



RESEARCH ARTICLE

Genetic mechanism governing fibre quality and yield in the cultivated jute (*Corchorus* sp.)- Breeders' perspective

Sourav Hazari¹, Kumaresh Dasgupta², Sri Sai Subramanyam Dash¹, Soham Hazra³, G Parimala¹,
Surendra Kumar Pandey⁴ & Anita Roy^{1*}

¹Department of Genetics and Plant Breeding, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur 741 252, West Bengal, India

²Department of Genetics and Plant Breeding, Uttar Banga Krishi Viswavidyalaya, Pundibari 736 165, West Bengal, India

³Department of Agriculture, Brainware University, Barasat 700 125, West Bengal, India

⁴ICAR-Central Research Institute for Jute and Allied Fibres, Barrackpore 700 120, West Bengal, India

*Correspondence email - royanita1925@gmail.com

Received: 14 November 2025; Accepted: 01 April 2026; Available online: Version 1.0: 18 June 2026

Cite this article: Sourav H, Kumaresh D, Sri SSD, Soham H, Parimala G, Surendra KP, Anita R. Genetic mechanism governing fibre quality and yield in the cultivated jute (*Corchorus* sp.)- Breeders' perspective. Plant Science Today. 2026;13(sp2):01–14. <https://doi.org/10.14719/pst.12727>

Abstract

Jute is valued for its biodegradability and industrial versatility. *Corchorus capsularis* L. (White jute) and *Corchorus olitorius* L. (Tossa jute) are the two commercially cultivated species, each exhibiting distinct morphological and physiological traits. Breeding efforts to develop superior cultivars combining desirable traits from both species are limited due to their sexual incompatibility. This study investigates the genetic control of 9 yield and quality traits in tossa and white jute through combining ability analysis, conducted during the rainy seasons of 2020 and 2021 at Bidhan Chandra Krishi Viswavidyalaya, West Bengal, India. Significant differences were observed among parents and hybrids for key traits, indicating genetic variability. Hybrid combinations such as BCCC 127 × BCCC 107 in white jute and BCCO 120 × BCCO 6 in tossa jute demonstrated the highest fibre yield (13.56 and 22.21 g plant⁻¹ respectively), while crosses like CIN 115 × CIN 111 and OIN 133 × OIN 95 produced the finest fibre (1.16 and 2.50 tex, respectively). Notable standard heterosis effects were recorded for fibre weight (up to 43.02 % in white jute and 58.85 % in tossa jute) and fineness (up to -33.33 and -15.73 %, respectively), with certain crosses exhibiting desirable transgressive segregation for improved fibre traits. Gene action analysis using Hayman's approach revealed the overwhelming importance of non-additive gene action, indicating that deferred selection in segregating generations or hybrid breeding is rewarding. The Vr Wr graphical analysis confirmed genetic variability among parental lines, indicating potential for effective selection. The findings highlight the potential of heterosis breeding and gene action analysis in optimising jute breeding programmes.

Keywords: combining ability; diallel analysis; gene action; heterosis; transgressive segregation

Introduction

Jute, frequently referred to as the "golden fibre," is the second most important natural and biodegradable fibre crop grown globally, after cotton (1). Jute is an essential bast fibre crop with around 40–100 species; however, only two are cultivated viz., *Corchorus capsularis* L. (white jute) and *Corchorus olitorius* L. (tossa jute). These two commercially significant species have distinct variations in appearance, physiology and fibre attributes. Jute farming is predominantly located in tropical areas, especially the lower Gangetic delta. Worldwide, the crop is cultivated on around 1.93 million hectare, producing about 3.27 million metric tonnes, with an average yield of 1700 kg per hectare (2). India dominates in both cultivation area and production, accounting for 51 % of the global share (3). Jute has been mostly utilised in the production of ropes and as a material for the packaging sector. However, the quality attributes viz., smooth texture, higher tensile strength, resistance to abrasion and heat, durability and extended staple length render it a versatile and economical material for several industries, including textiles, paper, construction and automobile manufacture (4). Jute can be integrated with various natural and

synthetic fibres. Additionally, the affordability and abundance as a source of cellulose and cellulose nanocrystals, amplifies its commercial importance (5). Fibres exhibiting exceptional bundle strength, breaking load and tenacity are highly esteemed in the textile sector (6). Therefore, enhancing both fibre yield and quality is crucial for maintaining competitiveness in the global market.

However, limited genetic improvement work pertaining to combining the best traits of both species viz., tossa jute and white jute has been done owing majorly to their sexual incompatibility leads (7). This leads to a restricted genetic pool which necessitates a robust breeding strategy for improving of jute yield and fibre quality. The success of any breeding programme depends upon the understanding of the genetic control underlying the important characters. Breeding techniques utilising diallel mating designs, as described (8), offer significant insights into combining aptitude, heterosis and genetic factors, facilitating the selection of ideal parents. Precise selection of parents is crucial for effective hybridisation. Diallel analysis encompasses not just gene action but also examines aspects like as epistasis, linkage, maternal effects and diploid segregation, thereby providing a thorough comprehension of the underlying genetic mechanisms (9).

Keeping this backdrop in mind, this study provides a combining ability analysis of traits affecting fibre yield and quality features in tossa jute (*C. olitorius*) and white jute (*C. capsularis*). The primary objective is to identify ideal parents and crossbreed combinations that exhibit increased production and quality potential, thereby facilitating the advancement of superior jute cultivars for the future. We hypothesised that systematically crossing these diverse parental lines would reveal significant additive and non-additive gene interactions, leading to the expression of exploitable heterosis and the emergence of superior transgressive segregants for fibre yield and fineness.

Materials and Methods

Experimental site and plant materials

The experiment was conducted in the rainy season for two consecutive years, 2020 and 2021 at the Teaching Farm, Mondouri of Bidhan Chandra Krishi Viswavidyalaya, Nadia, West Bengal, India located at 22.87° N latitude and 88.59° E longitude, with an elevation of 9.75 m above mean sea level. The soil is characterised as Gangetic alluvial sandy loam, with a neutral pH (measured using a 1:2.5 soil: water ratio), medium fertility and possessing both good water retention and drainage capabilities. Baseline soil nutrient status at the experimental site is typically reported around 168 kg ha⁻¹ of available N, 26 kg ha⁻¹ of available P₂O₅ and 287 kg ha⁻¹ of available K₂O (10). The experimental material consisted of 28 jute hybrids developed through 8 × 8 half diallel crossing design without reciprocals from both *Corchorus olitorius* and *C. capsularis* (Table 1). As standard checks for white jute and tossa jute, respectively, BCCC 1 and BCCO 6 were used because they have better fibre yield and good quality. In the first year (2020), a crossing programme was initiated to develop the hybrids. In the second year (2021), the 28 crosses, along with their 8 parental lines and the respective standard checks from each species, were assessed.

Field evaluation and agronomic practices

The genotypes were evaluated in a randomised complete block design (RCBD) with 3 replications. A strict plant geometry was maintained with a row-to-row spacing of 30 cm and a plant-to-plant spacing of 6–7 cm. The established protocols for crop cultivation were adhered meticulously. The field was prepared by deep ploughing followed by cross-harrowing to obtain fine tilth. Fertilisers were applied at the recommended dose of 60:30:30 kg ha⁻¹ of N:P₂O₅:K₂O. The entire dose of phosphorus and potassium, along with one-third of the dose of nitrogen, was applied as a basal dressing at the time of final land preparation. The remaining amount of nitrogen was applied at two splits of 20 and 40 days after sowing. Manual weeding was done twice at 15–20 days after sowing and again at 35–40 days after sowing to reduce competition between the crops and weeds. Thinning was done at the same time to maintain optimal spacing between the plants.

Since it was a rain-fed kharif crop, it was dependent on the monsoon rains. However, life-saving irrigation was also supplied during the dry spell.

Data collection

Observations were recorded from five randomly chosen plants in the middle row of each plot, focusing on nine yield and quality attributing traits viz., plant height (m), basal diameter (mm), mid diameter (mm), bark thickness (mm), green weight per plant (g), dry stick weight per plant (g), dry fibre weight per plant (g), fibre fineness (tex) and fibre strength (g tex⁻¹) at 120 days after sowing.

Statistical analysis

Analysis of variance (ANOVA) for the RCBD was performed to test the significance of differences among the genotypes. Combining ability analysis was executed following Griffing's method II (parents and one set of F₁s included), assuming model I (fixed effects). The mathematical model for the analysis was:

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + e_{ijk} \quad (\text{Eqn. 1})$$

Where

Y_{ij} is the mean phenotypic value of the cross between the i^{th} and j^{th} parents; μ is the general population mean; g_i and g_j are the general combining ability (GCA) effects of the i^{th} and j^{th} parents, respectively; s_{ij} is the specific combining ability (SCA) effect of the cross $i \times j$; and e_{ijk} is the environmental effect associated with the ijk^{th} observation.

The genetic components of variance (D , H_1 , H_2 , F and h^2) were estimated using standard diallel analysis approach (9). The Vr Wr graphical analysis was constructed by plotting the variance of each array (Vr) against the covariance between parents and their offspring in that array (Wr) to assess the degree of dominance and allelic distribution among the parents.

Standard heterosis (SH) was calculated to evaluate the superiority of the hybrids over the standard commercial check varieties (BCCC 1 for *C. capsularis* and BCCO 6 for *C. olitorius*), using the following formula:

$$\text{Standard heterosis (SH)} = \frac{F_1 - SV}{SV} \times 100 \quad (\text{Eqn. 2})$$

Note: Average values of F_1 and standard variety (SV) to be used.

