**
H21	-7.40	-6.88	-7.74	-8.02	34.14**	-16.65**	30.41**	-38.24**	9.09**	2.24**	3.49**	-9.65**
H22	-15.31	2.45	-19.56	-1.32**	34.59**	39.87**	28.59**	18.89**	43.58**	10.86**	34.44**	-6.95**
H23	-1.64	1.34	-9.20	-0.68**	54.20**	75.70**	38.19**	56.67**	51.85**	16.64**	29.45**	0.35**
H24	-19.26	-7.21	-19.35	-12.62	5.04**	32.31**	1.57**	22.86**	14.84**	13.63**	-9.07**	-0.57**
H25	-9.14	-3.53	-14.68	-5.06**	5.39**	72.31**	0.34**	60.00**	12.44**	29.55**	9.01**	27.46**
H26	-4.88	8.96**	-5.22	2.73**	137.35**	13.06**	136.99**	2.86**	78.56**	2.40**	63.73**	-13.05**
H27	-9.33	-8.70	-20.14	-10.31	9.50**	43.82**	17.10**	36.17**	18.20**	22.67**	6.85**	19.09**
H28	4.90	-8.12	-0.46	-10.25*	26.56**	-14.22**	17.10**	-31.43**	24.92**	-8.43**	4.23**	-12.78**
H29	-22.56	-8.29	-30.69	-10.27	97.44**	23.21**	80.02**	-1.43**	80.75**	13.30**	74.36**	-3.62**
H30	4.52	-8.97	9.93	-6.88**	31.89**	25.49**	25.82**	36.19**	38.00**	17.72**	34.93**	19.43**
H31	-15.90	6.67**	-22.29	2.40**	34.69**	-14.53**	24.49**	-28.57**	37.63**	0.60**	25.78**	-1.37**
H32	-6.57	-2.97	-8.26	-3.37**	37.86**	-11.34**	29.33**	-25.91**	23.74**	-12.25**	8.32**	-23.45**
H33	-3.33	-12.32	-11.05	-15.72	70.04**	-4.33**	52.59**	-6.44**	62.26**	-6.31**	49.73**	-7.76**
H34	-19.90	-9.97	-24.71	-13.91	27.82**	5.58**	25.79**	5.58**	16.19**	4.38**	-5.80**	-7.36**
H35	-3.32	-11.11	-3.76	-11.23	86.05**	20.28**	80.17**	2.38**	61.75**	22.61**	37.48**	18.39**
H36	-4.79	-9.70	-10.89	-13.55	29.02**	32.59**	23.02**	12.86**	14.64**	20.29**	8.21**	3.55**
LSD5%	1.24	2.05	1.43	2.37	16.73	56.48	19.32	65.22	4.84	6.85	5.59	7.91
LSD1%	1.647	2.72	1.90	3.14	22.193	74.91	25.63	86.50	6.424	9.09	7.42	10.49

Legend: *Significant at 0.05 probability level; **highly significant at 0.01 probability level; MPH, Mid-parent heterosis; BPH, Better parent heterosis; ENV, Environment; LSD, Least significant difference.



Table 8. Half diallel's analysis for analyzed features in two growing environments using Jones (1965) modifications.

