

Genetic Analysis of some Important Seed Yield Related Traits in Kenaf (*Hibiscus cannabinus* L.)

Md. Golam Mostofa¹, Lutfur Rahman² and Ranjit Kumar Ghosh^{1,*}

ABSTRACT

Genetic analyses for the days to first flowering, the number of fruits per plant, the number of seeds per fruit and the 1,000 seed-weight were carried out using six-parents half diallel crosses in kenaf to determine the inheritance pattern and genetic behavior of these characters. Hayman's analysis of variance and components of variations related to gene actions indicated the involvement of both additive and dominance effects for all the traits, but the value of additive (D) and dominance (H_1) of $(H_1/D)^{1/2}$ indicated predominant additive effects for the days to first flowering (0.91) and 1,000 seed-weight (0.81), while there were dominance effects for the number of fruits per plant (28.35) and the number of seeds per fruit (2.58). Variance and covariance graphs revealed a partial dominance for all the traits except the number of seeds per fruit which showed over-dominance. Parents Acc.5030, Acc.4197 and Acc.2922 possessed the most recessive genes, while parents Acc.4659 and Acc.2731 had maximum dominant alleles for all the studied traits. The value of heritability in the narrow sense (h^2_{ns}) was comparatively high for the days to first flowering (0.59) and 1,000 seed-weight (0.56), but it was low for the number of seeds per fruit (0.09) and the number of fruits per plant (0.01). Therefore, the improvement of seed yield can be enhanced through pedigree selection considering the desired traits in the early or segregating generation based on appropriate parents in the breeding program.

Keywords: Covariance, dominance effects, half-diallel cross, Hayman's analysis of variance, kenaf

INTRODUCTION

Kenaf (*Hibiscus cannabinus* L.) is a fast growing annual plant that is harvested mainly for its bast fiber. It is closely related to cotton and okra (*H. esculentus*). Kenaf is an important jute substitute in Bangladesh as it is tolerant to moisture stress and it can be grown in drought-prone areas and in low fertile soils where jute cannot be grown (Ahmad and Khatun, 1992). It is biodegradable and an environment friendly crop. Kenaf is commercially cultivated in more than 20

countries, particularly in India, China, Thailand and Vietnam (Food and Agriculture Organization, 2003), while in Bangladesh, around 19,611 ha of land is now under kenaf cultivation (International Jute Study Group, 2012). It is a short-day plant remaining vegetative until the day length falls below 12 hr (Carberry *et al.*, 1992) or 12 hr and 45 min (Alexopoulou *et al.*, 2000). Flowering of late-maturity cultivars is under photoperiodic control; conversely photoperiod does not influence the flowering of early-maturity cultivars (Alexopoulou *et al.*, 2000), which are less productive in terms

¹ Bangladesh Jute Research Institute, Manik Mia Avenue, Dhaka-1207, Bangladesh.

² Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh, Bangladesh.

* Corresponding author, e-mail: ranjit.bjri@yahoo.com

of final biomass (Patane and Sortino, 2010). Seed availability is a prerequisite for the widespread distribution of the crop for biomass production in the whole country. Seed production of kenaf is also economically important since it is a good source (16–22%) of oil (Patane and Sortino, 2010). Kenaf oil is characterized by a fatty acid composition and very similar to cotton seed oil. It is comparable to the most common edible oils and excellent for human consumption (Mohamed *et al.*, 1995). It is also important for reducing cholesterol and heart diseases (Mohamed *et al.*, 1995). The seeds can also be used for cooking (flour) and lubrication, soap manufacture, cosmetics, linoleum, paints and varnishes (Coetzee *et al.*, 2008).

Since kenaf is an annual crop, seeds are needed in a continuous supply (Ten and Wong, 2006). However, the problem of kenaf seed production is the high sensitivity to photoperiod. In the Bangladeshi context, kenaf plants keep the land occupied for about 8–9 mth (April to November/December) or more for seed production. Farmers face serious problems if they want to produce both fiber and seed from the same crop. Many small growers customarily leave an uncut portion of the field as a source of seed. Such seed crops suffer badly from natural hazards like hailstorm, heavy rainfall and foggy weather which can hamper normal crop growth; some plants dry up and the major part of the crop becomes senescent and incapable of producing fruits. On the other hand, only a few plants can produce fruits but do not exceed 15 fruits per plant. More importantly, the seeds frequently mature before the end of the rainy season, causing difficulty in drying the fruits; the mature seeds often germinate in the fruits before they can be threshed (Dempsey, 1975). Such seeds can never be treated as a quality product with respect to germination, viability and vigor. Therefore, early maturing and high seed-yielding kenaf varieties are needed to overcome these problems and one possibility is hybridization among appropriate parents. However, prior to undertaking any breeding program, information

on the inheritance of yield and yield-contributing characters is very important. Hence, this study aimed to identify the inheritance pattern and genetic behavior for the days to first flowering, the number of fruits per plant, the number of seeds per fruit and 1,000 seed-weight related to kenaf seed yield.