All the statistical analysis were conducted utilising INDOSTAT and OriginPro software.

Results and Discussion

Analysis of variance and mean performance

Analysis of variance for the parents and hybrids, as presented in Tables 2 and 3, indicated significant differences in the mean sum of squares for the 9 yield and quality attributing traits across the genotypes and hybrids of both species under investigation. All the

Table 1. List of parents

<i>Corchorus capsularis</i> (White jute)		<i>Corchorus olitorius</i> (Tossa jute)	
BCCC 102	Advanced breeding lines	BCCO 105	
BCCC 127		BCCO 115	
BCCC 116		BCCO 120	
BCCC 107		OIN 133	
CIN 106		OIN 128	
CIN 115	Germplasm	OIN 95	
CIN 111		OIN 122	
JRC 321		BCCCO 6	
	Realised variety		

Table 2. Analysis of variance of yield and quality traits of parents and hybrids of *Corchorus capsularis*

Source of variation	df	Mean sum of squares								
		PH	BD	MD	BT	GW	FW	STWT	FINE	STREN
Treatments	35	0.186**	2.866**	5.221**	0.064**	2793.994**	10.741**	47.489**	0.239**	20.150**
Parents	7	0.221**	2.101**	1.471**	0.0503**	595.071*	12.387**	8.167	0.307**	5.419**
Hybrids	27	0.166**	2.959**	6.362**	0.070**	3395.369**	8.772**	50.528**	0.197**	24.248**
Parents vs hybrids	1	0.463**	5.703**	0.614	0.005	1949.340**	52.360**	240.666**	0.859**	12.633**
Error	70	0.027	0.657	0.360	0.009	276.426	0.578	6.43	0.013	1.322

*, ** Significant at 5 % and 1 % levels of probability, respectively. PH: Plant height; BD: Basal diameter; MD: Mid diameter; BT: Bark thickness; GW: Green weight; FW: Dry fibre weight; STWT: Stick weight; FINE: Fibre fineness; STREN: Tensile strength.

Table 3. Analysis of variance of GCA and SCA in *Corchorus capsularis* genotypes

Source of variation	df	Mean sum of squares								
		PH	BD	MD	BT	GW	FW	STWT	FINE	STREN
GCA	7	0.159**	1.430**	1.864**	0.052**	1175.497**	10.111**	24.144**	0.211**	6.521**
SCA	27	0.038**	0.836**	1.710**	0.014**	870.293**	1.947**	13.755**	0.047**	6.767**
Error	70	0.009	0.219	0.120	0.003	92.150	0.193	2.144	0.004	0.441

*, ** Significant at 5 % and 1 % levels of probability, respectively. PH: Plant height; BD: Basal diameter; MD: Mid diameter; BT: Bark thickness; GW: Green weight; FW: Dry fibre weight; STWT: Stick weight; FINE: Fibre fineness; STREN: Tensile strength.

parameters under study displayed significant disparity amongst parents in both of the species except stick weight in white jute. Similarly, all traits showed substantial differences between parents and hybrids, with the exception of mid-diameter and bark thickness in white jute and plant height and stick weight in tossa jute. The mean value of the 9 yield and quality attributing traits of 28 hybrids along with their parents of *C. capsularis* and *C. olitorius* are presented in Fig. 1 and 2, respectively. The highest plant height (3.80 m), basal diameter (19.33 mm), mid diameter (14.70 mm) and bark thickness (1.99 mm) among white jute hybrids were documented in BCCC 102 × JRC 321, BCCC 102 × BCCC 116, BCCC 102 × BCCC 116 and BCCC 107 × CIN 115 respectively. BCCC 107 × CIN 115 demonstrated the most exceptional performance, achieving a value of 40.15 g plant⁻¹, which was statistically equivalent to the hybrid BCCC 127 × BCCC 107. In case of tossa jute hybrids the highest plant height (3.72 m), basal diameter (15.33 mm) and mid diameter (11.47 mm) was recorded in the cross OIN 133 × OIN 122 and BCCO 120 × BCCO 6 respectively. The hybrid combinations of *C. olitorius*, those had high bark thickness were recorded in BCCO 120 × BCCO 6 (1.55 mm) and OIN 122 × BCCO 6 (1.41 mm). There was a notable disparity in the stick weight per plant observed within the parental population of tossa jute. BCCO 115 displayed the highest value, measuring 46.19 g plant⁻¹, whereas OIN 95 recorded the lowest value of 28.49 g plant⁻¹. Among the hybrid combinations, OIN 133 × BCCO 6 demonstrated the most exceptional performance, achieving a score of 49.15 g plant⁻¹. Among the hybrids, highest fibre yield was shown by the combination BCCC 127 × BCCC 107 (13.56 g plant⁻¹) and

BCCO 120 × BCCO 6 (22.21 g plant⁻¹) in white jute and tossa jute respectively. Among the hybrid combinations, maximum coarse fibre observed in BCCC 127 × CIN 115 (2.31 tex) and BCCO 120 × OIN 122 (3.37 tex) respectively in white and tossa jute. Conversely, CIN 115 × 111 (1.16 tex) and OIN 133 × OIN 95 (2.50 tex) exhibited the finest fibre among the crosses of 2 species. Among the hybrid combinations, BCCC 127 × BCCC 116 had maximum fibre strength of 24.15 (g tex⁻¹) followed by BCCC 107 × CIN 106 (23.97 g tex⁻¹) and BCCC 127 × CIN 115 (23.93 g tex⁻¹) in white jute whereas in tossa jute BCCO 105 × BCCO 115 demonstrated the most exceptional performance, achieving a value of 27.23 g tex⁻¹ followed by hybrids like BCCO 115 × OIN 128 (26.66 g tex⁻¹) and BCCO 105 × OIN 133 (25.94 g tex⁻¹).

Combining ability analysis

General combining ability is mainly controlled by additive gene action, which refers to the ability of a parent to transmit desirable genes to its offspring. On the contrary, specific combining ability is controlled by non-additive gene action, which includes dominance and epistasis, thus pointing to unique gene interactions occurring during a specific cross. Analysis of variance for GCA and SCA (Tables 3–5) indicated significant variations for GCA and SCA among parents and hybrids respectively for all the 9 characters in both of the species under study. All the 16 parental genotypes exhibited significant GCA effects for multiple yield and quality traits evaluated in this study (Tables 6 and 7). However, deviations were observed for specific genotypes. BCCC 127, BCCC 116 and JRC 321 showed

Table 4. Analysis of variance of yield and quality traits of parents and hybrids of *Corchorus olitorius*

Source of variation	df	Mean sum of squares								
		PH	BD	MD	BT	GW	FW	STWT	FINE	STREN
Genotypes	35	0.10**	2.85**	2.55**	0.13**	3743.30**	19.53**	87.38**	0.25**	13.37**
Parents	7	0.08*	3.33**	1.00*	0.11**	4494.93**	35.78**	123.87**	0.77**	30.73**
Hybrids	27	0.11**	2.34**	2.76**	0.10**	3341.08**	15.48**	79.21**	0.11**	9.02**
Parent vs hybrid	1	0.002	13.46**	7.55**	0.84**	9341.91**	15.09*	52.50	0.31**	9.27*
Error	70	0.03	0.42	0.44	0.01	972.51	2.86	15.37	0.02	1.91

*, ** Significant at 5 % and 1 % levels of probability, respectively. PH: Plant height; BD: Basal diameter; MD: Mid diameter; BT: Bark thickness; GW: Green weight; FW: Dry fibre weight; STWT: Stick weight; FINE: Fibre fineness; STREN: Tensile strength.

Table 5. Analysis of variance of GCA and SCA in *Corchorus olitorius* genotypes

Source of variation	df	Mean sum of squares								
		PH	BD	MD	BT	GW	FW	STWT	FINE	STREN
GCA	7	0.03**	0.50**	1.53**	0.04**	1706.55**	9.77**	19.88**	0.12**	8.26**
SCA	27	0.04**	1.07**	0.68**	0.04**	1133.07**	5.70**	31.44**	0.07**	3.51**
Error	70	0.01	0.14	0.15	0.00	324.18	0.96	5.12	0.01	0.64

*, ** Significant at 5 % and 1 % levels of probability, respectively. PH: Plant height; BD: Basal diameter; MD: Mid diameter; BT: Bark thickness; GW: Green weight; FW: Dry fibre weight; STWT: Stick weight; FINE: Fibre fineness; STREN: Tensile strength.