Traits	Env.	a	b	b ₁	b ₂	b ₃	Baker ratio
Degree of freedom	1	8	36	1	8	27	
Plant height	Env1	4271.90**	1214.27**	2583.36	1026.19*	1219.29	0.88
	Env2	2604.07	415.38	219.98	104.41	514.76	0.93
Stem base diameter	Env1	54.24**	62.60**	490.89*	30.15*	56.36**	0.63
	Env2	35.15	7.49	50.75	3.40	7.10	0.90
Core diameter	Env1	48.31**	63.98**	483.62*	25.76*	59.76**	0.60
	Env2	31.10	7.56	49.33	2.61	7.48	0.89
Stem middle diameter	Env1	13.61**	7.22**	8.12	3.44	8.30**	0.79
	Env2	10.59	1.86	11.62	1.43	1.62	0.92
Stem top diameter	Env1	60.10**	17.08**	125.22*	5.76**	16.42**	0.88
	Env2	39.21**	14.89**	13.16	15.29**	14.84**	0.84
Number of nodes	Env1	11.08**	19.68**	236.22*	15.19**	12.99**	0.53
	Env2	2.42	1.54	2.13	2.57	1.21	0.76
Days to first flowering	Env1	126.12**	25.87	16.36	12.84	30.09*	0.91
	Env2	9.11**	1.68*	0.03	1.68	1.80*	0.92
Days to 50% flowering	Env1	97.58**	58.34**	363.42	50.33**	49.42**	0.77
	Env2	221.51	47.89	4.27	35.63	53.14	0.90
Stem weight with leaves and pod	Env1	20.17**	36.37**	590.01**	17.69**	29.88**	0.53
	Env2	418094.2	106164.9	348691.8	132382.3	89414.3	0.89
Fresh stem weight	Env1	21635.6**	22257.7**	196640.5*	8445.2*	19891.7**	0.66
	Env2	28799.3	3097.7	10698.3	1759.3	3212.7	0.95
Number of pods per plant	Env1	12075.56**	10297.52**	126802.93**	558.09*	8868.26**	0.70
	Env2	2.07	1.15	2.20	0.76	1.28	0.78
Number of seeds per pod	Env1	89.14**	65.30**	732.09**	24.35**	52.73**	0.73
	Env2	178.02**	30.04**	23.83	19.99*	33.24**	0.92
1000 seeds weight	Env1	1.35**	1.11**	7.04*	0.86**	0.96**	0.71
	Env2	2.35	1.53	13.81*	0.51	1.38	0.75
Dry stick weight	Env1	1562.64**	2651.59**	23683.01**	818.33**	2415.83**	0.54
	Env2	7773.80	1893.84	3518.70	2190.80	1745.68	0.89
Dry fiber weight	Env1	178.16**	198.39**	1602.80**	94.40**	177.18**	0.64
	Env2	108.70	17.16	85.02	3.70	18.63	0.93

Legend: *Significant at 0.05 probability level; **highly significant at 0.01 probability level; ENV, Environment; a Additive genetic effects; b Dominance effects; b₁, b₂ and b₃ Subcomponents of B.

Table 9. Homogeneity tests for hypothesis validity were performed on fifteen characters of kenaf in a 9 × 9 half diallel's analysis in two environments.

Traits	Env.	a	b ^{wr/vr}	SE (b ^{wr/vr})	b ^{wr/vr} = 0	l - b ^{wr/vr}	t ²	r _{xy}
Plant height	Env1	37.237	0.272	0.129	2.103	5.625**	9.766**	-0.19
	Env2	-8.958	0.653	0.187	3.494*	1.856	0.774	0.66
Stem base diameter	Env1	-1.061	0.149	0.131	1.139	6.482**	10.667**	-0.60
	Env2	0.740	0.242	0.204	1.186	3.725**	2.559*	0.11
Core diameter	Env1	-1.548	0.167	0.131	1.276	6.355**	10.562**	-0.63
	Env2	0.552	0.287	0.237	1.210	3.004*	1.216	-0.06
Stem middle diameter	Env1	0.033	0.222	0.075	2.950*	10.332**	36.602**	-0.01
	Env2	0.262	0.238	0.159	1.500	4.807**	5.857**	-0.26
Stem top diameter	Env1	-0.151	0.525	0.399	1.315	1.191	0.239	-0.49
	Env2	-0.004	0.214	0.154	1.388	5.107**	6.556**	-0.59
Number of nodes	Env1	-1.277	0.337	0.132	2.557*	5.030**	8.416**	-0.83
	Env2	0.370	-0.567	0.440	-1.287	3.558**	0.593	0.23
Days to first flowering	Env1	-0.010	0.394	0.077	5.114**	7.859**	27.127**	0.61
	Env2	0.829	0.655	0.214	3.066*	1.613	0.345	-0.49
Days to 50% flowering	Env1	-4.755	0.420	0.404	1.040	1.434	0.157	0.27
	Env2	-8.672	0.881	0.144	6.126**	0.824	0.074	0.11
Stem weight with leaves and pod	Env1	-25220.871	0.165	0.100	1.646	8.339**	20.309**	0.06
	Env2	-1965.299	0.298	0.190	1.564	3.693**	2.993*	-0.75
Fresh stem weight	Env1	-1099.558	0.269	0.119	2.273	6.164**	12.235**	-0.56
	Env2	174.470	0.705	0.221	3.193*	1.333	0.132	-0.24
Number of pods per plant	Env1	-339.710	0.298	0.141	2.112	4.974**	7.478**	0.37
	Env2	24.107	0.130	0.214	0.607	4.066**	2.396*	-0.29
Number of seeds per pod	Env1	-2.650	0.267	0.303	0.881	2.422*	0.225	0.64
	Env2	7.170	0.122	0.267	0.456	3.290*	0.830	-0.52
1000 seeds weight	Env1	0.061	0.468	0.313	1.495	1.701	0.024	0.52
	Env2	1.094	0.043	0.326	0.133	2.936*	0.153	0.43
Dry stick weight	Env1	-124.716	0.207	0.097	2.122	8.135**	20.864**	-0.34
	Env2	-0.078	0.384	0.242	1.586	2.540*	0.828	-0.07
Dry fiber weight	Env1	-0.745	0.107	0.081	1.312	11.002**	33.670**	-0.49
	Env2	0.351	0.605	0.157	3.865**	2.523*	2.180	-0.04

