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DISSECTION OF GENETIC VARIABILITY AND STABILITY ANALYSIS FOR FIBRE YIELD IN WHITE JUTE (*CORCHORUS CAPSULARIS* L.) GENOTYPES UNDER SUB-HIMALAYAN PLAINS

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ABSTRACT

The analysis of variance for phenotypic expression of the genotypes of any crop showed that the variation was due to genotype by environment (G×E) interaction and this is a major challenge faced by the plant breeders. The present investigation was undertaken with objectives to determine genetic variability and association for fibre yield and its component traits and stability in fibre yield and to measure the effect of G×E interaction in white jute (*Corchorus capsularis* L.). So, it was thought to apply the different stability parameters such as, Eberhart and Russell (1966), Shukla Stability variance (σ_i^2), Wricks Ecovalence (W_i^2), Perkins and Jinks, Cultivar performance measure (P) and non-parametric, for the assessment of stability of different genotypes over three years in whitejute. Among all the genotypes assessed over three succeeding years, the highest fibre yield was exhibited by the genotype JRC-698 (32.43 q ha⁻¹) followed by NCJ-27-40121(31.06 q ha⁻¹). Highest mean genotypic coefficient of variation and heritability was recorded for basal diameter, followed by plant height. The fibre yield was significantly and positively correlated with basal diameter (rG = 0.98), green weight (rG = 0.92) and plant height (rG = 0.68). As per the result of stability performance according to Eberhart and Russell model, the genotype KJC-11 was found to be stable and adaptable to all the temporal environments in the three years. According to Ecovalence (W_i^2) and Shukla's stability variance ($Sh-\sigma_i^2$), the genotype KJC-11 was the most stable and the higher yielding genotype followed by JRC-9057 and JRCM-9-1. On the basis of P_i values, JRC-698 was the most stable genotype followed by NCJ-27-40121, JRCM-9-1, KJC-11 and JRC-9057. According to Huehn's non-parametric measures of stability, the most stable and comparatively higher fibre yielding genotype was KJC-11, which had the smallest changes in ranks of $S_i^{(1)}$ and $S_i^{(2)}$. Based on AMMI stability value (ASV), KJC-11 was the most stable genotype. According to yield selection index (YSI), JRCM-9-1 was the high yielding and stable genotype followed by genotype KJC-11. According to GGE biplot, the genotype JRCM-9-1 had high stability and high fibre yield followed by KJC-11. Among the three environments (E_1 , E_2 and E_3) and environment 2009 (E_1) was the most discriminating one.

Key words : Jute, Genetic variability, Stability, G×E interaction, ASV, YSI, GGE biplot.

Introduction

White Jute (*Corchorus capsularis* L.) is a herbaceous annual plant which belongs to Tiliaceae family, commonly grown in Southeast Asian countries (José et

al., 2009). A good number of fabrics such as Hessian cloth, scrim, sacking, canvas and carpet backing cloth (CBC), etc. are manufactured from jute. The ideal genotype or variety of any crop is one that consists of

high mean yield associated with a lesser fluctuation of yield or has the consistency in yield or in its performance when it is cultivated over different environments. The genotype×environment (G×E) interaction is very important for the plant breeders because G×E interaction helps to develop improved varieties by minimizing the effect of environments. The G×E interaction helps in the improvement of quantitative traits like yield and helps in the introduction of new crop cultivars (McLaren and Chaudhary, 1994 and Prasad and Singh, 1990).

According to Breese (1969), the incidence of G×E interaction has provided challenge for better understanding of genetic control of variability and thus to rationalize procedures for breeding improved genotypes in crop plants. It is very important to the plant breeders to identify the genetic factors that provide wide and specific adaptation. The genotypes which show low level of response to various environmental situation, would be considered as wide adaptation, while the genotypes which show maximum response to specific factors of environments, would be considered as specific adaptation. The quantum jump can be realized by breeding, when a genotype would be performing good and would give identical performance over all the environments.

The present investigation was carried out to study the nature of genetic variability and association of fibre yield with its attributing traits in combination with the estimation of the magnitude of G×E interaction for fibre yield and to find out the stable and adaptable high yielding genotypes of whitejute, which would be suitable for the Terai Zone of West Bengal.

Materials and Methods

The investigation was conducted with jute (*Corchorus capsularis* L.) at Regional Research Station, Terai Zone, Uttar Banga Krishi Vishwavidyalaya, under Sub-Himalayan plains of West Bengal, over three consecutive years of 2009-10, 2010-11 and 2011-12 which were treated as three environments of E_1 , E_2 and E_3 , respectively. In this context, nine genotypes of white jute (*Corchorus capsularis* L.) were obtained under AINP on Jute and Allied Fibres and cultivated. The genotypes were tested during the pre-kharif season (April - July) in each year. Among the nine promising whitejute genotypes namely NDC-2013, JRCM-9-2, KJC-11, JRC-9057, JRCM-9-1, NCJ-27-40121, JRC-698 (Check-1), JRC-9097 and JRC-321 (Check-2) which were evaluated in trials, two of them were checks namely JRC-698 and JRC-321. The experiment was laid out in randomized complete block design (RCBD) with three replications. Net Plot size was 4m × 2m for each year under study.

Inter and intra row spacing was 20cm and 15cm, respectively. Recommended cultural practices and plant protection measures were followed in each trial in each year.

The general statistical procedure was followed according to standard method proposed by Steel and Torrie (1980). The analysis of variance (ANOVA) and broad sense heritability (h^2_b) were estimated from the pooled data over three years (2009-10, 2010-11 and 2011-12). The phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV) were estimated according to the procedure proposed by Burton (1952). The expected genetic advance and the genotypic correlation were calculated by the method described by Johnson *et al.* (1955). The path analysis was carried out by the method described by Dewey and Lu (1959).