MATERIALS AND METHODS

Six kenaf accessions CPI-72126, Acc.4197, Acc.2922, Acc.5030, Acc.4659 and Acc.2731 representing different agro-ecological conditions were used in this study. Diallel mating was conducted in all possible combinations excluding reciprocals at the glasshouse premises of the Bangladesh Jute Research Institute (BJRI) during October and November 2009 and thus 15 F_1 hybrids were obtained. Seeds of 21 entries (six parents and 15 F_1 s) were sown on 6 April 2010 at the Central Station of BJRI in a randomized complete block design with three replications. Each plot consisted of 3 rows of 1 m length. The spacing was maintained at 30 cm between rows and 8–10 cm between plants. The replications (blocks) were interspaced by 1 m. The recommended intercultural operations (weeding, thinning, plant protection measures and supplemental irrigation among others) were undertaken whilst raising the crop throughout the cropping season.

The data were recorded on five randomly selected plants from each entry for the days to first flowering, the number of fruits per plant, the number of seeds per fruit and 1,000 seed-weight. Mean data for each entry were used for statistical analysis. Analysis of variance was carried out for genotypes, parents (P), crosses (F_1) and P versus F_1 . From the analysis, the least significant difference was calculated which was used to compare the entries. Hayman's analysis of variance (ANOVA), array variance (V_r) and parent-offspring covariance (W_r) were calculated according to Hayman (1954a) following Jones (1965) modification. A V_r - W_r graph (Hayman

1954a; Jinks 1954) and components of genetic variations along with related genetic parameters were estimated according to Hayman (1954b).

RESULTS AND DISCUSSION

Mean performance of parents and F₁ hybrids

Days to first flowering

The genotypes, parents (P), crosses (F₁) and P versus F₁ interaction in the analysis of variance for the days to first flowering were highly significant ($P < 0.01$) indicating considerable differences among the genotypes for this trait (Table 1). The average days from sowing to first flowering in F₁ ranged from 69 to 190 d compared to the parental values ranging from 80 to 191 d (Table 2). The parent with the lowest ranking was Acc.5030 followed by Acc.2922 and Acc.4197. Parent Acc.5030 differed significantly ($P < 0.05$) from other parents. The parent with the highest ranking was Acc.4659, which also differed significantly from other parents. Among the crosses, the hybrid Acc.2922 × Acc.5030 took the shortest period of flowering (69 d), which was 35 and 11 d earlier than its female and male parents, respectively. Hence, Acc.2922 × Acc.5030 was the best performing hybrid followed by Acc.4197 × Acc.2922, Acc.4197 × Acc.5030 and CPI-72126 × Acc.2922. These crosses were significantly different from all the other crosses. However, the longest period (190 d) was observed for the hybrid Acc.4659 × Acc.2731, which was one day earlier

than its female parent (191 d) but markedly later than its male parent (182 d).

Number of fruits per plant

Table 1 shows significant differences in the number of fruits per plant among genotypes, crosses and P versus F₁ but the difference was not significant in case of the parents. The average number of fruits per plant in F₁ ranged from 4 to 21 compared with the parental values of 5 to 8 (Table 2). Parents Acc.4197, Acc.5030 and Acc.2731 were equal performers and for each one, there was no significantly higher difference than for the remainder of the parents. The parent with the lowest ranking was Acc.4659. The cross combination Acc.4197 × Acc.2922 produced the highest number of fruits per plant (21), which was much higher than that of any of the parents, indicating the presence of transgressive segregation in the cross. In decreasing order, the crosses Acc.4197 × Acc.5030, Acc.2922 × Acc.2731 and CPI-72126 × Acc.5030 also showed higher numbers of fruits per plant, following Acc.4197 × Acc.2922. The lowest number of fruits per plant (4) was produced from CPI-72126 × Acc.2731, which was lower than either of its parents (Table 2).