Legend: *Significant at 0.05 probability level; **highly significant at 0.01 probability level; ENV, Environment.



Table 10. Components of genetic variance (Hayman 1954) for all nine parents and their crosses over two environments for all traits tested.

Traits	D	F	H ₁	H ₂	h ²	(H ₁ /D) ^{1/2}	H ₂ /4 H ₁	h ² /H ₂	h ²
PH	-369.83**	-1025.68**	-1161.29**	-775.20**	-96.75**	1.77	0.17	0.12	23.05
SBD	-4.29	-10.58**	3.45**	6.56**	28.28*	0	0.48	4.31	14.41
CD	-4.56	-10.64**	2.60**	6.48**	27.74*	0	0.62	4.28	10.50
SMD	-1.29	-3.15	-2.56	-1.28	0.57	1.41	0.12	-0.44	13.35
STD	-0.87	-1.29	-1.56	-1.03	-0.32	1.34	0.16	0.31	0
NN	-0.95	-1.30	0.73	1.20	9.46	0	0.41	7.88	0
D1FF	-4.80	-22.32**	-17.37**	-10.13*	-4.07	1.90	0.15	0.40	34.40
D50%F	-13.39**	-40.67**	-56.91**	-37.47**	3.25**	2.06	0.16	-0.09	14.16
FW1	-43359.99**	-94759.01**	96084.93**	129965.29**	364591.81**	0	0.34	2.81	8.17
FW2	-2032.35**	-6796.38**	-4058.43**	-1318.11**	9217.05**	1.41	0.08	-6.99	20.06
DSW	-633.49**	-1306.31**	-1372.45**	-870.14**	1316.32**	1.47	0.16	-1.51	11.44
DFW	-4.33**	-22.32**	14.03**	20.65**	81.72**	0	0.37	3.96	19.83
NF	-182.73**	-1090.80**	1524.86**	1899.41**	4912.29**	0	0.31	2.59	19.21
NS	5.75*	-9.70**	16.77**	16.30**	16.57**	1.71	0.24	1.02	50.93
SW	0.48	-2.41*	7.75*	7.40*	7.45	4.04	0.24	1.01	32.84