The yield data was analyzed on individual year basis and pooled basis, as per the RCBD design. The same yield data was also used to estimate different stability parameters as follows:

a) Eberhart and Russell model (1966) : The model deals with the regression approach with a purpose to study the G×E interaction and therein the interaction sum of squares is partitioned into two components. Among of these two components, one component describes the heterogeneity of linear regression (b_i), while the other component illustrates pooled deviations from individual regression lines (S^2_{di}). The b_i and the S^2_{di} are calculated as:

$$b_i = 1 + \frac{\sum (X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X}_{..}) (\bar{X}_{.j} - \bar{X}_{..})}{\sum_{ij} (\bar{X}_{.j} - \bar{X}_{..})^2}$$

$$S^2_{di} = \frac{1}{E-2} \left[\sum_i (X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X}_{..}) - (b_i - 2)^2 \sum_j (\bar{X}_{.j} + \bar{X}_{..})^2 \right]$$

Where, X_{ij} is the performance of the genotype i in environment j , \bar{X}_i is the mean performance of the environment j , \bar{X}_j is the grand mean performance of the environment j , $\bar{X}_{..}$ is the grand mean and E is the number of environments. Depending upon the value of b_i , the adaptability of the genotypes change, *i.e.*, when $b_i > 1$, the genotypes would be adapted to favourable environments, when $b_i < 1$, the genotypes would be adapted to unfavourable environmental conditions and genotypes with $b_i = 1$ would have an average adaptation to all environments. Genotypes with $S^2_{di} = 0$ would be most stable whereas, if $S^2_{di} > 0$, it would indicate that the

genotypes have lower stability across the environments. In overall a genotype is said to be stable if the following conditions are fulfilled:

i. The mean of the genotypes greater than the population mean

ii. $b_i = 1$

iii. $S^2_{di} = 0$

b) Coefficient of Variation (CV) : Francis and Kaunenberg (1978) used both the coefficient of variation (CV) and mean yield to describe the stability. The genotypes which had low CV but high mean yield, were recognized as the most stable and desirable genotypes.

c) Shukla's stability Variance (1972) : On the basis of residuals in a two-way classification, the variation in a genotype over environments is considered as the stability measure. According to this parameter, the genotypes, which have low stability variance, are considered as more stable genotypes.

d) Perkins and Jinks model (1968) : In this model, regression adjusts the observed value for location effects. The regression coefficient for each genotype is considered as the stability parameter.

e) Wricke's Ecovalence (W_i^2) : Wricke's Ecovalence for the genotype "i" was calculated as follows:

$$W_i^2 = \sum (X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X})^2$$

Where, X_{ij} is the observed yield response, \bar{X}_i is the mean performance of the genotype i, \bar{X}_j is the mean performance of the environment j and \bar{X} is the grand mean.

f) Superiority index (P_i) : It is a measurement of genotype adaptability over a wide range of environments. It is estimated by the use of the highest-yielding genotype within each environment as a reference point. The genotypes which have the largest yield difference in comparison to the reference genotype, would have the maximum P_i value (Lin and Bins, 1988).

$$P_i = \frac{\sum_{j=1}^n (X_{ij} - M_j)^2}{2E}$$

Where, X_{ij} is the grain yield of the genotype "i" in the jth environment, M_j is the yield of the genotype with maximum yield at environment j and E is the number of environments.

g) Nassar and Huehn (1987) non-parametric measure : The non-parametric stability statistics which consider both mean yield and stability parameters (Nassar and Huehn, 1987). The $Si^{(1)}$ and $Si^{(2)}$ statistics have developed on the basis of ranks of the genotypes over different environments and they give equal priority to each environment. According to Becker and Leon (1988), the genotypes which change their rank very few, are considered as more stable genotypes. A genotype would be considered as stable if it's rank remains similar unchanged across environments *i.e.*, maximum stability is found with equal ranks across environments. The parameters based on yield ranks of genotypes in each environment are derived as follows:

$$S_i^{(1)} = 2 \sum_j^{m-1} \sum_{j=j+1}^m [r_{ij} - r_{ij}^*] / [m(m-1)]$$

$$S_i^{(2)} = \sum_{j=1}^m (r_{ij} - \bar{r}_i)^2 / [(m-1)]$$

Where, m is the number of environments, i is the number of genotypes, r_{ij} is the rank of the ith genotype in the jth environment, r_{ij}^* is the adjusted rank.

h) AMMI stability value (ASV) : According to Purchase *et al.* (2000), in the AMMI model, the ASV is the difference between the coordinate point and the origin in a two-dimensional scatter diagram representing IPCA1 scores against IPCA2 score. Because the IPCA1 score has more contribution to the G×E interaction sum of squares. So, a weighted value is needed. This weight is calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 to the interaction Sum of squares as follows:

$$ASV_i = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA1Score) \right]^2 + (IPCA2Score)^2}$$

Where, $\frac{SS_{IPCA1}}{SS_{IPCA2}}$ is the weight given to the IPCA1

value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. The larger the IPCA score, either negative or positive the more specifically adapted a genotype is to certain environments. Smaller IPCA scores indicate a more stable genotype across environments.

i) Yield stability index (YSI) : For the selection of a genotype, stability should not be the only parameter, as the most stable genotype might not necessarily give the best yield performance (Mohammadi *et al.*, 2007; Mohammadi and Amri, 2008). Therefore, there is a requirement for integrating both mean yield and stability

into a single selection index. So, the various authors and scientists proposed different selection criteria for simultaneous selection of yield and stability (Bajpai and Prabhakaran, 2000; Rao and Prabhakaran, 2005; Babarmanzoor *et al.*, 2009). In this context, the rank of ASV and rank of mean performance of a trait is considered. The lowest ASV value occupies rank one, while the highest mean value of a trait occupies rank one and then both the ranks summed into a single selection index of stability, called yield stability index (YSI) and that is considered as the most stable as well as high yielding genotype.