Number of seeds per fruit

The genotypes, parents, crosses and P versus F₁ interaction for the number of seeds per fruit were not significant in the analysis of variance (Table 1). The highest magnitude of the parental mean was obtained from both Acc.4197

Table 1 Analysis of variance for four seed yield related characters of kenaf in a 6 x 6 half-diallel cross.

Source of variation	df	Days to first flowering	Number of fruits per plant	Number of seeds per fruit	1,000 seed-weight (g)
Replication	2	1.00 ns	0.33 ns	6.30 ns	0.03 ns
Genotypes	20	4161.34**	45.57**	21.61 ns	3.99 ns
Parents (P)	5	6646.50**	4.80 ns	14.13 ns	5.98 ns
Crosses (F ₁)	14	3449.57**	55.49**	25.80 ns	3.45 ns
P versus F ₁	1	1700.36**	110.63*	0.31 ns	1.62 ns
Error	40	16.60	4.83	6.57	0.06

df = Degrees of freedom, ns = Not significant, * = $P < 0.05$, ** = $P < 0.01$.

and Acc.4659 (19.00) followed by Acc.2731 (17.00) and CPI-72126 (16.67) as shown in Table 2. The parent with the lowest ranking was Acc.2922, which differed significantly from the highest ranking two parents. Among the crosses, Acc.2922 × Acc.4659 produced the highest (22.33)

and Acc.5030 × Acc.2731 produced the lowest (12.33) number of seeds per fruit. The crosses Acc.4197 × Acc.2922 and Acc.4197 × Acc.5030 also showed higher numbers of seeds per fruit following Acc.2922 × Acc.4659. A higher number of seeds per fruit was obtained from the hybrids

Table 2 Mean performance and general combining ability effects (in parentheses) of six parental accessions and averages of their half-diallel crosses for four seed-yield related characters.

Parents and their crosses	Days to first flowering	Number of fruits per plant	Number of seeds per fruit	1,000 seed-weight (g)
Parents				
CPI-72126 (P ₁)	179 (15.25**)	6 (-2.08**)	16.67 (-0.49**)	23.88 (0.34**)
Acc.4197 (P ₂)	173 (3.38**)	8 (2.04**)	19.00 (1.68**)	22.02 (-0.58**)
Acc.2922 (P ₃)	104 (-29.88**)	7 (1.42**)	14.00 (0.18**)	22.65 (-0.40**)
Acc.5030 (P ₄)	80 (-27.13**)	8 (0.92**)	14.33 (-1.86**)	23.72 (0.26**)
Acc.4659 (P ₅)	191 (22.00**)	5 (-1.58**)	19.00 (1.26**)	21.28 (-0.79**)
Acc.2731 (P ₆)	182 (16.38**)	8 (-0.71**)	17.00 (-0.78**)	25.17 (1.18**)
F ₁ s				
CPI-72126 × Acc.4197	178	7	16.67	22.82
CPI-72126 × Acc.2922	164	8	17.33	22.30
CPI-72126 × Acc.5030	169	11	12.67	24.04
CPI-72126 × Acc.4659	189	5	16.67	21.80
CPI-72126 × Acc.2731	182	4	15.33	24.08
Acc.4197 × Acc.2922	98	21	21.67	21.58
Acc.4197 × Acc.5030	160	17	19.33	21.23
Acc.4197 × Acc.4659	186	9	17.33	21.44
Acc.4197 × Acc.2731	177	10	16.33	24.30
Acc.2922 × Acc.5030	69	10	13.00	22.62
Acc.2922 × Acc.4659	172	10	22.33	21.53
Acc.2922 × Acc.2731	168	12	15.00	23.52
Acc.5030 × Acc.4659	175	9	15.00	22.98
Acc.5030 × Acc.2731	168	8	12.33	23.82
Acc.4659 × Acc.2731	190	8	16.67	23.45
Mean	159.71	9.10	16.56	22.87
LSD _(0.05)	3.33	3.63	4.23	0.40
CV (%)	23.32	42.88	16.18	5.03

** = $P < 0.01$, LSD = Least significant difference, CV = Co-efficient of variation.

produced by the parental lines Acc.4197, Acc.2922 and Acc.4659 indicating their high contribution to the hybrids. Highly significant and positive general combining ability (GCA) effects also confirmed their higher potential. Therefore, these three parents were considered as the best general combiners for this trait.