Legend: **Highly significant at P ≤ .01 level; *Significant at P ≤ .05 level; D, Additive; H₁, Dominance; H₂, Dominance × dominance; h₂, Overall dominance; h²N, Narrow-sense heritability; PH, Plant height; SBD, Stem base diameter; CD, Core diameter; SMD, Stem middle diameter; STD, Stem top diameter; NN, Number of nodes; D1FF, Days to first flowering; D50%F, Days to 50% flowering; FW1, Stem weight with leaves and pod; FW2, Fresh stem weight; DSW, Dry stick weight; DFW, Dry fiber weight; NF, Number of pods per plant; NS, Number of seeds per pod; SW, 1000 seeds weight.

pod, dry fiber weight, pods number, seeds number, and 1000 seeds weight were positive and more than unity, indicating that at least one group of the dominant gene(s) controlling these traits exhibited dominance; however, it was negative for the stem middle diameter, days to 50% flowering, fresh stem weight, and dry stick weight indicating only one group of the recessive gene(s) showing a dominance effect on these traits. Seeds number had the highest narrow-sense heritability of 50.93% in the combined environment, followed by days to 1st flowering (34.40%), 1000 seed weight (32.84%), plant height (23.05%), and fresh stem weight (20.06%). Conversely, the remaining traits had a low, narrow sense heritability, indicating that non-additive gene effects predominated in trait inheritance.

Discussion

All studied traits exhibited a GCA/SCA ratio greater than unity in the 2nd environment, showing that additive gene action effects played a significant role in character inheritance. In the 1st environment, however, a more significant ratio of GCA/SCA than unity was observed for eight of the 15 analyzed traits, although seven showed lower than unity, indicating that additive and additive × additive gene effects dominated the inheritance of studied traits. While additive gene effects contributed the most to variability in most traits, indicating that the parental materials studied had a lot of genetic variabilities.

This finding usually favors the breeding selection strategy due to significant additive gene effects (Sarker, Rasul, and Mian 2002). According to Mostofa, Rahman, and Hussain (2011), the development of traits such as days to 1st flowering, dry fiber weight, and 1000-seed weight all imply the presence of additive gene effects. A single dominant gene pair influenced days to 1st flowering and plant height, but raw fiber yield was influenced by three genes (Thombre and Patil 1985). Mukewar, Zope, and Lahane (1997) discovered that additive gene activity predominated in kenaf seed yield and the number of pods. Pace, Piscioneri, and Settanni (1998) found that additive gene action was more important for yield components, including plant height, fresh and dry weight of bark, and usable stick in kenaf. In addition, the environment had a tremendous impact on how these characters evolved (Abu et al. 2017). Mostofa, Rahman, and Ghosh (2013) and Youcai, Anping, and Weijie (1998) discovered similar results in kenaf, Sobhan (1993) in *Hibiscus sabdariffa*, and Khatun et al. (2007) in *Corchorus capsularis*, respectively, using combining ability investigations.

Parent P₄ was the best parental line in terms of plant height, stem base diameter, core diameter, stem middle diameter, stem weight with leaves and pods, fresh stem weight, seed number, dry stick weight and dry fiber weight content, indicating that the hybrids had accumulated beneficial additive genes for these traits. Plant height, fresh stem weight, and dry fiber weight were all positively affected by the parent P₃, whereas the parent P₁ was the best general combiner for days to 1st flowering, fresh stem weight, dry fiber weight, and pods number contributed positively to the hybrid for these traits.

SCA effects were found to be substantial for most yield characteristics in both environments. According to the results for all genotypes, the best cross combinations for stem base diameter, core diameter, stem weight with leaves and pod, and fresh stem weight were H9, H23, H29, and H35. The hybrids H9, H29 and H35 were the most effective specific combiners for dry fiber weight. The cross H23 is a good combiner for pod number per plant, whereas H29 is good for plant height, stem middle diameter, stem top diameter, 1000 seed weight, dry stick weight and dry fiber weight. The hybrids H3, H28, and H35 were identified as the best specific combiners for dry stick weight and pods per plant. The best specific combiners for dry fiber weight and seed number per pod were hybrid H2. The hybrids H3 and H28 were chosen as good specific combiners for pods per plant and seeds per pod. The hybrids H4, H20, H24, and H34 were selected as good specific combiners for another feature, 1000 seed weight (smaller seed size). Hybrid vigor can be induced by dominant, over-dominant, or epistatic gene action in any combination of parents, according to Moll and Stuber (1974). In this study, both additive and non-additive genetic components influenced morphological and yield-related traits, with non-additive gene activity predominating in most characters.