The experimental data was subjected to statistical analysis using Windowstat, Cropstat version 7.2 and OPSTAT.

Results and Discussion

Analysis of Variance

Data on fibre yield and its attributing traits were recorded from the nine white jute genotypes over a period of three years (2009-10, 2010-11 and 2011-12), each of which was treated to be a separate environment (E_1 , E_2 and E_3) and were subjected to pooled analysis of variance (ANOVA) over the three years (environments). The ANOVA over the three environments (E_1 , E_2 and E_3) is presented in Table 1, which gives the overall picture of the relative magnitude of the genotypes (G), environments (E) and genotype \times environment interaction (GEI) variance. The $G \times E$ interactions for all the traits were non-significant except fibre yield, which was found to be significant. A wide range of variation was noticed in all the traits, which offered scope of selection for improvement of desirable types. There is limited scope for further improvement of cultivated variety of white jute in the absence of required variability (Sinha *et al.*, 2004). The genotypes differed significantly for plant height, basal diameter, green weight and fibre yield.

The environments differed significantly only for two

traits namely plant height and fibre yield which is a clear indication that the three different environments varied over three years. The mean performance of the nine jute genotypes over the three environments (Table 2 and Fig. 1) showed good promising genotypes among the white jute varieties for almost all the four traits, indicating the suitability of the genotypes for carrying out the study of genetic variability for different traits. The mean fibre yield of genotypes over environments ranged from 27.26 q ha⁻¹ to 32.43 q ha⁻¹ (Table 2). The Fig. 1 revealed that during 2009 (E_1) and 2010 (E_2), the genotype JRC-698 (Check-1) was the highest fibre yielder and during 2011 (E_3), the genotype JRC-698 (Check-1) gave a moderate fibre yield. So, among all the genotypes over the three succeeding years in the three environments E_1 , E_2 and E_3 (Fig. 1), the highest fibre yielding genotype was the check JRC-698 (32.43 q ha⁻¹), followed by NCJ-27-40121 (31.06 q ha⁻¹).

Genetic parameters

Range, coefficient of variation, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (h^2_b) and genetic advance as a percentage of mean (GAM) measured the extent of variability, which was present among the genotypes. The PCV and the GCV were low to moderate (Table 3). Highest GCV was recorded for basal diameter (12.32%) followed by plant height (9.78 %). Similar result was observed by Islam *et al.* (2002), Ghoshdastidar (2003), Senapati *et al.* (2006), Shreshtha (1991) and Kumer and Modak (1990). The high broad sense heritability (60% and above) was recorded for plant height, basal diameter and green weight. Similar result was reported by Nayak *et al.* (2007). High estimates of broad sense heritability in the quantitative traits have been found to be useful from plant breeder's point of view, as this would enable the basis for selection based on the phenotypic performance. High genetic advance as percentage of mean was found for basal diameter (24.44%) and plant

Table 1 : ANOVA for fibre yield and its attributing traits in *capsularis* jute over three years (2009-10, 2010-11 and 2011-12).

Sources of variation	df	Mean sum of squares			
		Plant height (cm)	Basal diameter (cm)	Green weight (qha ⁻¹)	Fibre yield (qha ⁻¹)
Replications	3	5842.64**	0.51**	40342.09**	91.01*
Genotypes (G)	8	11954.91**	0.65**	34345.29**	45.14
Environments (E)	2	820.10*	0.02	521.05	69.26*
Interactions (G×E)	6	262.98	0.02	1598.51	21.51*
Total	11	1886.00**	0.15**	11969.04**	49.14
Error	88	701.36	0.05	4209.42	32.36

* Significant at 5% probability level; ** Significant at 1% probability level.

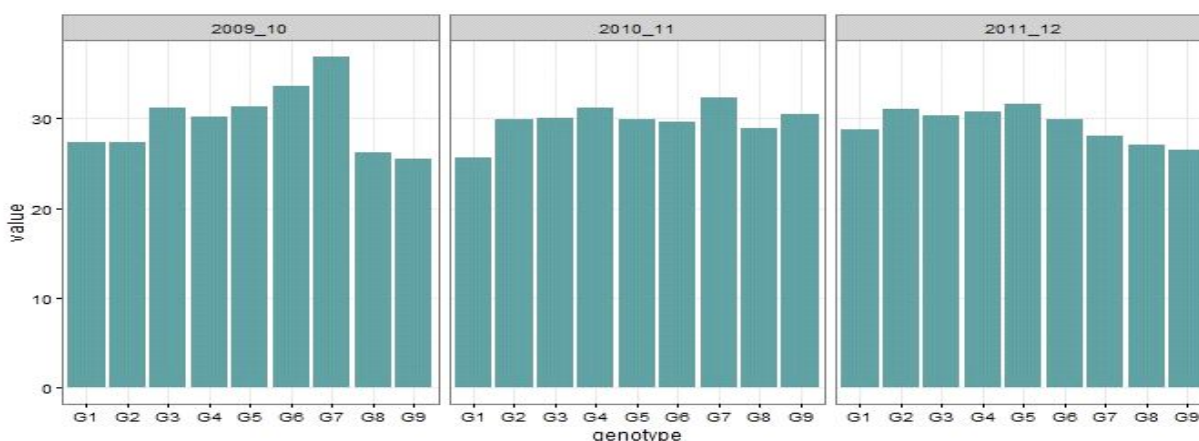


Fig. 1 : Performance of the nine capsularis jute genotypes over three years (2009-10, 2010-11 and 2011-12) for the trait fibre yield (q/ha).