Table 6. Combining ability effects (GCA and SCA) of yield and quality traits in hybrids (F1s) and parents of *Corchorus capsularis*

Parents	GCA effects								
	PH	BD	MD	BT	GW	FW	STWT	FINE	STREN
BCCC 102 (P1)	0.05 ns	0.40 **	0.56 **	0.01 ns	2.07 ns	0.78 **	-1.39 **	0.09 **	0.76 **
BCCC 127 (P2)	0.15 **	0.22 ns	-0.29 **	-0.02 ns	1.67 ns	1.20 **	0.47 ns	0.26 **	0.91 **
BCCC 116 (P3)	0.12 **	0.08 ns	0.47 **	-0.01 ns	1.67 ns	0.32 *	-0.08 ns	0.02 ns	0.75 **
BCCC 107 (P4)	0.01 ns	0.01 ns	0.04 ns	-0.05 **	14.38 **	0.91 **	2.09 **	0.04 *	-0.48 *
JRC 321 (P5)	0.07 *	0.35 *	-0.25 *	-0.06 **	3.02 ns	-0.19 ns	0.99 *	0.02 ns	0.15 ns
CIN 106 (P6)	-0.20 **	-0.66 **	-0.30 **	-0.07 **	-23.52 **	-1.56 **	-2.99 **	-0.17 **	0.02 ns
CIN 115 (P7)	-0.14 **	-0.47 **	-0.61 **	0.15 **	-4.33 ns	-1.25 **	0.51 ns	-0.19 **	-1.33 **
CIN 111 (P8)	-0.06 *	0.07 ns	0.39 **	0.05 **	5.02 ns	-0.22 ns	0.39 ns	-0.07 **	-0.77 **
Hybrids	SCA effects								
PH	BD	MD	BT	GW	FW	STWT	FINE	STREN	
P1 × P2	-0.13 ns	0.30 ns	1.65 **	-0.03 ns	3.56 ns	-0.62 ns	0.15 ns	0.02 ns	0.00 ns
P1 × P3	-0.00 ns	1.22 **	2.22 **	0.13 **	33.56 **	1.82 **	1.47 ns	0.04 ns	0.30 ns
P1 × P4	0.15 *	-1.60 **	-1.35 **	-0.07 ns	-24.65 **	-0.24 ns	-2.04 ns	0.16 **	-0.02 ns
P1 × P5	0.48 **	0.15 ns	0.06 ns	0.14 **	51.71 **	1.75 **	5.08 **	-0.03 ns	-1.08 *
P1 × P6	-0.23 **	0.95 *	1.99 **	0.08 ns	2.75 ns	0.28 ns	-0.35 ns	0.12 *	1.18 *
P1 × P7	0.01 ns	-0.49 ns	-2.16 **	-0.05 ns	-52.94 **	-0.86 *	-5.63 **	0.25 **	0.86 ns
P1 × P8	0.02 ns	-0.56 ns	-0.23 ns	0.11 *	-7.29 ns	1.38 **	0.72 ns	0.07 ns	1.39 **
P2 × P3	0.04 ns	-0.02 ns	-1.41 **	0.03 ns	-9.04 ns	-0.31 ns	0.26 ns	0.09 ns	2.12 **
P2 × P4	0.16 *	0.13 ns	0.41 ns	0.04 ns	16.75 *	1.41 **	4.52 **	0.07 ns	-3.27 **
P2 × P5	0.24 **	-0.01 ns	-0.48 ns	-0.07 ns	-8.39 ns	0.25 ns	-0.83 ns	0.02 ns	-1.04 *
P2 × P6	0.17 *	-0.08 ns	-0.90 **	0.07 ns	-19.85 *	-1.41 **	-3.79 **	-0.15 **	-1.61 **
P2 × P7	-0.02 ns	0.06 ns	-0.73 **	-0.13 **	-0.04 ns	3.05 **	4.42 **	0.61 **	3.97 **
P2 × P8	-0.05 ns	0.45 ns	0.24 ns	-0.10 *	-13.89 ns	-0.05 ns	-1.86 ns	-0.17 **	-0.11 ns
P3 × P4	0.12 ns	0.30 ns	1.06 **	0.00 ns	38.75 **	-0.95 **	1.00 ns	-0.23 **	-4.16 **
P3 × P5	-0.17 *	-0.23 ns	1.86 **	0.03 ns	-8.39 ns	0.22 ns	-0.99 ns	0.01 ns	-2.20 **
P3 × P6	0.11 ns	-1.59 **	-0.58 *	-0.14 **	-22.35 **	-0.57 ns	-2.55 *	0.05 ns	-0.93 ns
P3 × P7	0.05 ns	1.44 **	-0.25 ns	0.02 ns	16.46 *	2.04 **	2.57 *	0.14 **	4.14 **
P3 × P8	-0.05 ns	-0.50 ns	-2.20 **	-0.14 **	-29.89 **	0.28 ns	0.66 ns	0.30 **	2.85 **
P4 × P5	-0.08 ns	0.84 *	-0.80 **	0.00 ns	-13.10 ns	1.45 **	1.49 ns	0.25 **	0.43 ns
P4 × P6	-0.26 **	-1.14 **	1.03 **	-0.16 **	-13.43 ns	0.53 ns	-0.55 ns	-0.06 ns	4.04 **
P4 × P7	0.07 ns	1.29 **	1.29 **	0.26 **	57.25 **	1.58 **	8.51 **	-0.15 **	-2.65 **
P4 × P8	-0.30 **	1.40 **	0.60 *	-0.02 ns	9.40 ns	-0.90 *	0.07 ns	-0.15 **	-1.21 *
P5 × P6	0.15 *	0.26 ns	-1.89 **	-0.12 **	-25.20 **	0.74 *	0.93 ns	0.17 **	3.09 **
P5 × P7	0.08 ns	0.63 ns	0.34 ns	0.05 ns	3.61 ns	-0.51 ns	0.84 ns	-0.13 *	-0.72 ns
P5 × P8	0.11 ns	0.28 ns	1.37 **	0.15 **	59.26 **	0.39 ns	4.50 **	0.01 ns	-0.06 ns
P6 × P7	0.16 *	0.57 ns	-0.25 ns	-0.01 ns	-4.85 ns	-0.09 ns	1.01 ns	0.14 **	-1.88 **
P6 × P8	0.19 *	1.00 **	-1.08 **	-0.09 *	8.30 ns	-0.07 ns	0.41 ns	0.10 ns	-3.25 **
P7 × P8	-0.04 ns	-1.60 **	1.33 **	0.10 *	15.61 *	-0.17 ns	2.33 *	-0.21 **	-5.30 **

PH: Plant height; BD: Basal diameter; MD: Mid diameter; BT: Bark thickness; GW: Green weight; FW: Dry fibre weight; STWT: Stick weight; FINE: Fibre fineness; STREN: Tensile strength.

Table 7. Combining ability effects (GCA and SCA) of yield and quality traits in hybrids (F1s) and parents of *Corchorus olitorius*

Parents	GCA effects						
	PH	BD	MD	BT	GW	FW	STWT
BCCO 105 (P1)	0.08 **	0.14 ns	-0.23 *	0.10 **	13.29 *	2.07 **	0.90 ns
BCCO 115 (P2)	-0.05 ns	-0.19 ns	-0.56 **	-0.01 ns	-10.13 ns	-0.33 ns	0.59 ns
BCCO 120 (P3)	-0.06 *	0.02 ns	-0.21 ns	-0.07 **	-10.27 ns	-0.22 ns	-0.23 ns
OIN 133 (P4)	0.02 ns	-0.02 ns	0.55 **	0.03 *	22.04 **	0.25 ns	2.47 **
OIN 128 (P5)	0.05 ns	-0.02 ns	0.18 ns	-0.08 **	1.62 ns	-0.65 *	-0.76 ns
OIN 95 (P6)	-0.05 ns	0.08 ns	-0.08 ns	-0.05 **	-13.47 *	-1.26 **	-2.42 **
OIN 122 (P7)	0.02 ns	-0.38 **	-0.19 ns	0.08 **	-9.77 ns	-0.32 ns	-0.34 ns
BCCO 6 (P8)	-0.01 ns	0.37 **	0.54 **	-0.00 ns	6.70 ns	0.47 ns	-0.22 ns
Hybrids	SCA effects						
	PH	BD	MD	BT	GW	FW	STWT
P1 × P2	0.06 ns	0.07 ns	-0.11 ns	0.05 ns	13.83 ns	1.34 ns	2.47 ns
P1 × P3	0.20 **	-0.13 ns	-0.68 *	-0.20 **	-19.36 ns	-0.24 ns	0.80 ns
P1 × P4	0.09 ns	0.06 ns	0.65 *	-0.01 ns	-0.84 ns	-1.58 *	1.98 ns
P1 × P5	0.07 ns	-1.03 **	-0.77 *	-0.14 **	-37.09 *	-1.04 ns	0.68 ns
P1 × P6	-0.01 ns	-1.24 **	0.33 ns	-0.09 *	-13.67 ns	-2.74 **	-2.57 ns
P1 × P7	-0.08 ns	0.12 ns	-0.58 ns	-0.07 ns	-8.20 ns	-0.92 ns	-10.52 **
P1 × P8	-0.22 **	-1.21 **	0.03 ns	-0.05 ns	-38.84 **	-3.61 **	-6.49 **
P2 × P3	0.19 *	0.06 ns	-0.48 ns	-0.12 **	-0.95 ns	1.50 ns	-0.88 ns
P2 × P4	-0.03 ns	-1.12 **	-0.91 **	0.03 ns	-43.25 **	-1.22 ns	-7.21 **
P2 × P5	-0.23 **	-0.55 ns	-0.94 **	0.03 ns	-12.00 ns	-2.83 **	-3.69 *
P2 × P6	-0.11 ns	0.55 ns	-0.04 ns	0.09 *	23.08 ns	0.04 ns	-0.24 ns
P2 × P7	-0.41 **	-0.79 **	-0.77 *	-0.40 **	-61.45 **	-1.11 ns	-9.06 **
P2 × P8	0.26 **	-0.98 **	0.20 ns	-0.09 *	19.58 ns	-0.10 ns	0.99 ns
P3 × P4	0.15 *	0.21 ns	0.80 **	0.24 **	14.39 ns	0.31 ns	-0.88 ns
P3 × P5	-0.17 *	-0.07 ns	-0.27 ns	-0.25 **	-6.86 ns	0.54 ns	0.14 ns
P3 × P6	-0.28 **	0.24 ns	-0.25 ns	-0.01 ns	-10.11 ns	-1.88 *	-4.85 **
P3 × P7	-0.07 ns	-0.94 **	-1.29 **	-0.12 **	-21.89 ns	-1.04 ns	-1.24 ns
P3 × P8	0.14 ns	1.81 **	1.07 **	0.43 **	59.72 **	7.00 **	4.86 **
P4 × P5	0.15 *	-0.59 ns	0.46 ns	-0.01 ns	22.50 ns	1.44 ns	2.61 ns
P4 × P6	-0.14 ns	-1.85 **	-0.69 *	-0.37 **	-57.42 **	-0.77 ns	-5.70 **
P4 × P7	0.35 **	0.41 ns	0.61 *	-0.12 **	-8.61 ns	0.16 ns	-0.32 ns
P4 × P8	0.09 ns	0.99 **	0.23 ns	-0.27 **	37.41 **	2.57 **	10.68 **
P5 × P6	0.10 ns	-0.04 ns	-1.46 **	-0.03 ns	-15.34 ns	0.15 ns	-1.06 ns
P5 × P7	0.03 ns	0.14 ns	0.73 *	0.07 ns	-2.36 ns	-0.56 ns	8.41 **
P5 × P8	0.02 ns	-0.92 **	-0.46 ns	-0.11 **	-23.00 ns	-0.13 ns	3.48 ns
P6 × P7	0.14 ns	0.41 ns	1.05 **	0.16 **	43.56 **	1.01 ns	6.12 **
P6 × P8	-0.03 ns	-0.32 ns	-0.34 ns	-0.11 **	-24.59 ns	-2.56 **	-0.64 ns
P7 × P8	-0.19 *	1.43 **	-0.09 ns	0.14 **	32.55 *	0.68 ns	1.69 ns