According to Liu (2005), there is a lot of heterosis in yield characteristics depending on the mid-parent and better parent. Heterosis estimates based on mid-parental values ranged from 10% to 55%,

with stalk dry weight and bast percentages ranging from 10% to 55% (Behmaram et al. 2014). In both environments, hybrid H3 showed the greatest mid-parent and better parent heterosis for 8 of the 15 phenotypic parameters. In addition, for nodes number and dry fiber weight, H4 had the highest mid-parent and better parent heterosis. In contrast, H9 had the largest stem base diameter, core diameter, and dry fiber weight. In terms of the features indicated, the hybrids exceeded their mutant parents. Therefore, the hybrid H11 will be the best choice for 1st flowering and days to 50% flowering features in late-maturity cultivars. Furthermore, in terms of stem base diameter, core diameter, fresh stem weight, dry stick weight, and dry fiber weight, hybrids H23 and H35 were chosen as the best combiners. Hybrid H29, on the other hand, had high mid-parent and improved parent heterosis estimations for Plant height, stem base diameter, core diameter, stem weight with leaves and pods, and fresh stem weight.

Compared to the better-parent and the mid-parent, higher heterosis values indicated the absence of epistasis and the frequency of partial or total dominance of genes for fiber and seed yield. By examining the proportion F_1 heterosis over the high parent, crosses that yield superior transgressive segregants with higher fiber output could be identified. The strongest positive estimates of mid-parent and better parent heterosis were found, showing the accumulation of desirable genes inherited from their parents. According to hybrids studied in both environments, H3, H4, H9, H11, H23, H29, and H35 had the best yield and yield component quality.

For most of the traits, additive genetic effects (a) were significantly larger than dominant genetic effects (b) in both environments, showing the presence of both additive and dominant gene activities in the inheritance of these traits (Table 8). The findings agree with those of Akter (2009). Except for stem base diameter, core diameter, nodes number, stem weight with leaves and pods, fresh stem weight, dry stick weight, and dry fiber weight in the 1st environment, additive genetic effects (a) were found to be significantly larger than dominance genetic effects (b) in both environments, indicating the presence of both additive and dominance gene actions in the inheritance of these traits. Xu (1990) discovered a larger magnitude of the additive genetic variance than dominance in the inheritance of kenaf flowering days. Baker ratios greater than 0.80 indicated that additive gene effects were more important in the genetic control of plant height, stem top diameter, and days to 1st flowering in both environments and most traits in the 2nd environment. Additive influences contributed more to genetic variation, according to the Baker ratio. In addition, a significant mean square due to changes in the environment was detected for most of the traits, demonstrating that differences in soil types and climate conditions in each environment influenced the F_1 's mean deviation from their mid-parental values for two attributes.

A graphical analysis of parent-offspring covariance (W_r) and array variance (V_r) revealed that the plant height (2nd env.), days to 1st flowering (2nd env.), days to 50% flowering (2nd env.), and fresh stem weight (2nd env.), fitted with a simple additive-dominance genetic model ($H_0: b > 0$ and $H_0: b = 1$) involving all the nine parents studied. They are considerably different from zero but not from unity, showing that there is no non-allelic interaction for these features' inheritance. The findings were comparable to those of Sobhan (1993), who found that the days to flower fit the model well and the regression coefficient was substantially different from zero but not from unity.

However, stem middle diameter (1st env.), nodes number (1st env.), days to 1st flowering (1st env.) and dry fiber weight (2nd env.) showed highly significant "b" values and therefore did not follow the model clearly which were significantly different both from zero and unity indicating the presence of an inter-allelic interaction in the inheritance of these traits. Days to 1st flowering in kenaf did not match the model (Mostofa, Rahman, and Ghosh 2013). The remaining traits in both environments were considered to follow epistatic or non-allelic gene interaction as the regression coefficient significantly differed from unity but not zero involving all the nine parents studied. Similar results were obtained by Khatun et al. (2007) reported pods numbers with *Corchorus capsularis*, a similar bast fiber plant to kenaf. The non-significant t^2 values supported the validation of assumptions for these qualities by satisfying the uniformity of covariance and variance (W_r - V_r).