Table 2 : Mean performance of nine *capsularis* genotypes over three years.

Genotype	Plant height (cm)	Basal diameter (cm)	Green weight (q/ha)	Fibre yield (q/ha)
NDC-2013	351.20	2.05	529.09	27.26
JRCM-9-2	355.95	1.98	539.47	29.44
KJC-11	345.47	1.84	515.51	30.56
JRC-9057	271.97	1.48	438.46	30.71
JRCM-9-1	290.90	1.59	505.82	30.95
NCJ-27-40121	276.87	1.49	443.10	31.06
JRC-698+	304.18	1.87	563.10	32.43
JRC-9097	305.87	1.93	582.29	27.39
JRC-321+	315.37	2.07	582.90	27.54
Grand Mean	313.09	1.81	522.19	29.70
CV (%)	8.46	12.02	12.42	19.15
SEm (\pm)	7.65	0.06	18.73	1.64
CD (5%)	21.49	0.18	52.64	-

CV (%) = Coefficient of variation; SEm (\pm) = Standard error of mean; CD (5%) = Critical distance at 5% probability level, + : local standard check varieties.

height (19.55%). Johnson *et al.* (1955) suggested that for a more reliable conclusion, heritability and genetic advance should be considered together. Thus, basal diameter with high heritability and genetic advance as a percentage of mean is under additive gene control and hence can be improved further, as selection would be rewarding.

Trait association and Path Co-efficient analysis

Wright (1921) coined the term path coefficient and gave the theory of path analysis on the basis of standardized partial regression analysis. Selection of a trait for its improvement may simultaneously lead to selection of the associated traits. Therefore, it is essential

to understand the inter-relationship among different traits so that improvement of the targeted trait does not carry with it the non-targeted traits, rather desirable traits could be simultaneously included which may lead to ultimate success on breeding programme. Therefore, according to Pervin and Haque (2012), the measurement of correlation and path analysis illustrate a clear idea regarding the union between two traits and dividing the relationship into direct effect and indirect effect, reflecting the comparative influence of each factors for the sake of the trait yield. In this regard, many workers such as Islam *et al.* (2001) and Alam *et al.* (2011) had done multiple research works on jute. Dewey and Lu (1959) outlined the technique to partition the genotypic and phenotypic correlations into path coefficient. Genotypic (G) correlation coefficients among the pair of fibre yield contributing traits pertaining to jute are presented in Table 4. The fibre yield ($q\ ha^{-1}$) was significantly and positively correlated with all the fibre yield attributing traits like basal diameter ($r_G = 0.98$), green weight ($r_G = 0.92$) and plant height ($r_G = 0.68$). Khatun and Sobhan (1992), Zhegh *et al.* (1985), Chaudhury *et al.* (1981) and Sasmal and Chakroborty (1978) also narrate the same identical relationship. Plant height was significantly and positively correlated with basal diameter whereas basal diameter was positively and significantly correlated with green weight.

Highest positive direct effect on fibre yield was exhibited by basal diameter (2.14), as presented in Table 5. According to Chaudhury *et al.* (1981), direct selection would be effective based on this trait. Out of these three traits, only basal diameter had significant and positive correlation with fibre yield, which indicated that linear correlation did not always suggest that the trait would exert high and positive direct effect on the dependent variable such as fibre yield in the present investigation.

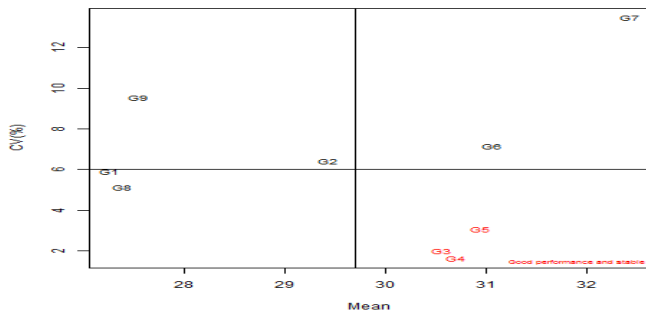


Fig. 2 : Plot for CV (%) versus mean for the trait fibre yield (q/ha) over three years (2009-10, 2010-11 and 2011-12).

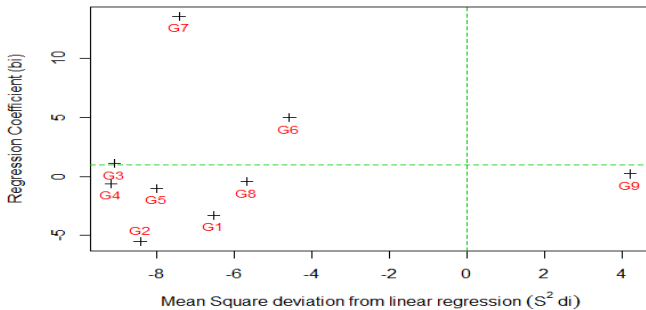


Fig. 3 : Plot for Regression Coefficient (b_i) versus mean square deviation from linear regression for the trait fibre yield (q/ha) pooled over three years (2009-10, 2010-11 and 2011-12).