PH: Plant height; BD: Basal diameter; MD: Mid diameter; BT: Bark thickness; GW: Green weight; FW: Dry fibre weight; STWT: Stick weight; FINE: Fibre fineness; STREN: Tensile strength.

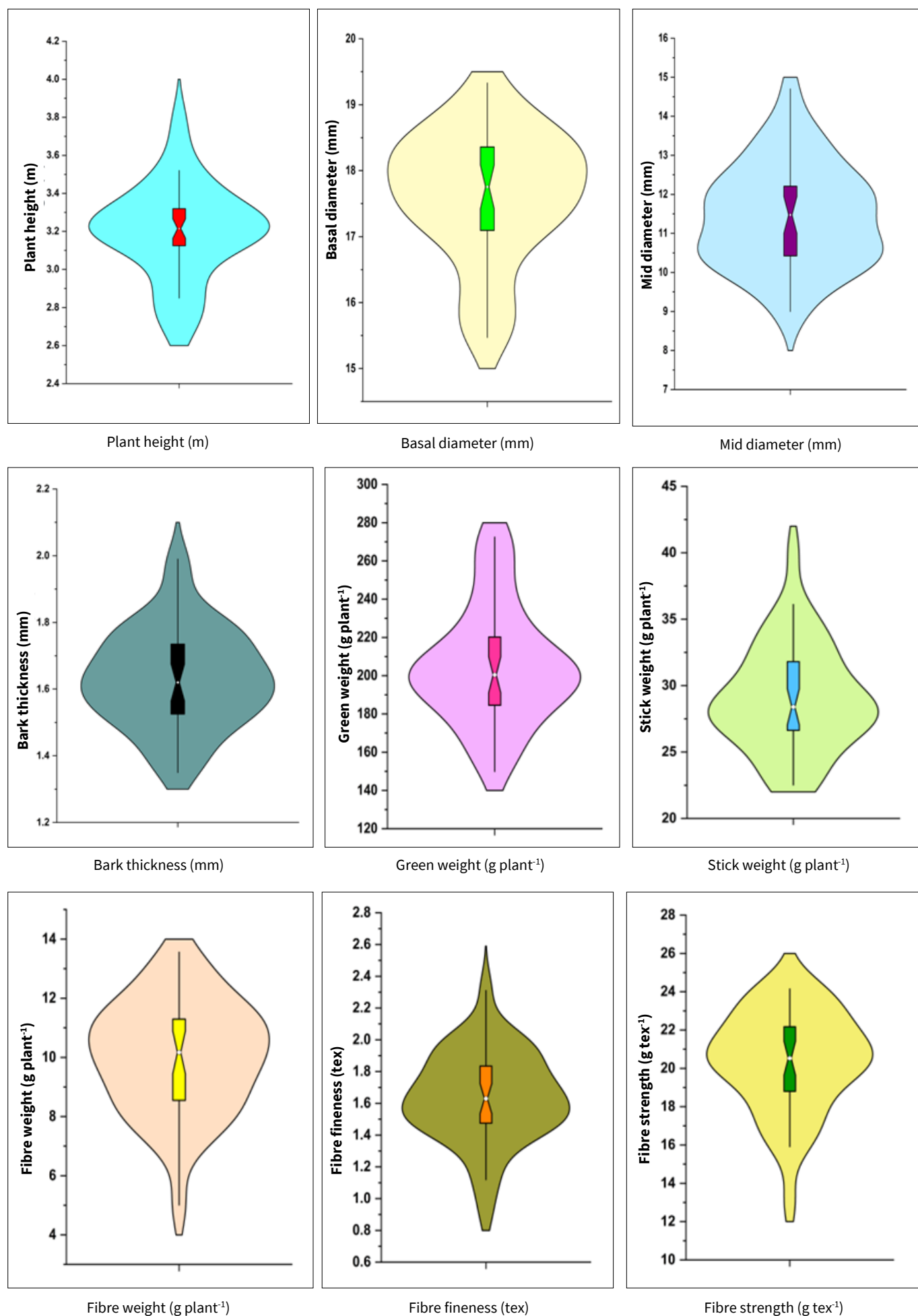


Fig. 1. Mean performances of yield and quality traits of parents and hybrids of *Corchorus capsularis*.

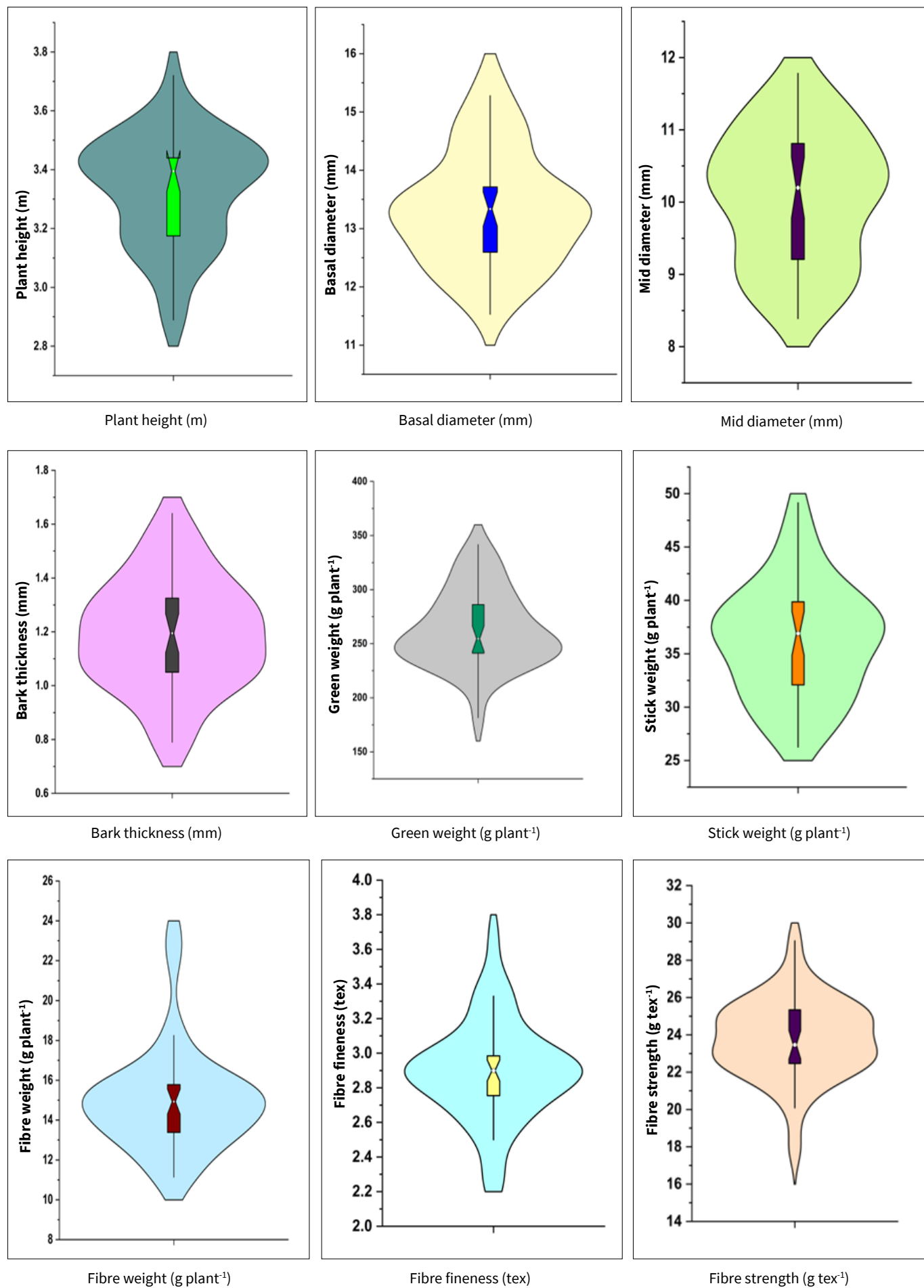


Fig. 2. Mean performances of yield and quality traits of parents and hybrids of *Corchorus olitorius*.

