



Variability, Heritability and Genetic Advance in Kenaf (*Hibiscus cannabinus* L.)

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ABSTRACT

An investigation was carried out to assess the variability, heritability and genetic advance for ten quantitative characters *viz.*, days to 50% flowering, plant height, basal stem diameter, bark thickness, number of nodes per plant, inter-nodal length, green plant weight, fibre length, fibre-wood ratio and fibre yield per plant in 28 genotypes (twenty one F₁S and seven parents) of kenaf (*Hibiscus cannabinus* L.). The analysis of variance indicated significant differences among the genotypes for all the characters studied. The results revealed high PCV and GCV for fibre yield per plant. The estimates of heritability and genetic advance as per cent of mean were high for the characters *viz.*, bark thickness, green plant weight and fibre yield per plant indicating that most likely the heritability is due to additive gene action and selection may be effective. High heritability coupled with moderate genetic advance as per cent of mean was observed for number of nodes per plant and fibre length whereas, moderate heritability combined with moderate genetic advance as per cent of mean for plant height and inter-nodal length indicating the role of both additive and non-additive gene actions; Moderate heritability coupled with low genetic advance as per cent of mean was observed for basal stem diameter while moderate heritability coupled with high genetic advance as per cent of mean for fibre-wood ratio whereas, high heritability coupled with low genetic advance as per cent of mean for days to 50% flowering indicating the role of non-additive gene action.

Key words : Genetic advance, Heritability, Kenaf, Variability.

Kenaf (*Hibiscus cannabinus* L.) is a diploid species ($2n = 36$), a member of the family Malvaceae. It is an important fibre yielding crop next to jute. Fibre extracted from bast region is used for non-traditional and value added non-textile products. Besides fibre, it also provides forage and paper pulp which in turn broadened the agricultural diversity of resources to reduce pressure on forest resources. Genetic variability is the pre requisite for any crop improvement programme. Improvement in any trait depends solely on the amount of variability present in the base material for that trait. Hence, insight into the magnitude of genetic variability present in a population is of paramount importance to a plant breeder for starting a judicious breeding programme. Heritability estimates along with genetic advance are also helpful in predicting the genetic gain under selection (Johnson *et al.*, 1955). Hence, the present study was carried out to have knowledge on genetic variability, heritability and genetic advance as per cent of mean present in the available genetic material

MATERIAL AND METHODS

Seven parental genotypes were mated in diallel fashion without reciprocals to produce twenty one F₁S. All these twenty one F₁S and seven parents were evaluated during *kharif* 2014 at Agricultural Research Station, Amadalavalasa in a randomized block design with two replications. The experimental material was raised in two rows for parental genotypes and three rows for F₁S of 3m length with the spacing of 30 x 10 cm. Observations were recorded on five randomly selected plants per replication in case of parents and ten for F₁'s for ten quantitative characters *viz.*, days to 50% flowering, plant height, basal stem diameter, bark thickness, number of nodes per plant, inter-nodal length, green plant weight, fibre length, fibre-wood ratio and fibre yield per plant. The data was subjected to statistical analysis and various genetic parameters such as genotypic and phenotypic coefficients of variation were calculated according to the method suggested by Burton (1952) and heritability estimates by the method of Hanson *et al.* (1956). The genetic advance as per cent of mean was calculated by the formula given by Johnson *et al.* (1955).

Table 1. Analysis of variance for yield and yield component characters in kenaf.

Source	d.f.	Days to 50% flowering	Plant height (cm)	Basal stem diameter	Bark thickness	Number of nodes per plant	Inter - nodal length	Green plant weight	Fibre length	Fibre - wood ratio	Fibre yield per plant
Replications	2	1.446	335.650	4.640**	0.115	10.200	0.075	62.160	0.679	0.0002	1.171
Crosses	27	3.721	1192.718**	1.533**	0.185**	69.839**	0.439**	2193.356**	737.609**	0.0086**	5.829**
Error	27	2.705	409.274	0.760	0.028	13.199	0.115	157.808	115.034	0.0023	1.071
Total	55	3.181	792.535	1.126	0.107	40.949	0.273	1155.338	418.583	0.0054	3.409

*Significant at 5% level ** Significant at 1% level

Table 2. Estimates of variability, heritability and genetic advance as per cent of mean for fibre yield and yield components in kenaf.