1,000 seed-weight

No significant variations for 1,000 seed-weight were found due to genotypes, parents, crosses and P versus F_1 in the analysis of variance (Table 1). The highest and the lowest 1,000 seed-weight were found in parents Acc.2731 (25.17 g) and Acc.4659 (21.28 g), respectively (Table 2). The lowest ranking parent Acc.4659 differed significantly from the rest of the parents. Most of the F_1 hybrids showed 1,000 seed-weight values between the weights of their parents indicating incomplete dominance for the inheritance of this trait. The highest (24.30 g) and the lowest (21.23 g) mean 1,000 seed-weight values were found in hybrids Acc.4197 \times Acc.2731 and Acc.4197 \times Acc.5030, respectively. The crosses Acc.4197 \times Acc.4659, Acc.2922 \times Acc.4659, Acc.4197 \times Acc.2922 and CPI-72126 \times Acc.4659 also showed lower 1,000 seed-weight values. These crosses were significantly different from all other crosses.

Of the six parental lines, Acc.4197 had the top value for two characters (number of fruits per plant and number of seeds per fruit), whereas Acc.5030 and Acc.4659 had the lowest value for the days to first flowering and 1,000 seed-weight, respectively. Significant GCA effects were found among the parents for the different characteristics estimated. Parents with high GCA effects for different characters may be extensively used in a hybridization program as the donor parents for the improvement of these traits. The GCA effects of parents revealed that the best general combiners were: Acc.5030 and Acc.2922 for the days to first flowering; Acc.4197, Acc.2922 and Acc.5030 for the number of fruits per plant; Acc.4197, Acc.4659 and Acc.2922 for the number of seeds per fruit;

and Acc.4659, Acc.4197 and Acc.2922 for 1,000 seed-weight. Among all the F_1 hybrids, it was revealed that if earliness of flowering is the most important selection criteria, the hybrids Acc.2922 \times Acc.5030 and Acc.4197 \times Acc.2922 will be the best in a breeding program. Otherwise, if seed yield and seed size are important in the breeding program, the hybrids Acc.4197 \times Acc.5030, Acc.4197 \times Acc.2922 and Acc.2922 \times Acc.4659 will be the best choice.

Hayman's analysis of variances

The results of Hayman's ANOVA following Jones (1965) modification for the days to first flowering, the number of fruits per plant, the number of seeds per fruit and 1,000 seed-weight are presented in Table 3. Both the additive genetic effects (A) and dominance effects (B) were found significant for all the characters indicating the presence of both additive and dominance gene actions in the inheritance of these traits. The results are in accordance with the findings of Akter (2009). The magnitude of A was much higher than B indicating the greater importance of the additive effects. The involvement of a larger magnitude of additive genetic variance than dominance was also reported by Xu (1990) in the inheritance of the days to flower in *Hibiscus cannabinus*. Among the sub-components of B, significant mid-parental deviation (b_1) provided information on the directional dominance, while asymmetry of the gene distribution (b_2) suggested that some parents contained more dominant alleles and the residual dominance effects (b_3) indicated the specific dominant alleles in individual cases.

Vr-Wr regression analysis

Graphical analysis of the parent-offspring covariance (Wr) and array variance (Vr) for all the characters and their related statistics are presented in Table 4 and Figures 1 to 4.

Days to first flowering

In testing the validity of the additive-

dominance model, the regression coefficient ($b = 0.774 \pm 0.031$), which was significantly different from both zero and unity (Table 4), did not follow the model, clearly indicating the presence of an interallelic interaction in the inheritance of this trait. The results differed from the findings of Sobhan (1993) with *Hibiscus sabdariffa*, a close species of *H. cannabinus*, where it was reported that the days to flower fitted the model well as the regression coefficient was significantly different from zero but not from unity. The regression line cut the Wr axis above the origin at an intercept of $a = 299.767$ indicating partial dominance controlling the trait (Figure 1). The array points 5 (Acc.4659), 6 (Acc.2731) and 1 (CPI-72126) were the nearest to the origin, thus they carried a relatively large number of dominant genes. On the other hand, the array point 4 (Acc.5030) was located furthest from the origin indicating a relative abundance of recessive genes. The significant correlation coefficient value between parental measurement (Yr) and the parental order of dominance (Wr

+ Vr) was -0.96 . This significant negative correlation indicated that positive genes, that is, those for a higher number of days to flowering (late flowering), were barely dominant over those for a lower number of days to flowering (early flowering).