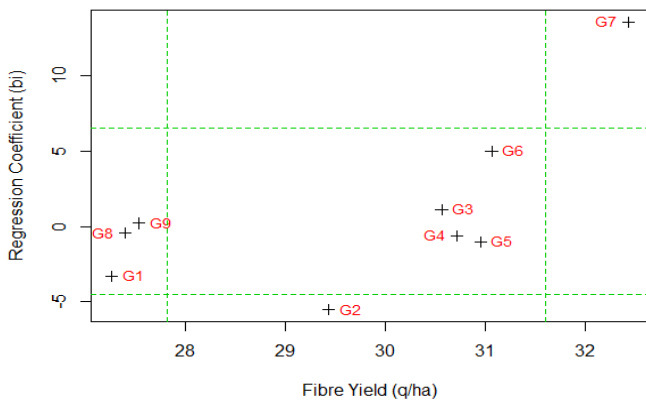


Fig. 4 : Plot for Regression Coefficient (b_i) versus the trait fibre yield (q/ha) pooled over three years (2009-10, 2010-11 and 2011-12). The two vertical lines on fibre yield indicate the points on X-axis at average Fibre yield \pm Standard deviation. Similarly the two horizontal lines on Regression Coefficient indicate the points on Y-axis at average Regression Coefficient \pm Standard deviation.

Similar result was observed by Das and Rakshit (1988), Saradana *et al.* (1990), Nayak and Baisakh (2007).

Stability for fibre yield over three years

Coefficient of variation (CV) : According to Francis and Kannenberg (1978), stability can also be estimated by integrating both coefficient of variation (CV) and the mean yield. The genotype which consists of low CV and average high yield would be stable and most desirable for a breeding programme. The CV of all the genotypes over the three environments was low except for the check variety JRC-698 (13.47), which had the maximum CV for fibre yield (Fig. 2). It was also revealed from Fig. 2, that JRC-9057 (1.62) had the lowest CV, followed by KJC-11 (1.99). Among these two genotypes (Table 2), JRC-9057 had high mean fibre yield (30.71 qha⁻¹) followed by KJC-11 (30.56 q ha⁻¹). So, JRC-9057 was found to be the most stable followed by KJC-11.

Eberhart and Russell model : The data of mean performance (X_i), regression coefficient (b_i) and deviation from regression (S^2_{di}) are shown in the Table 6. None of the genotypes were found to be widely adapted ($X_i >$ population mean, $b_i = 1$ and $S^2_{di} = 0$) for the trait fibre yield. Based on the observed results, the genotype KJC-11 exhibited comparatively high mean of fibre yield than grand mean yield and where the regression coefficient was near unity (Figs. 3 and 4) with low deviation from regression (Fig. 3). Therefore, KJC-11 can be considered to be superior to others and is strongly recommended for planting at multi-location trials at Terai Region of West Bengal. However, among the high performing group consisting of KJC-11, NCJ-27-40121 and JRC-698 (Check-1) were highly stable (non-significant S^2_{di}) and recorded above average response ($b_i > 1$). Therefore, they were found to be adapted specifically to favourable or rich environments, while the genotypes NDC-2013, JRCM-9-2, JRC-9057, JRCM-9-1, JRC-9097 and JRC-321 (Check-2) showed less yield than grand mean fibre yield (Fig. 4), which indicated their specific adaptability to unfavourable environments ($b_i < 1$ and S^2_{di} non-significant) for fibre yield.

Table 3 : Genetic parameters for the nine *capsularis* genotypes pooled over three years.

Traits	Mean	Range	GCV (%)	PCV (%)	h^2_b	GAM
Plant height (cm)	313.09	271.97 - 355.95	9.78	10.08	0.94	19.55
Basal diameter (cm)	1.81	1.48 - 2.07	12.32	12.80	0.93	24.44
Green weight (q/ha)	522.19	438.46 - 582.90	9.60	10.25	0.88	18.52
Fibre weight (q/ha)	29.70	26.93 - 33.29	3.47	6.53	0.28	3.81

GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; h^2_b = Broad sense heritability; GAM = Genetic advance as percentage of mean.

Shukla's stability variance ($Sh-\sigma_i^2$) : According to Shukla (1972), the $G \times E$ interaction sum of square of each genotype is divided into variance components (σ_i^2). Based on these variance components, a genotype would be called stable, if it has stability variance (σ_i^2) is equivalent to environmental variance (σ_o^2), which indicate that $Sh-\sigma_i^2 = 0$. The comparatively high value of σ_i^2 means more instability of genotype 'i', while those genotypes having low value of stability variance (σ_i^2), would be considered as stable genotypes. This has given rise to the practical application as it has the ability to find out the environmental factors which have influence on the heterogeneity in the $G \times E$ interaction. Results from Shukla's stability variance and overall means are summarized in Table 6 for fibre yield of white jute. Based on the values of Shukla's stability variance for fibre yield, it was found that the most stable genotypes were KJC-11 (-0.39), followed by JRC-9057 (-0.11) and JRCM-9-1 (0.82), while the genotypes JRC-698 (20.54), JRC-321 (8.23), JRCM-9-2 (5.38), NCJ-27-40121 (4.51), NDC-2013 (3.56) and JRC-9097 (2.07) were least stable ones, according to this procedure.

Perkins and Jinks' model : According to Perkins and Jinks (1968) linear regression model, it was revealed that the genotype JRC-698 (12.59), which is the first check variety was the most stable, followed by NCJ-27-40121 (3.99) and KJC-11 (0.11), because of high value of regression coefficient (B_i) with non-significant DJ_i , indicating that these genotypes were suitable for favourable environment (Table 6).