positive GCA for plant height, while BCCC 102 and JRC 321 enhanced basal diameter in white jute. Notably, desirable negative GCA in relation to the attainment of finer fibre in parental varieties, specifically CIN 106, CIN 115 and CIN 111 in *C. capsularis*, as well as BCCO 120, OIN 128 and OIN 95 in *C. olitorius*. The study revealed some parental lines viz, BCCC 102, BCCC 127 and BCCC 116 in *C. capsularis*, as well as BCCO 105 in *C. olitorius*, were good general combiners for both fibre strength and fibre weight. BCCC 107 and JRC 321 in *C. capsularis* and OIN 133 in *C. olitorius*, were effective general combiners in terms of stick weight. General combining is a measure of additive genetic variance. The genotypes exhibiting significant GCA effect could be used as valuable breeding stock and lead to major genetic advancements with wide adaptability. Furthermore, it has been noticed that an elevated degree of GCA is associated with a decrease in environmental influences and gene interactions. This characteristic renders these lines well-suited of selecting preferred parents. The analysis of specific combining ability (SCA) identified promising hybrid combinations for key traits in white jute. Positive SCA effects were observed in several crosses of white jute, such as P1 × P4, P2 × P5, P4 × P7 and P5 × P8 for plant height, basal diameter, bark thickness and fibre traits respectively. Notable hybrids like P1 × P6, P3 × P7 and P4 × P5 showed strong potential for strength. However, some combinations, including P2 × P6, P2 × P8, P3 × P4, P4 × P7, P4 × P8, P5 × P7 and P7 × P8 exhibited negative SCA

effects, indicating fine fibre producing combinations. Significant positive SCA effects were observed in tossa jute hybrids like P3 × P8, P4 × P8, P6 × P7 and P7 × P8 for traits such as plant height, basal diameter, fibre weight and fibre strength. These findings highlighted the best hybrid combinations for breeding programmes aimed at improving jute yield and fibre quality. Negative SCA impacts for particular traits in some crossings, on the other hand, might result from harmful gene interactions in the parental lines.

Gene action and Vr Wr graphical analysis through Hayman's approach

In white jute both additive (D) and dominant (H_1 and H_2) gene components were significant for plant height, bark thickness, fibre weight and fibre fineness, whereas non-additive gene action primarily regulated basal diameter, mid diameter, green weight, stick weight and fibre strength (Table 8). Conversely, in tossa jute, both additive and dominant gene actions governed basal diameter, bark thickness, green weight, stick weight, fibre weight, fibre fineness and fibre strength, while plant height and mid diameter were predominantly controlled by non-additive gene action (Table 9). In both cultivated species of jute, the majority of cases demonstrated contributions from mutually additive and non-additive gene actions, while for some traits, non-additive gene actions primarily controlled the expression. But, the significant test of validity (t^2) also showed the indication that some of the traits in white jute like plant height, basal

Table 8. Estimates of different genetic components of yield and quality traits by Hayman's approach in *Corchorus capsularis*

Genetic components	PH	BD	MD	BT	GW	FW	STWT	FINE	STREN
D (Additive component)	0.06**	0.47	0.37	0.01**	104.55	3.94*	0.59	0.10*	1.34
F (Mean of Fr)	0.03	-0.003	0.15	0.01	253.41	0.86	2.55	0.04	1.99
H_1 (Dominant component)	0.14**	2.73*	6.99*	0.06**	3733.03*	6.94*	54.96*	0.18*	28.30*
H_2 (Symmetry or asymmetry)	0.11**	2.67*	6.27*	0.04**	2886.00*	5.80*	38.53*	0.15*	24.03*
h_2 (Dominant component)	0.07**	0.83	0.05	-0.0005	278.78	8.50*	38.56*	0.14*	1.87
E (Environmental component)	0.01	0.23	0.12	0.003	93.8	0.19	2.13	0.004	0.46
t^2 (Test of validity)	5.38*	13.69*	2.02	2.49	22.24*	0.54	24.60*	3.25	10.94*
a (point of intercept)	0.01	0.26	-0.2	0	-15.61	-0.13	-2.66	0.01	-0.4
b (slope)	0.35	0.01	0.2	0.33	0.02	0.73	0.18	0.44	0.09
$H_2/4H_1$ (Proportion of alleles with positive and negative effects in parents)	0.2	0.24	0.22	0.17	0.19	0.21	0.18	0.21	0.21
$(4DH_1)0.5 + F / (4DH_1)0.5 - F$ (Proportion of dominant and recessive alleles in parents) [KD/KR]	1.35	1	1.1	1.29	1.51	1.18	1.58	1.37	1.39

*, ** Significant at 5 % and 1 % levels of probability, respectively. PH: Plant height; BD: Basal diameter; MD: Mid diameter; BT: Bark thickness; GW: Green weight; FW: Dry fibre weight; STWT: Stick weight; FINE: Fibre fineness; STREN: Tensile strength.

Table 9. Estimates of different genetic components of yield and quality traits by Hayman's approach in *Corchorus olitorius*

Genetic components	PH	BD	MD	BT	GW	FW	STWT	FINE	STREN
D (Additive component)	0.02	0.97*	0.19	0.03*	1182.58*	10.98*	36.26*	0.25*	9.56*
F (Mean of Fr)	0.04	2.08	0.11	0.03	1417.53	16.46	73.25*	0.41*	11.68*
H_1 (Dominant component)	0.15*	4.46*	2.66*	0.15*	4122.99*	25.76*	140.18*	0.39*	14.97*
H_2 (Symmetry or asymmetry)	0.11*	3.13*	1.93*	0.14*	3270.36*	16.65	95.04*	0.20*	10.44*
h_2 (Dominant component)	-0.004	2.15*	1.18*	0.14*	1394.52*	2.06	6.41	0.05	1.22
E (Environmental component)	0.01	0.14	0.14*	0.002	315.74*	0.94	5.03	0.005	0.69
t^2 (Test of validity)	0.07	7.53*	12.46*	0.08	0.06	0.08	0.99	0.78	2.11
a (point of intercept of regression line)	-0.003	1.3	-0.24	0.03	-121.13	1.17	-2.46	-0.03	-0.22
b (slope of regression line)	0.08	-1.44	0.42	-0.45	0.35	0.06	0.1	0.84	0.6
$H_2/4H_1$ (Proportion of alleles with positive and negative effects in parents)	0.19	0.18	0.18	0.23	0.2	0.16	0.17	0.13	0.17
$(4DH_1)0.5 + F / (4DH_1)0.5 - F$ (Proportion of dominant and recessive alleles in parents) [KD/KR]	2.2	2.99	1.16	1.56	1.95	2.92	3.11	4.81	2.91

*, ** Significant at 5 % and 1 % levels of probability, respectively. PH: Plant height; BD: Basal diameter; MD: Mid diameter; BT: Bark thickness; GW: Green weight; FW: Dry fibre weight; STWT: Stick weight; FINE: Fibre fineness; STREN: Tensile strength.

diameter, fibre strength, green weight and stick weight and in tossa jute basal diameter and mid diameter did not maintain the additive dominance model properly. Other genetic mechanisms, such as epistasis, might also contribute to the manifestation of these features. The proportion of alleles with positive and negative effects ($H_2/4H_1$) in parents of approximated 0.25, suggesting a balanced division of positive and negative alleles amongst the parental individuals of white jute for traits such as basal diameter (0.24) and mid diameter (0.22) whereas bark thickness (0.23) in tossa jute. The remaining traits showed a much lower value of 0.25 of $H_2/4H_1$ which indicated unequal allocation of positive and negative alleles between the parents. The proportions of dominant and recessive alleles (K_D/K_R) were more than unity showed the excess of dominant alleles present in parents of white jute in characters like plant height (1.35), mid diameter (1.10), bark thickness (1.29), fibre fineness (1.37), fibre strength (1.39), green weight (1.51), fibre weight (1.18) and stick weight (1.58). In tossa jute, excess of dominant alleles present in parents in characters like plant height (2.20), basal diameter (2.99), mid diameter (1.16), bark thickness (1.56), green weight per plant (1.95), fibre weight per plant (2.92), stick weight (3.11), fibre fineness (4.81) and fibre strength (2.91). The proportions of dominant and recessive alleles (K_D/K_R) were almost equal to unity in basal diameter (1.00) of white jute parents showed the equal distribution of dominant and recessive alleles present in parents. Negative slopes observed in the regression line of the Vr Wr graph for basal diameter and bark thickness in *C. olitorius* (Fig. 3) may suggest the presence of non-allelic interactions in these traits. Conversely, all evaluated traits in *C. capsularis* exhibited positive slopes (Fig. 4). The widely scattered array points of parents on the graph indicated considerable genetic dissimilarity amongst the parental lines of the species for all the nine characters under study. The regression line intercepted Wr axis above the origin in some characters of white jute viz., plant height, basal diameter and fibre fineness whereas in tossa jute basal diameter, bark thickness and fibre weight which indicated presence of partial dominance ($h = d$) indicating additive component more prevalent in controlling those characters. The regression line intercepted Wr axis through the origin in some traits in white jute like bark thickness, mid internode length, green weight and fibre weight and in tossa jute stick weight and fibre strength which indicated the presence of complete dominance ($h = d$) that means additive and dominance both the components were equally responsible for controlling those characters. The regression line intercepted Wr axis below the origin in some characters like mid diameter, fibre percentage, stick weight and fibre strength in white jute and plant height, mid diameter, green weight and fibre fineness in tossa jute which indicated the incidence of over dominance ($h = d$) that means dominant component was more prevalent in controlling those characters.