Number of fruits per plant

The analysis of all arrays (six parents) for the number of fruits per plant gave a regression slope of $b = 0.038 \pm 0.030$ which was significantly different from unity but not from zero (Table 4) because of epistasis effects indicating the presence of a non-allelic gene interaction for the inheritance of this trait. Similar results were obtained by Khatun (2007) with *Corchorus capsularis*, a similar bast fiber plant to kenaf. The regression line cut the Wr axis above the point of origin at an intercept of $a = 1.187$ showing partial dominance controlling the trait (Figure 2). The order of parental measurement (Yr) was 6, 2, 4, 3, 1 and 5 and the parental order of dominance (Wr + Vr) was 5, 1, 6, 4, 3 and 2. The positive correlation coefficient of $r = 0.44$ between

Table 3 Hayman's ANOVA following Jones (1965) modification for different characters of kenaf in a 6×6 half-diallel cross.

Source of variation	Degrees of freedom	Days to first flowering	Number of fruits per plant	Number of seeds per fruit	1,000 seed-weight (g)
A	5	4199.000**	22.983**	14.015**	4.315**
B	15	449.819**	12.593**	4.933*	0.336**
b ₁	1	566.786**	0.076 ns	199.469**	395.319**
b ₂	5	279.800**	14.183**	6.681*	0.117**
b ₃	9	531.278**	13.100**	-17.653**	-43.429**
Error	40	5.533	1.611	2.189	0.021

A = Additive genetic effects, B = Dominance effects, b₁, b₂, b₃ = Sub components of B.
ns = Not significant, * = $P < 0.05$, ** = $P < 0.01$.

Table 4 Statistics related to Vr-Wr analysis for different characters of kenaf in a 6×6 half diallel cross.

Character	a	b	SE(b)	Ho: b=1	Ho: b=0	t ²
Days to first flowering	299.767	0.774	0.031	**	**	41.070**
Number of fruits per plant	1.178	0.038	0.030	**	ns	274.564**
Number of seeds per fruit	-1.646	0.562	0.251	ns	ns	0.746 ns
1,000 seed-weight (g)	0.597	0.502	0.187	ns	ns	2.622 ns

ns = Not significant, * = $P < 0.05$, ** = $P < 0.01$.

parental measurement (Y_r) and the parental order of dominance ($W_r + V_r$), which was not significant, suggested the presence of negative genes, that is, those for a lower number of fruits per plant were barely dominant over those for a higher number of fruits per plant.

Number of seeds per fruit

The Hayman's additive-dominance model was found partially valid from the b value (0.562 ± 0.251), which did not differ significantly from both zero and unity (Table 4), indicating the absence of a non-allelic interaction in the inheritance of the number of seeds per fruit and that the genes among the parents were distributed independently. Over-dominance type of inheritance was observed as the regression line touched the W_r axis below the origin ($a = -1.646$) as shown in Figure 3. These results are in agreement with the findings of Akter

(2009) for *Corchorus olitorius* and Khatun (2007) for *C. capsularis* from V_r - W_r regression analysis. The order of parental measurement (Y_r) was 2, 5, 6, 1, 4 and 3, the parental order of dominance ($W_r + V_r$) was 2, 1, 6, 5, 4 and 3 and the coefficient of correlation was $r = -0.79$ which revealed that the parent with the higher value of Y_r and lower value of ($W_r + V_r$) contained the most dominant alleles and confirmed the parental order of dominance in the V_r - W_r graph.

1,000 seed-weight

The regression coefficient ($b = 0.502 \pm 0.187$) of 1,000 seed-weight did not differ significantly from both unity and zero (Table 4), indicating a partial failure of the model. This result indicated that there wasn't a non-allelic interaction in the inheritance of this trait and the alleles among the parents were distributed independently. Similar

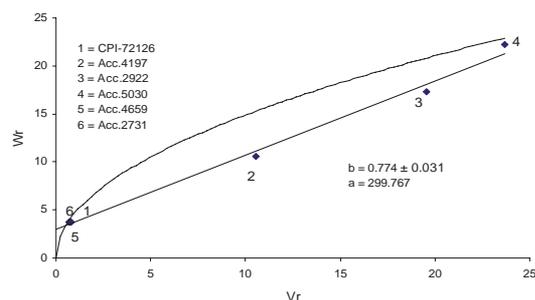


Figure 1 Array variance (V_r) and parent-offspring covariance (W_r) graph for days to first flowering.