Hayman's ANOVA and components of variation related to gene actions revealed that both additive and dominant (non-additive) gene actions governed all the characters (Table 10). It also revealed that positive and negative alleles were not equally common in the parents and asymmetrical gene distribution at the loci, indicating that all these characteristics were dominant. These findings agreed with Akter (2009), who reported that positive and negative alleles were not equal in the parents since H_1 and H_2 were not equal for all traits (the days to 1st flowering, nodes number, pods number and seeds number) in *C. olitorius*. But the value of additive (D) and dominance (H_1) of $(H_1/D) \frac{1}{2}$ showed zero indicating presence of no dominance effects for the stem base diameter, core diameter, nodes number, stem weight with leaves and pod, dry fiber weight, and pods number, while there were dominance effects for the other traits showed 1.34 to 4.04. Patil and Thombre (1981) reported a more significant proportion of additive genetic components concerning days to flowering, plant height and length of fiber in kenaf. Heritability in the narrow sense (h^2_N), as measured from genetic components appeared to be moderate to low in the combined two environments for most of the traits. Khatun et al. (2007) found similar results for *C. capsularis*, finding that the narrow sense heritability in F_1 was moderate for the number of seeds (47%) and 1000 seed weight (37%) yet low for the number of fruits per plant (15%). All parameters of kenaf (plant yield, stalk yield, plant height, basal diameter, middle diameter, dry stalk yield) had a low narrow-sense heritability, according to Liu (2005). According to Falconer and Mackay (1996), low additive effects and high dominant gene action caused reduced narrow-sense heritability. Pedigree selection based on plant height, days to 1st flowering, and fresh stem weight can improve kenaf fiber yield.

Conclusion

Additive and non-additive variations played a role in the genetic control of all variables, including fiber yield and yield-related traits. The strongest positive estimates of mid-parent and better-parent heterosis for the qualities examined indicate the accumulation of favorable genes inherited from their parental mutant lines. The combining ability analysis revealed significant GCA and SCA were observed in seed number per pod and 1000 seed weight, controlled by both additive and non-additive gene effects. In contrast, the hybrids H3 ($P_1 \times P_4$), H4 ($P_1 \times P_5$), H9 ($P_2 \times P_3$), H11 ($P_2 \times P_5$), H23 ($P_4 \times P_6$), H29 ($P_5 \times P_8$), and H35 ($P_7 \times P_9$) showed promising heterotic responses and could benefit future breeding programs. Because the traits have a high Baker ratio and moderate to low narrow sense heritability, it was decided that selection should be made in advanced generations after homozygosity and genetic fixation. Variance and covariance graphs revealed an over-dominance for most traits except for stem middle diameter, pod number and 1000 seed weight, showing a clear-cut case of partial dominance. Parents P_2 , P_8 and P_9 possessed the most recessive genes, while parents P_1 , P_3 and P_4 had maximum dominant alleles for most of the studied traits.

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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 and Mohd Y. Rafii; Investigation, Mohd Y. Rafii, Zulkarami Berahim, Azizah Misran and Zaiton Ahmad; Supervision, Mohd Y. Rafii; Writing – original draft, Md Al-Mamun; Writing – review & editing, Yusuff Oladosu. All authors have read and agreed to the published version of the manuscript.

Disclosure statement

No potential conflict of interest was reported by the authors.

Conflicts of benefits

Regarding the research of this manuscript, the authors disclosed no potential conflicts of interest.

Highlights

- Additive and non-additive gene action varied between the evaluated traits.
- The expression of additive genes was highly influenced by the environment
- High GCA parents did not always produce the best performers.
- GCA and SCA effects indicated the necessity for distinct breeding strategies.

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