Standard heterosis for yield and quality traits

Significant desirable standard heterosis coupled with significant desirable specific combining ability (SCA) was observed in 10 hybrids for fibre weight (8 in *C. capsularis*, 2 in *C. olitorius*), 6 hybrids for fibre strength (all in *C. capsularis*) and 11 hybrids for fibre fineness (5 in *C. capsularis*, 6 in *C. olitorius*). Among 28 crosses, 13 white jute hybrids and 6 tossa jute hybrids exhibited significant positive heterosis for fibre weight over the standard check (BCCC1 and BCCO 6 in white and tossa jute respectively) (Tables 10 and 11). In white jute, significant positive heterosis for fibre weight was recorded in 13 crosses, ranging from 15.68 % (BCCC 127 × CIN 111) to 43.02 % (BCCC 127 × BCCC 107). In tossa jute, 6 hybrids displayed significant

positive heterosis for fibre weight, ranging from 13.73 % (BCCO 115 × BCCO 120) to 58.85 % (BCCO 120 × BCCO 6). For stick weight, 17 crosses in *C. olitorius* and 9 crosses in *C. capsularis* demonstrated a significant positive advantage over the standard checks. Since lower fibre fineness values indicate finer fibres, negative heterosis is a favourable trait. Nine white jute crosses exhibited desirable negative heterosis for this trait, ranging from -11.30 % (BCCC 116 × CIN 106) to -33.33 % (CIN 115 × CIN 111). Similarly, 7 tossa jute hybrids displayed desirable negative heterosis, ranging from -8.09 % (OIN 128 × BCCO 6) to -15.73 % (OIN 133 × OIN 95). Finally, for fibre strength, 6 white jute crosses displayed significant positive heterosis, peaking at 15.35% in the BCCC 107 × CIN 115 hybrid. There was no evidence of statistically significant positive heterosis in any of the 28 tossa jute crosses that were tested. However, the commercial implementation of heterosis breeding remains unattained in jute to date. Consequently, hybrids lacking significant SCA (indicating an absence of dominance), but exhibiting significant general combining ability (GCA) effects in either or both parents, could be employed in recombination breeding to obtain transgressive segregants viz., BCCC 127 × CIN 111, BCCC 107 × CIN 106 and JRC 321 × CIN 111 in *C. capsularis* and BCCO 115 × OIN 133, OIN 133 × OIN 128, OIN 133 × BCCO 6 and OIN 128 × OIN 122 in *C. olitorius*. Those above-mentioned hybrids showed yield increments without sacrificing quality.

The pre-requisite of crop improvement is plant diversity, which is defined by both allelic richness (11), which includes the number of different genotypes in a population and allelic evenness, which represents the relative abundance of each genotype (12). The significant mean sum of squares observed for yield and quality traits across both *C. capsularis* and *C. olitorius* genotypes indicated robust genetic variability. Extensive work has been done to identify and catalogue important agronomic features in various germplasm collections, which will provide priceless resources for upcoming breeding initiatives (13, 14). The genetic diversity within a crop species facilitates the development of superior genotypes through the implementation of systematic genetic improvement strategies (15).

Combining ability analysis indicated that both additive and non-additive effects were present in the inheritance of yield and quality attributes of jute, though their importance differed. General combining ability is a measure of additive genetic variation. Plant breeding material with significant general combining ability effects can be exploited as valuable breeding material. High levels of general combining ability are related to low levels of environmental effects, thus making them highly stable (16, 17). The inclusion of these parents in hybridisation programmes has the potential to be advantageous in harnessing heterosis and acquiring desired transgressive segregants, as proposed (17).

The significant specific combining ability effects seen in numerous crosses suggest that distinct and advantageous genetic interactions between particular parental lines produce innovative and advantageous genetic recombination, which in turn lead to enhanced hybrid performance (18). The success of heterosis breeding operations depends on determining which specific combiners are most effective. Novel and superior genetic combinations can be developed by intercrossing these superior parental lines, which can help break down unfavourable linkage blocks (19, 20).

The standard method adopted confirmed the combining ability results, where complex interactions of mutually additive and non-additive gene actions were seen (9). This is in accordance with

Table 10. Standard heterosis (%) over BCCC1 of two major yield and quality traits in hybrids of White jute

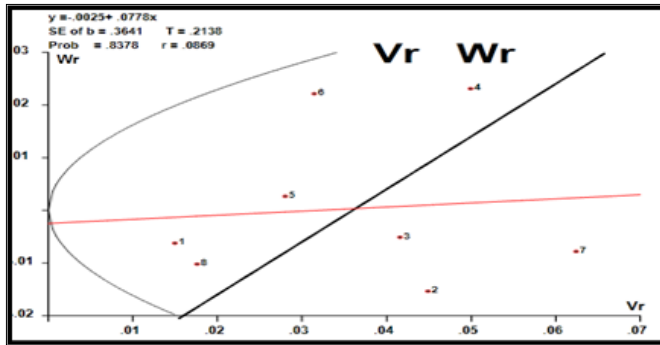
Hybrids	Fibre weight	Stick weight	Fibre fineness	Fibre strength
P1 × P2	20.18 **	2.30 ns	15.33 **	5.30 ns
P1 × P3	36.63 **	5.12 ns	2.68 ns	5.94 ns
P1 × P4	21.20 **	0.25 ns	11.30 *	-1.40 ns
P1 × P5	30.51 **	22.02 **	-1.34 ns	-3.47 ns
P1 × P6	0.56 ns	-12.04 ns	-2.87 ns	6.70 ns
P1 × P7	-8.19 ns	-18.47 *	2.68 ns	-1.26 ns
P1 × P8	26.26 **	4.10 ns	-0.96 ns	3.88 ns
P2 × P3	18.63 **	7.43 ns	15.52 **	15.35 **
P2 × P4	43.02 **	30.72 **	15.33 **	-16.21 **
P2 × P5	19.16 **	7.36 ns	11.49 *	-2.56 ns
P2 × P6	-12.83 ns	-17.78 *	-9.39 ns	-5.92 ns
P2 × P7	37.54 **	24.66 **	32.95 **	14.31 **
P2 × P8	15.68 *	1.46 ns	-5.36 ns	-2.56 ns
P3 × P4	8.86 ns	16.00 *	-15.33 **	-21.25 **
P3 × P5	9.56 ns	4.79 ns	-2.87 ns	-8.87 *
P3 × P6	-13.22 *	-15.26 *	-11.30 *	-3.45 ns
P3 × P7	17.57 **	15.95 *	-7.66 ns	14.31 **
P3 × P8	9.84 ns	8.63 ns	8.24 ns	10.84 *
P4 × P5	28.75 **	21.62 **	11.88 *	-2.17 ns
P4 × P6	4.57 ns	-0.16 ns	-16.09 **	14.47 **
P4 × P7	18.95 **	45.32 **	-23.18 **	-23.95 **
P4 × P8	3.69 ns	14.35 ns	-16.09 **	-14.41 **
P5 × P6	-4.78 ns	1.17 ns	-4.21 ns	12.91 **
P5 × P7	-14.73 *	13.56 ns	-23.18 **	-11.72 *
P5 × P8	5.66 ns	26.36 **	-8.24 ns	-5.91 ns
P6 × P7	-24.71 **	-0.25 ns	-18.39 **	-17.90 **
P6 × P8	-13.74 *	-2.85 ns	-13.98 *	-21.76 **
P7 × P8	-11.49 ns	16.81 *	-33.33 **	-38.00 **

*, ** Significant at 5 % and 1 % levels of probability, respectively. P1- BCCC 102; P2- BCCC 127; P3- BCCC 116; P4- BCCC 107; P5- JRC 321; P6- CIN 106; P7- CIN 115; P8- CIN 111.