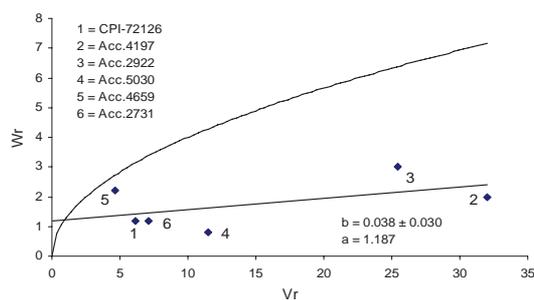


Figure 2 Array variance (V_r) and parent-offspring covariance (W_r) graph for number of fruits per plant.

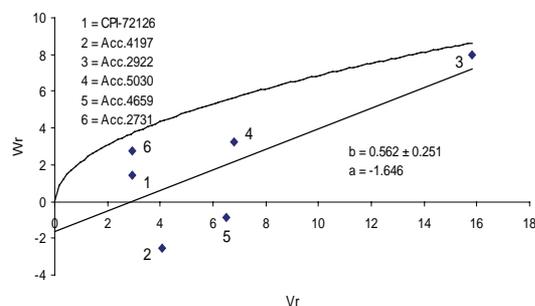


Figure 3 Array variance (V_r) and parent-offspring covariance (W_r) graph for number of seeds per fruit.

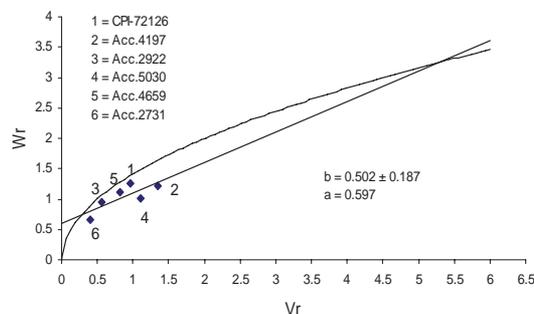


Figure 4 Array variance (V_r) and parent-offspring covariance (W_r) graph for 1,000 seed-weight.

results were obtained by Sobhan (1993) for roselle (*Hibiscus sabdariffa*) and by Khatun (2007) for white jute (*C. capsularis*). The regression line of W_r on V_r passed above the point of origin at an intercept of $a = 0.597$ (Figure 4), which indicated the presence of partial dominance. Figure 4 also suggests that the array point 6 (Acc.2731) possessed more dominant alleles and that point 2 (Acc.4197) had the predominant recessive alleles. Array points 3 (Acc.2922) and 5 (Acc.4659) contained relatively higher numbers of dominant genes but the remaining two array points possessed larger amounts of recessive alleles. The correlation coefficient between parental measurement (Y_r) and the parental order of dominance ($W_r + V_r$) was $r = -0.51$. This negative correlation, which was not significant, showed the positive genes, that is, a lower value of ($W_r + V_r$) had a higher value of Y_r and confirmed the partial order of dominance.

Components of variation and genetic parameters

Estimated genetic components for the days to first flowering, the number of fruits per plant, the number of seeds per fruit and 1,000 seed-weight are presented in Table 5. The significant values of additive (D), dominance (H_1), dominance \times dominance (H_2) and overall dominance (h^2) indicated the control of both additive and dominance gene actions in the inheritance of these traits. Hayman's ANOVA also showed similar results and confirmed these genetic effects. Positive and significant F values for the days to first flowering indicated the predominance of dominant alleles in the parents, which was supported by the ratio $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ (greater than unity). However, significant negative F values for the number of fruits per plant, the number of seeds per fruit and 1,000 seed-weight revealed the predominant recessive genes in the parents controlling these traits. The influence of environment was severe for all the characters studied since the component