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (broad sense) (%)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Days to 50% flowering	102.26	99.50	105.50	1.48	1.15	60.40	1.85
2	Plant height (cm)	208.83	170.40	252.90	13.55	9.47	48.90	13.65
3	Basal stem diameter (mm)	12.86	10.94	14.27	8.32	4.83	33.70	5.78
4	Bark thickness (mm)	1.62	1.16	2.19	20.14	17.25	73.40	30.43
5	Number of nodes per plant	52.32	41.70	66.80	12.31	10.17	68.20	17.30
6	Inter-nodal length (cm)	4.73	3.10	5.65	11.11	8.49	58.40	13.37
7	Green plant weight (g)	160.87	97.50	219.00	21.31	19.83	86.60	38.01
8	Fibre length (cm)	205.65	162.25	237.00	10.03	8.57	73.00	15.10
9	Fibre-wood ratio	0.43	0.36	0.72	17.11	12.94	57.20	20.17
10	Fibre yield per plant (g)	7.35	4.00	11.00	25.24	20.95	68.90	35.84

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among all the 28 genotypes for all the characters studied indicating a high degree of variability in the material (Table 1). In the present study, the phenotypic coefficient of variance (PCV) was slightly higher in magnitude than genotypic coefficient of variance (GCV) for all the characters studied indicating the influence of environment on expression of these traits (Table 2). High PCV and GCV were recorded for fibre yield per plant whereas, bark thickness and green plant weight shows high PCV alone. Moderate PCV and GCV were recorded for number of nodes per plant and fibre-wood ratio whereas, moderate PCV alone is recorded for plant height, inter-nodal length and fibre length while moderate GCV alone were recorded

for bark thickness and green plant weight. The characters days to 50% flowering and basal stem diameter exhibited low PCV and GCV whereas plant height, inter-nodal length and fibre length showed low GCV alone.

In the present study, heritability estimates were high for days to 50% flowering, bark thickness, number of nodes per plant, green plant weight, fibre length and fibre yield per plant. Moderate heritability was recorded for plant height, basal stem diameter, inter-nodal length and fibre-wood ratio. The maximum value for heritability was recorded by green plant weight (86.60%) and minimum was recorded by basal stem diameter (33.70%).

High heritability alone is not sufficient enough to exercise selection unless the information is accompanied with substantial amount of genetic

advance. The estimates of heritability and genetic advance as per cent of mean were high for bark thickness, green plant weight and fibre yield per plant indicating the predominance of additive gene action and hence simple selection may be rewarding. These findings were in agreement with Pulli Bai *et al.* (2005), Rani *et al.* (2006) for bark thickness; Mostofa *et al.* (2002) for green plant weight and Subramanyam *et al.* (1995), Adilakshmi (1992) for fibre yield per plant.

High heritability coupled with moderate genetic advance as per cent of mean was observed for number of nodes per plant and fibre length indicating the role of both additive and non-additive gene actions in the inheritance of these traits and can be improved by population improvement method. While moderate heritability coupled with low genetic advance as per cent of mean was observed for basal stem diameter indicating the role of non-additive gene action and can be improved by population improvement methods involving selection, inter-mating among selected ones and reselection may help to improve these traits besides exploiting the methods of heterosis breeding.

Thus, the characters *viz.*, bark thickness, green plant weight and fibre yield per plant having high heritability and genetic advance as per cent of mean can be exploited in the breeding programmes by using simple selection.

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