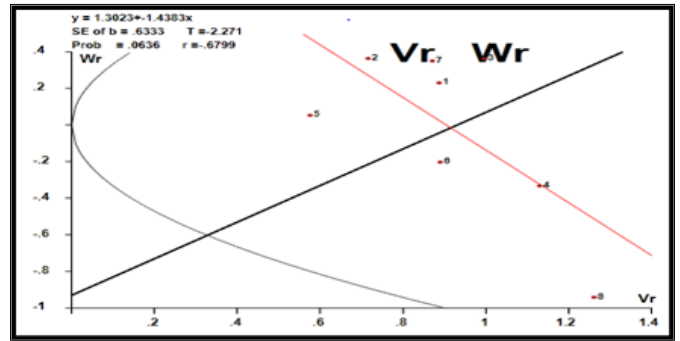
Table 11. Standard heterosis (%) over BCCO 6 of two major yield and quality traits in hybrids of Tossa jute

Hybrids	Fibre weight	Stick weight	Fibre fineness	Fibre strength
P1 × P2	28.99 **	40.99 **	0.67 ns	7.46 ns
P1 × P3	18.45 *	32.26 **	-2.58 ns	-9.59 *
P1 × P4	12.21 ns	45.88 **	-1.24 ns	2.35 ns
P1 × P5	9.68 ns	29.98 **	-4.38 ns	-1.42 ns
P1 × P6	-6.84 ns	12.74 ns	-1.01 ns	0.50 ns
P1 × P7	12.92 ns	-7.87 ns	4.83 ns	-14.59 **
P1 × P8	-0.67 ns	6.73 ns	8.20 *	-3.22 ns
P2 × P3	13.73 *	25.28 *	-3.71 ns	-13.53 **
P2 × P4	-2.36 ns	12.54 ns	-10.79 **	0.71 ns
P2 × P5	-20.31 *	13.55 ns	-5.28 ns	5.21 ns
P2 × P6	-4.15 ns	19.81 *	-3.03 ns	-2.56 ns
P2 × P7	-5.65 ns	-3.83 ns	-4.72 ns	1.78 ns
P2 × P8	7.30 ns	31.87 **	-3.60 ns	-14.22 **
P3 × P4	9.35 ns	31.88 **	-8.99 **	-8.85 *
P3 × P5	4.60 ns	24.13 *	-3.60 ns	-11.18 *
P3 × P6	-17.05 *	0.77 ns	0.34 ns	-2.39 ns
P3 × P7	-4.36 ns	20.77 ns	13.60 **	-8.65 ns
P3 × P8	58.85 **	42.61 **	-1.24 ns	-2.67 ns
P4 × P5	14.40 *	42.27 **	-13.15 **	-2.67 ns
P4 × P6	-5.79 ns	7.27 ns	-15.73 **	-12.10 **
P4 × P7	7.58 ns	33.46 **	-6.29 ns	1.05 ns
P4 × P8	30.54 **	72.50 **	-1.91 ns	-7.35 ns
P5 × P6	-5.58 ns	12.23 ns	2.02 ns	-9.52 *
P5 × P7	-3.96 ns	52.76 **	-12.70 **	-4.26 ns
P5 × P8	4.77 ns	35.91 **	-8.09 *	-11.29 *
P6 × P7	2.91 ns	38.89 **	-9.66 **	-11.82 **
P6 × P8	-16.98 *	15.58 ns	-0.56 ns	0.00 ns
P7 × P8	12.90 ns	31.09 **	0.00 ns	-20.73 **

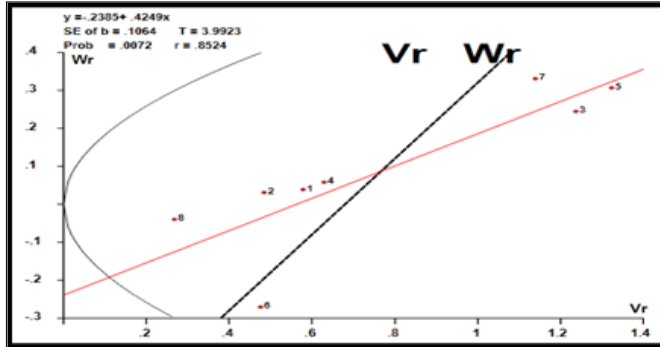
*, ** Significant at 5 % and 1 % levels of probability, respectively. P1: BCCO 105; P2: BCCO 115; P3: BCCO 120; P4: OIN 133; P5: OIN 128; P6: OIN 95; P7: OIN 122; P8: BCCO 6.



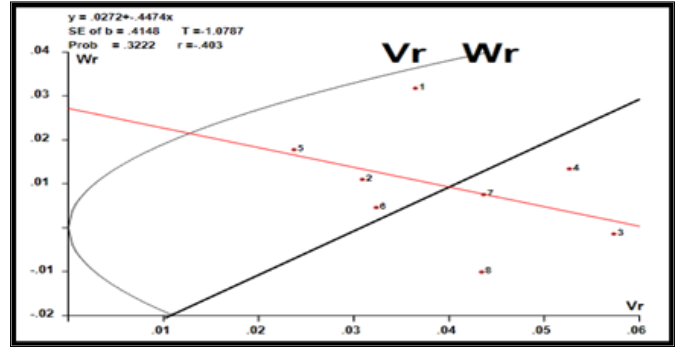
Plant height



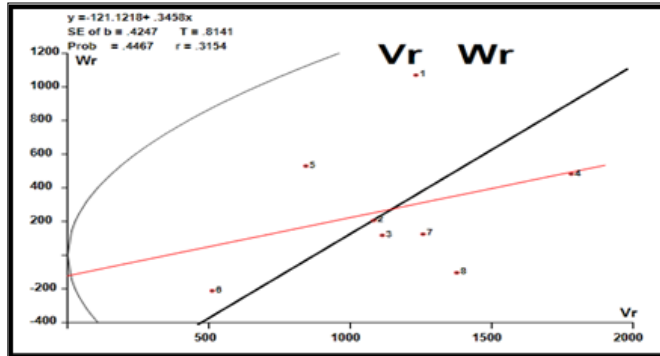
Basal diameter



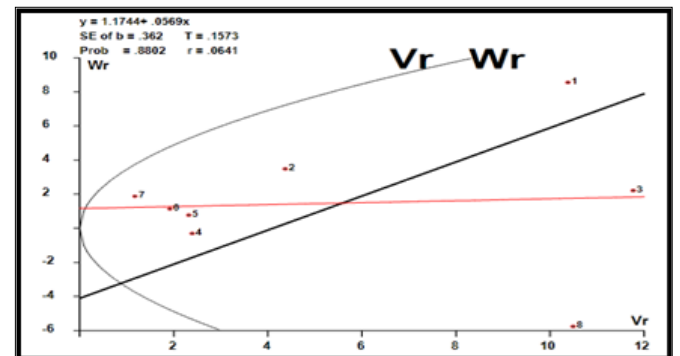
Mid diameter



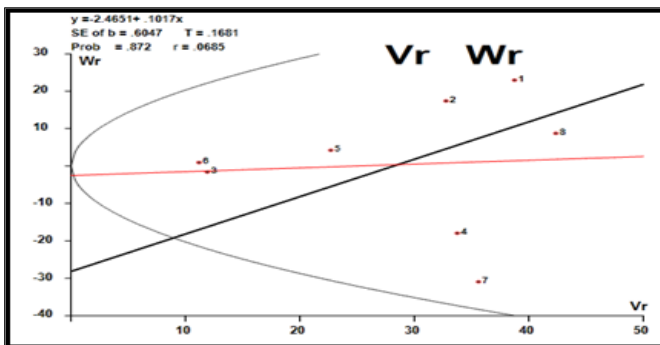
Bark thickness



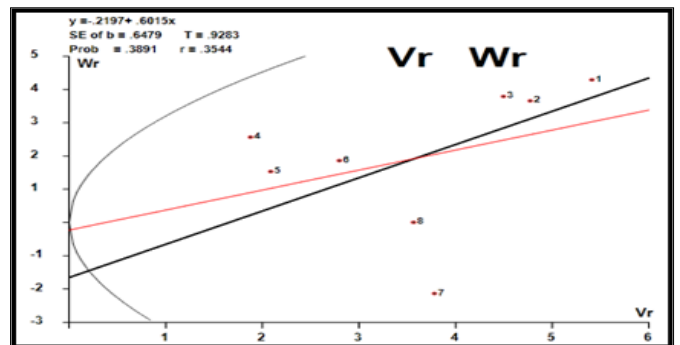
Green weight



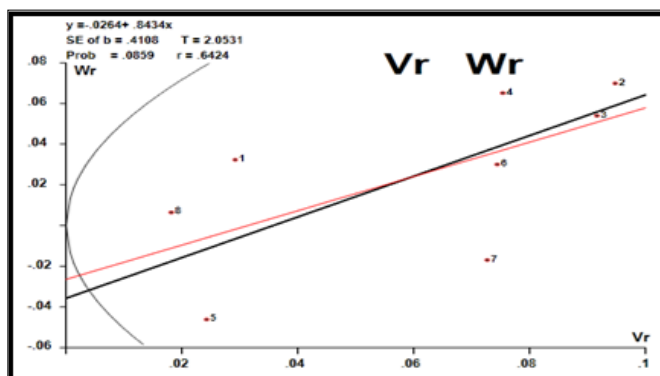
Fibre weight



Stick weight



Fibre strength



Fibre fineness

Parents on graph: 1- BCCO 105, 2- BCCO 115, 3- BCCO 120, 4- OIN 133, 5- OIN 128, 6- OIN 95, 7- OIN 122 & 8- BCCO 6

Fig. 3. Vr Wr graph of yield and quality traits in *Corchorus olitorius*.