E was highly significant. The mean degree of dominance as measured by $(H_1/D)^{1/2}$ was less than unity for the days to first flowering and 1,000 seed-weight indicating the occurrence of partial or incomplete dominance for the inheritance of these two traits, as was observed from the V_r - W_r graph. Whereas, the number of fruits per plant and number of seeds per fruit exhibited dominance to over-dominance since the ratio was greater than unity for these traits, as was also observed in the V_r - W_r graph. Patil and Thombre (1981) reported a greater proportion of additive genetic components with respect to days to flowering, plant height and length of fiber in kenaf. The ratio of $H_2/4H_1$ measures the proportion of dominant genes with positive and negative effects at all loci. The value of $H_2/4H_1$ deviated from the expected value of 0.25 for all the characters indicating an asymmetrical distribution of positive and negative alleles among the parents. These findings were in agreement 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 first flowering, the number of nodes per plant, the number of pods per plant and the number of seeds per pod) in tossa jute (*C. olerarius*). The total number of groups of genes which control the character and exhibited dominance was measured by h^2/H_2 . The h^2/H_2 ratio for the days to first flowering, number of fruits per plant and 1,000 seed-weight were positive and less than unity, indicating that at least one group of dominant gene(s) controlling these traits exhibited dominance; however, it was negative (-0.09) for the number of seeds per fruit indicating only one group of recessive gene(s) showing a dominance effect on the trait. A negative r_{xy} value was observed for all the characters except the number of fruits per plant which indicated that increasing genes were dominant in nature, but for the number of fruits per plant, increasing genes were recessive in nature, since the r_{xy} value of this trait was positive. Heritability in the narrow sense

(h^2_{ns}) was low for the number of seeds per fruit (0.09) and the number of fruits per plant (0.01), whereas, it was high for the days to first flowering (0.59) and 1,000 seed-weight (0.56), indicating the predominance of additive gene effects for these two traits. More or less similar findings were also reported by Khatun (2007) for *C. capsularis*. She showed that the narrow sense heritability in F_1

was high for the number of seeds per fruit (0.47) and 1,000 seed-weight (0.37), and moderately high for the number of fruits per plant (0.15). High heritability values of these two traits (days to first flowering and 1,000 seed-weight) were thus indicative of their effectiveness for selection in the early generation of the breeding improvement program.

Table 5 Genetic components and their ratios for different seed yield related characters of kenaf in a 6 x 6 half-diallel cross.

Genetic component	Estimated value \pm SE			
	Days to first flowering	Number of fruits per plant	Number of seeds per fruit	1,000 seed-weight (g)
E	5.29** \pm 0.79	1.54** \pm 0.04	2.19** \pm 0.01	0.02** \pm 0.001
D	2210.21** \pm 2.09	0.06 ns \pm 0.01	2.53** \pm 0.03	1.97** \pm 0.002
F	334.15** \pm 5.12	-5.79** \pm 0.23	-1.52** \pm 0.07	-0.17** \pm 0.005
H ₁	1846.56** \pm 5.32	48.47** \pm 0.24	16.86** \pm 0.07	1.28** \pm 0.005
H ₂	1601.37** \pm 4.75	36.89** \pm 0.22	12.38** \pm 0.06	1.19** \pm 0.004
h ²	364.42** \pm 3.20	23.05** \pm 0.15	-1.15** \pm 0.04	0.34** \pm 0.003
Ratio	Proportional value			
(H ₁ /D) ^{1/2}	0.91	28.35	2.58	0.81
H ₂ /4H ₁	0.22	0.19	0.18	0.23
[(4DH ₁) ^{1/2} + F]/ [(4DH ₁) ^{1/2} - F]	1.18	-0.26	0.79	0.90
r _{xy}	-0.96*	0.44	-0.79	-0.51
r ²	0.92	0.20	0.62	0.26
h ² /H ₂	0.23	0.62	-0.09	0.29
h ² _{ns}	0.59	0.01	0.09	0.56

H₂ = Dominance \times dominance, h² = Overall dominance, H₁ = Dominance, D = Additive, r_{xy} = Correlation between parental measurement (Yr) and parental order of dominance (Wr + Vr), r² = Prediction for measurement of completely dominant and recessive parents, h²_{ns} = Heritability in the narrow sense. ns = Not significant, * = $P < 0.05$, ** = $P < 0.01$.

CONCLUSION

Hayman's ANOVA, variance-covariance regression and other parameters related to genetic phenomena underlay the inheritance of major seed yield-related characters pertinent to genetic improvement of *H. cannabinus* L. Earliness of flowering (short crop duration) in kenaf is a desirable character for its better fit into current cropping patterns. Acc.2922 showed earliness of flowering with smaller seed size and therefore may be useful for developing high yielding and early maturing (short field duration) kenaf varieties with smaller seed size characteristics. According to the genetic analysis, both additive and non-additive gene actions were found to be important with the predominance of additive gene action in the inheritance of all the traits. The Vr-Wr regression analysis also provided some information on the studied characters. Partial dominant and over-dominant gene action or both were involved with all the characters. Since the number of fruits per plant, the number of seeds per fruit and the days to first flowering were inherited additively with various degrees of dominance, there does not appear to be any difficulty in breeding for improvement of the crop plant.