Wricke's ecovalence (W_i^2) : Wricke (1962) applied the word "ecovalence" to denote the relative influence of genotype 'i' to the total $G \times E$ interaction. The genotypes which have low value of W_i^2 , would be considered as the stable genotypes. The ecovalence values (W_i^2) were worked out for the white jute genotypes over three years and are presented in Table 6. The results indicated that the genotypes KJC-11 (0.50), JRC-9057 (0.93), JRCM-9-1 (2.37) and JRC-9097 (4.32) had the lowest ecovalence values and therefore, could be considered to be most stable. The ranks of these genotypes for the mean fibre yield were 5, 4, 3 and 8, respectively. The genotype JRC-9097 had lower ecovalence values and had lower mean yield than grand mean yield. The genotypes JRC-321, JRCM-9-2, NCJ-27-40121 and NDC-2013 had higher ecovalence values but had lower mean yield than grand mean fibre yield, while the genotype JRC-698 produced the highest ecovalence values and highest mean fibre yield than grand mean fibre yield and thus could be considered as the most unstable genotype. So, KJC-11 was more stable and higher fibre yielding followed by

JRC-9057 and JRCM-9-1.

Superiority/ Cultivar performance measure (P_i) : According to Lin and Binns (1988), the mean square difference between the genotypes and the genotype 'i' which has the maximum reaction over all the environments, would be considered as Cultivar performance (P_i). The lesser value of P_i indicates the smaller difference between the maximum yielding genotype and the better performing genotype. The P_i value can be estimated based on overall environmental mean and it shows the superiority on account of general adaptability, which is also called as wide adaptation. The Table 6 presents the Cultivar performance measure (P_i) for fibre yield of white jute. On the basis of P_i values, the first check variety JRC-698 (2.03) was the most stable genotype followed by NCJ-27-40121 (3.40), JRCM-9-1 (6.00), KJC-11 (6.34) and JRC-9057 (7.75). The most unstable genotypes according to this parameter were JRC-321 (26.12), JRC-9097 (24.34), NDC-2013 (23.87) and JRCM-9-2 (16.03).

Non-parametric measures of stability : Nassar and Huehn's (1987) non-parametric measures of stability for fibre yield of nine jute genotypes were evaluated in three years, and are shown in Table 6. The non-parametric statistics are very simple in use and they exhibit to explore the $G \times E$ interaction. It is very efficient in the explanation of $G \times E$ interaction and stability. It has been used and explained in several crops by applying non-parametric strategy. Different non-parametric measures were modified and proposed by Huhn (1979), Huhn and Nassar (1989), Lu (1995), Nassar and Huehn (1987) and Thennarasu (1995). Both $S_i^{(1)}$ (mean absolute rank differences of a genotype in multiple environments) and $S_i^{(2)}$ (variance of ranks over several environments) values of the genotypes across the tested environments, were used as measurements of stability (Huehn, 1990). The $S_i^{(1)}$ and $S_i^{(2)}$ statistics are based on ranks of the genotypes across over years and they give equal weight to environments. According to Becker and Leon (1988), the genotypes which change their rank very less frequently, are enumerated as stable genotypes. According to Nassar and Huehn (1987), the $S_i^{(1)}$ value is calculated for each genotype on the basis of pair-wise differences in rank over several environments, while $S_i^{(2)}$ is calculated for each genotype on the basis of variance in ranks over multiple environments. According to Huehn's non-parametric measures of stability for fibre yield of nine white jute genotypes, it was revealed that the genotype KJC-11 and JRC-9097 had $S_i^{(1)}$ and $S_i^{(2)}$ values of 0.00 each and could be considered as stable genotypes, because of minimum value for this statistics.

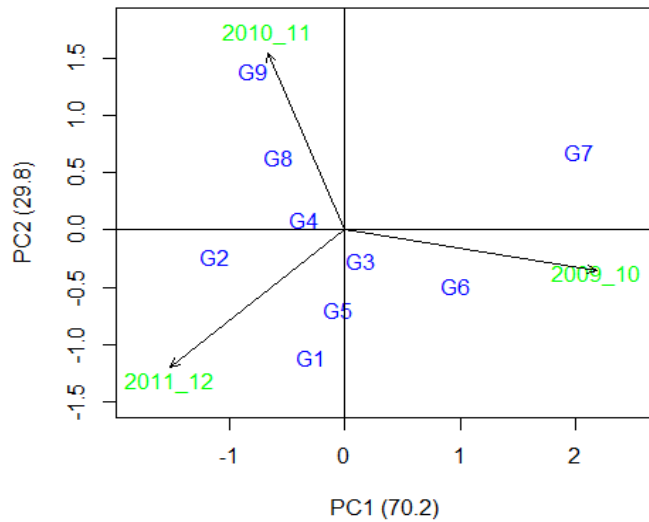


Fig. 5 : Biplot of genotype × environment interaction of nine white jute (*Corchorus capsularis* L.) genotypes in three environments, representing the effects of primary and secondary components (PC 1 and PC 2, respectively).

Table 4 : Genotypic correlation between the four traits for the nine genotypes of *capsularis* jute pooled over three years.

Traits	Basal diameter (cm)	Green weight (q/ha)	Fibre yield (q/ha)
Plant height (cm)	0.81*	0.56	0.68*
Basal diameter (cm)		0.96*	0.98*
Green weight (q/ha)			0.92*

* Significant at 5% probability level

But the genotype KJC-11 and JRC-9097 ranked 5 and 8 for the mean fibre yield, respectively. So, the genotype JRC-9097 was the low yielding genotype and its mean fibre yield was below the grand mean. Therefore, the most stable and comparatively higher fibre yielding genotype was KJC-11.

AMMI stability value (ASV) : In this study, for estimation of the stability of genotypes, the AMMI stability value (ASV) was applied. The genotype which has less ASV is considered as stable genotype and genotype which has higher ASV value, is considered as less stable

Table 5 : Direct (diagonal) and indirect (off-diagonal) effect of different yield attributes on the fibre yield of *capsularis* jute.

Traits	Plant height (cm)	Basal diameter (cm)	Green weight (q/ha)	Correlation coefficient with fibre yield (q/ha)
Plant height (cm)	-1.00	1.72	-0.04	0.68*
Basal diameter (cm)	-0.81	2.14	-0.35	0.98*
Green weight (q/ha)	-0.56	2.06	-0.58	0.92*

* Significant at 5% probability level; Residual Effect = 0.19

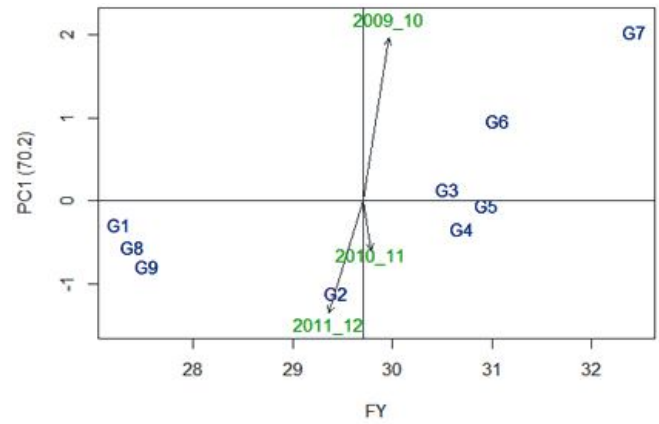


Fig. 6 : Biplot of the fibre yield (FY) and primary component (PC 1) of the environment on which the nine white jute genotypes tested in three environments. The vertical line represents fibre yield and while horizontal line for PC 1.

genotypes. A variety could be called as stable variety when it has ASV value close to Zero (Purchase, 1997). In this study, Table 6 reveals that KJC-11 has the lowest ASV value (0.43) followed by JRCM-9-1 (0.71) and both these ASV values were close to zero. So, KJC-11 is the top ranking ASV genotype, which implies that KJC-11 is the most stable genotype followed by JRCM-9-1, while the first check variety JRC-698 had the highest ASV value (4.84) and was the bottom ranking genotype based on ASV value, which implies that JRC-698 was least stable genotype among all the genotypes.

Yield stability index (YSI) : It is not mandatory that the most stable genotype would be the highest yielding one. Therefore, there is an approach, which will integrate both the stability measure and yield performance of the crop. Hence, the rank of AMMI stability value (ASV) and rank of mean of genotypes are fused together to form a single selection index, termed as yield stability index (YSI). The genotypes which have high mean yield as well as the least ASV value, is considered as ideally stable and good yielding. In this study, Table 6 shows that JRCM-9-2 consisted of high YSI value, which indicated that the genotype had comparatively low yield and could be considered the comparatively least stable genotype. The genotype JRCM-9-1 had low YSI value which

Table 6 : Stability parameters for fibre yield (q/ha) for the nine genotypes of *capsularis* jute.

Genotypes	Mean	Rank as per Mean	Standard deviation	Francis CV(%)	Eberhart and Russell			Shukla σ_i^2	Perkins and Jinks		Wricke's Ecoalence	Superiority Measure	Non parametric Nassar & Huehn		AMMI Stability Value (ASV)	Yield Stability Index (YSI)	
					bi	S ² di	R ²		Bi	Dji			Wi	Pi			Sj ⁽¹⁾
NDC-2013 (G1)	27.26	9	1.61	5.89	-3.29	-6.53	0.41	3.56	-4.29	3.05	6.63	23.87	1.67	2.50	1.30	4	13
JRCM-9-2 (G2)	29.44	6	1.89	6.41	-5.53	-8.42	0.84	5.38	-6.53	1.16	9.47	16.03	1.33	5.50	2.63	8	14
KJC-11 (G3)	30.56	5	0.61	1.99	1.11	-9.08	0.32	-0.39	0.11	0.50	0.50	6.34	0.00	0.00	0.43	1	6
JRC-9057 (G4)	30.71	4	0.50	1.62	-0.62	-9.16	0.15	-0.11	-1.62	0.42	0.93	7.75	1.33	2.50	0.82	3	7
JRCM-9-1 (G5)	30.95	3	0.94	3.05	-1.02	-8.00	0.11	0.82	-2.02	1.58	2.37	6.00	2.00	4.00	0.71	2	5
NCJ-27-40121 (G6)	31.06	2	2.22	7.15	4.99	-4.57	0.49	4.51	3.99	5.01	8.11	3.40	2.33	6.50	2.33	7	9
JRC-698+ (G7)	32.43	1	4.37	13.47	13.59	-7.42	0.94	20.54	12.59	2.17	33.05	2.03	2.00	12.00	4.84	9	10
JRC-9097 (G8)	27.39	8	1.41	5.13	-0.45	-5.67	0.01	2.07	-1.45	3.91	4.32	24.34	0.00	0.00	1.47	5	13
JRC-321+ (G9)	27.54	7	2.63	9.54	0.21	4.21	0.00	8.23	-0.79	13.79	13.91	26.12	4.00	12.00	2.32	6	13
Grand Mean	29.70																

indicated the genotype was comparatively high yielding and as well as comparatively stable followed by the genotype KJC-11. So, according to YSI model JRCM-9-1 could be considered the most potential stable genotype which was closely followed by KJC-11.