ACKNOWLEDGEMENTS

The authors thank the Bangladesh Jute Research Institute for supplying the kenaf seeds used in this research and also gratefully acknowledge the Bangladesh Agricultural Research Council (BARC) for providing financial support.

LITERATURE CITED

Ahmad, S. and R. Khatun. 1992. **Screening for Biomass and Oil Yield of Kenaf and Selection of Base Populations for the Breeding Program**. Technical Program, Bangladesh Jute Research Institute, Dhaka, Bangladesh.

- Akter, N. 2009. **Genetic Analysis of Fibre and Seed Yield in Tossa Jute (*Corchorus olitorius* L.)**. PhD. Thesis. Department of Genetics and Plant Breeding. Bangladesh Agricultural University, Mymensingh, Bangladesh.
- Alexopoulou, E., M. Christou, M. Mardikis and A. Chatziathanassiou. 2000. Growth and yields of kenaf varieties in central Greece. **Ind. Crop Prod.** 11: 163-172.
- Carberry, P.S., R.W. Muchow, R. Williams, J.D. Sturtz and R.L. McCown. 1992. A simulation model of kenaf for assisting fibre industry planning in Northern Australia. I. General introduction and phenological model. **Aust. J. Agric. Res.** 43: 1501-1513.
- Coetzee, R., M.T. Labuschagne and A. Hugo. 2008. Fatty acid and oil variation in seed from kenaf (*Hibiscus cannabinus* L.). **Ind. Crop Prod.** 27: 104-109.
- Dempsey, J.M. 1975. **Fibre Crops**. The University Presses of Florida, Gainesville, FL, USA. 470 pp.
- Food and Agriculture Organization. 2003. **Consultation on Natural Fibers. The Production and Consumption of Kenaf in China**. ESC-Fibers Consultation No: 03/6.
- Hayman, B.I. 1954a. The theory and analysis of diallel crosses. **Genetics** 39: 789-809.
- Hayman, B.I. 1954b. The analysis of variance of diallel crosses. **Biometrics** 10: 235-244.
- International Jute Study Group. 2012. **World Jute and Kenaf Statistics: At a Glance**. Dhaka, Bangladesh.
- Jinks, J.L. 1954. The analysis of continuous variation in a diallel crosses of *Nicotiana rustica* varieties. **Genetics** 39: 767-788.
- Jones, R.M. 1965. Analysis of variance of the half diallel table. **Heredity** 20: 117-121.
- Khatun, R. 2007. **Improvement of Fibre Yield and Associated Traits in White Jute (*Corchorus capsularis* L.)**. PhD. Thesis. Department of Botany, Dhaka University. Dhaka, Bangladesh.

- Mohamed, A., H. Bhardwaj, A. Hamama and C. Webber. 1995. Chemical composition of kenaf (*Hibiscus cannabinus* L.) seed oil. **Ind. Crop Prod.** 4: 157-165.
- Patane, C. and O. Sortino. 2010. Seed yield in (*Hibiscus cannabinus* L.) as affected by sowing time in South Italy. **Ind. Crop Prod.** 32: 381-388.
- Patil, R.C. and M.V. Thombre. 1981. Graphic and variance components analysis of five quantitative characters in *Hibiscus cannabinus*. **J. Maharashtra Agric. Univ.** 6(3): 221-224.
- Sobhan, M.A. 1993. **Heritability of Fibre, Fruit and Seed Yield in *Hibiscus sabdariffa* L.** PhD. Thesis. Department of Botany, Dhaka University. Dhaka, Bangladesh.
- Ten, S.T. and C.C. Wong. 2006. Design and development of kenaf seed thresher machine for seed production under rainshelter. **Acta Hort.** 710: 245-250.
- Xu, Z. 1990. **Genetic Evaluation of IJO Collected Kenaf (*Hibiscus cannabinus* L.) Germplasm.** MSc. Thesis. Bidhan Chandra Krishi Viswavidyalaya. West Bengal, India.