GGE Biplot Analysis : GGE biplot is a more powerful tool than AMMI model to elaborate G×E interaction for its discriminating power. The GGE biplots for nine white jute genotypes were evaluated over three consecutive years and are shown in Figs. 5 and 6. The value of the first principal component (PC1) was present along X-axis and the value of second principal component (PC2) was present along Y-axis. In Fig. 5, the GGE biplot represented that PC1 captured 70.2% and PC2 encompassed 29.8% of the total G×E interaction. The tested genotypes had made the clustering according to their principal component and secondary component value in biplot (Fig. 5) and the tested genotypes had formed clustering based on principal component value and average fibre yield on biplot (Fig. 6). In Fig 5, biplot also represented the similarities and dissimilarities among the genotypes and relationship among the genotypes (Shafii *et al.*, 1992). According to Anandan *et al.* (2009), the environments whose values are near to zero, have less interaction among genotypes and that create low discrimination among the genotypes. This type of pattern was not found in this study for any of the environments. The vectors of environments represent either the interaction between them is positive or negative. The interaction between environments is positive when the environment vector makes an acute angle (<90°) in between two vectors, while they form an obtuse angle (>90°), the interaction becomes negative. In Fig. 5, the environment vector 2009-10 (E1) made an obtuse angle with environment vector 2010-11 (E2) and 2011-12 (E3). So, the interaction between environment vector 2009-10 and 2010-11 was negative. Similarly, environment vector 2009-10 formed negative interaction with environment vector 2011-12. The environment vector 2010-11 and 2011-12 formed acute angle in between them. So, there was a positive interaction in between these two environments. The genotypes interacted differently with different environments. The environment and genotypes which are present on the right side of centre of origin consists of higher yield than the environment and genotypes present on the left side. In Fig. 5, the genotypes KJC-11, NCJ-27-40121 and JRC-698 and environment 2009-10 were located on the right side. So, the genotypes KJC-11, NCJ-27-40121 and JRC-698 and environment 2009-10 were higher yielding, while the genotypes NDC-2013, JRCM-9-2, JRC-9057, JRC-9097 and JRC-321 and

environment 2010-11 and 2011-12, which were presentation the left side of origin, were comparatively low yielding. In Fig. 5, the genotypes NDC-2013, JRCM-9-2, JRC-9057, JRC-9097 and JRC-321 interacted positively with the environments 2010-11 and 2011-12, but negatively with environment 2009-10. The genotypes KJC-11, NCJ-27-40121 and JRC-698 interacted positively with environment 2009-10, but negatively with environment 2010-11 and 2011-12. The genotype JRCM-9-1 with PC1 value near to zero, located at PC1 axis in both Figs. 5 and 6, indicated that it had high stability with high average fibre yield. Similarly, in both Figs. 5 and 6, it was found that genotype KJC-11 was located near to PC1 axis, which indicated that it was also stable and exhibited average high fibre yield, but comparatively far from JRCM-9-1. These types of genotypes are immensely desirable for white jute breeding programmes due to their high stability. Similar types of study was also performed by Kulsum *et al.* (2013), Kumar and Purushottam (2020), Lee *et al.* (2023) and Kiruba *et al.* (2023), Sujitha *et al.* (2024).

The Fig. 6 explained that the genotype KJC-11 (G3) was located close to the centre of the bisect, indicating that it was close to the general mean fibre yield of 29.70 q ha⁻¹. Therefore, it was distinguished to be of highest stability. According to Yan (2001), the genotypes which are located on the highest point in certain section of graph is considered as the best yielding genotypes on that environment, which is located in the same particular section. The genotype JRC-698 was far from origin and located on the highest point of the environment 2009-10. So, it was high fibre yielding genotype but specifically adapted to the first environment 2009-10. From the vector point of view of the GGE biplot, the length of the vector is an estimation of the discrimination ability of the environments (Yan and Kang, 2003). In Fig. 6, the vector which was representing the second environment 2010-11 was very short compared to others vectors and biplot size. So, the environment 2010-11 was least discriminating environment, while the vector of environment 2009-10 was very long, indicating that it was the most discriminating environment.

Conclusion

Among all the genotypes over three succeeding years, the highest fibre yield was exhibited by JRC-698 (32.43 q ha⁻¹) followed by NCJ-27-40121 (31.06 q ha⁻¹). The fibre yield (q ha⁻¹) was significantly and positively correlated consistently with all the attributing traits like basal diameter (rG = 0.98), green weight (rG = 0.92) and plant height (rG = 0.68). Result of stability performance

according to Eberhart and Russell model, revealed that KJC-11 was stable in all the environments. According to Ecovalence (W_i^2) and Shukla's stability variance ($Sh-\sigma_i^2$), KJC-11 was the most stable and comparatively higher yielding genotype followed by JRC-9057 and JRCM-9-1. On the basis of P_i values, JRC-698 was the most stable genotype followed by NCJ-27-40121, JRCM-9-1, KJC-11 and JRC-9057. According to Huehn's non-parametric measures of stability, the most stable and comparatively higher fibre yielding genotype was KJC-11, which had the smallest changes in ranks of $S_i^{(1)}$ and $S_i^{(2)}$ was thus regarded as the most stable genotype. Based on AMMI stability value, KJC-11 (G3) was the most stable genotype followed by genotype JRCM-9-1. According to Yield stability index (YSI), JRCM-9-1 was comparatively high yielding and as well as stable genotype followed by KJC-11. According to the GGE biplot, JRCM-9-1 had high stability with high average fibre yield followed by KJC-11. Thus, in overall from most of the stability models the white jute genotypes JRCM-9-1 and KJC-11 were identified to be the most stable for fibre yield, over the three years and can be recommended for cultivation in Terai Agro-climatic condition, which comes under sub-Himalayan zone. The first environment 2009-10 was the most discriminating one.

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