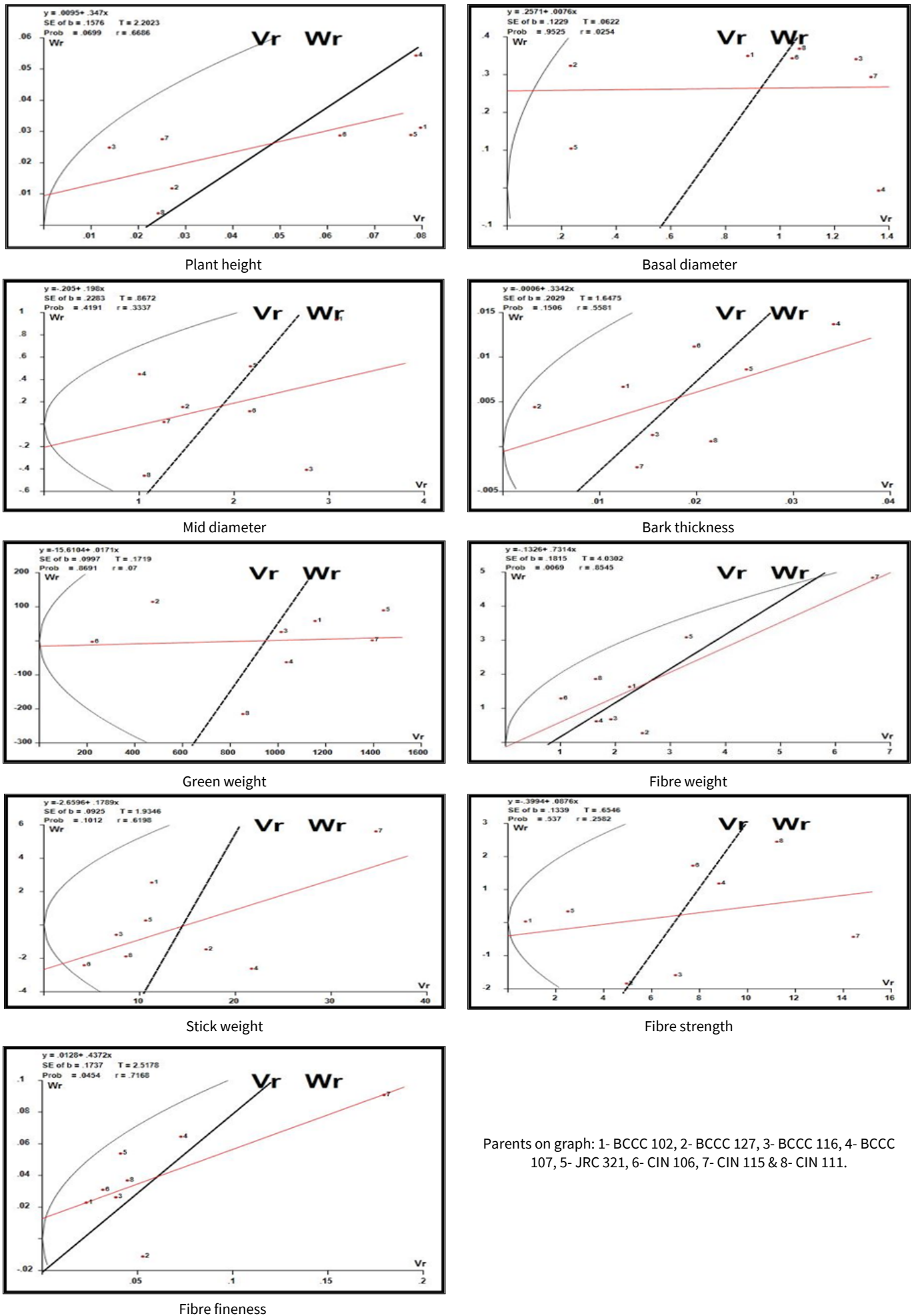


Fig. 4. Vr Wr graph of yield and quality traits in *Corchorus capsularis*.

previous studies in jute plants (21, 22). The unequal number of positive and negative alleles for certain characters, as well as the excess of dominant alleles, indicates the breeding strategy to be adopted (23). The Vr Wr method for graphical analysis indicated that over-dominance is seen in certain characters such as fibre fineness and green weight in tossa jute. This observation is consistent with the findings (24). The presence or absence of digenic epistatic interactions significantly aids the selection of potential parents or crosses for both pedigree selection and heterosis breeding programmes. Traits exhibiting substantial epistasis generally show limited response to selection in later generations (25), making breeding strategies that exploit non-additive gene action viz., heterosis breeding crucial. Single-plant selection in the F₂ generation may lack efficacy unless the trait's heritability is high (26). Subsequent generation selection methods, including bulk selection and single-seed descent, can aid in stabilising desired traits (27). However, the effectiveness of these approaches might be limited due to the progressive reduction of dominance genetic variance as homozygosity increases in later segregating generations, potentially hindering further trait improvement (28).

The fundamental basis of heterosis is primarily due to the genetic divergence between the parents (29). Phenotypic distinctions in hybrid offspring trace back to advantageous changes in genomic composition (30, 31). The level of heterosis tends to increase with greater genetic differences (32, 33). The notable standard heterosis recorded for fibre weight, strength and fineness underscored the immense potential of hybrid jute.

Conclusion

The study revealed considerable genetic variations and the predominant influence of both additive and non-additive gene actions in controlling yield and quality traits in *Corchorus capsularis* and *Corchorus olitorius*. Parents like BCCC 127 and BCCO 105 were found to have higher GCA, while specific hybrids such as BCCC 127 × BCC C 107 and BCCO 120 × BCCO 6 were found to have the maximum fibre yields and significant standard heterosis. Considering the overwhelming influence of non-additive gene actions and over-dominance in important traits, delayed selection in later segregating generations is recommended instead of early selection at the single-plant level. These findings will support plant breeders in selecting superior parents and designing effective breeding programmes for sustainable improvement of jute yield and fibre quality. Future efforts should prioritise multi-environment trials to validate the stability of these elite crosses, alongside the integration of molecular markers to facilitate marker-assisted selection for sustainable jute improvement.

Acknowledgements

The authors gratefully acknowledge the ICAR-Central Research Institute for Jute and Allied Fibres, West Bengal, India, for providing technical support in the assessment of fibre quality parameters.

Authors' contributions

The concept was developed by SH¹ and AR. Data curation was done by SH¹ and GP. Formal analysis was carried out by SH¹ and KD. Investigation and methodology were undertaken SH¹ and AR. The

project was supervised by AR and SKP. The original draft was prepared by SH¹, while writing-reviewing and editing were performed by SH², SSSD and GP. All authors have read and approved the final manuscript. [SH¹ stands for Sourav Hazari and SH² stands for Soham Hazra].

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

References

1. Marik S. A critical review of agro-based fibre applications in asphalt concrete mixtures. *Road Mater Pavement Des.* 2026;1–23. <https://doi.org/10.1080/14680629.2026.2633611>
2. CACP. Price Policy for Jute: 2021–22 Season. New Delhi: Department of Agriculture, Cooperation and Farmers Welfare, Ministry of Agriculture and Farmers Welfare, Government of India; 2020. p. 2–3.
3. FAOSTAT. Food and Agricultural Organization of the United Nations, FAO Statistical Database. 2019.
4. Wang H, Memon H, AM Hassan E, Miah MS, Ali MA. Effect of jute fiber modification on mechanical properties of jute fiber composite. *Materials.* 2019;12(8):1226. <https://doi.org/10.3390/ma12081226>
5. Jahan MS, Hossain S, Khan MA. Economic importance of jute. In: *The jute genome*. Cham: Springer International Publishing; 2022. p. 1–16. https://doi.org/10.1007/978-3-030-91163-8_1
6. Mukul MM, Akter N. Morpho-anatomical variability, principal component analysis and Euclidean clustering of tossa jute (*Corchorus olitorius* L.). *Heliyon.* 2021;7(5). <https://doi.org/10.1016/j.heliyon.2021.e07042>
7. Das A, Kumar D. Genetic divergence and character association for yield and quality attributing characters in tossa jute (*Corchorus olitorius* L.). *Electron J Plant Breed.* 2016;7(3):529–37. <https://doi.org/10.5958/0975-928X.2016.00068.5>
8. Griffing B. The concept of general and specific combining ability in relation to diallel crossing system. *Aust J Biol Sci.* 1956;9:463–93. <https://doi.org/10.1071/BI9560463>
9. Hayman BI. The theory and analysis of diallel crosses. *Genetics.* 1954;39(6):789. <https://doi.org/10.1093/genetics/39.6.789>
10. Sau SA, Ghosh BI, Sarkar SU. Correlation and path analysis studies for growth and yield contributing traits in guava as affected by micronutrients. *Ann Plant Soil Res.* 2016;18(4):370–74.
11. Laurentin H. Data analysis for molecular characterization of plant genetic resources. *Genet Resour Crop Evol.* 2009;56:277–92. <https://doi.org/10.1007/s10722-008-9397-8>
12. Ahmed SSU, Mukul MM, Fatema K, Akter N. Estimation and utilization of heterosis and heterobeltosis for yield and yield contributing traits in tossa jute hybrids (F₁) derived from diverse germplasms. *Int J Agric Sci.* 2022;3(1):97–101. <https://doi.org/10.52804/ijaas2022.3116>
13. Ene CO, Ogbonna PE, Agbo CU, Chukwudi UP. Studies of phenotypic and genotypic variation in sixteen cucumber genotypes. *Chil J Agric Res.* 2016;76(3):307–13. <https://doi.org/10.4067/S0718-58392016000300007>
14. Tiwari A, Tikoo SK, Angadi SP, Kadaru SB, Ajanahalli SR, Vasudeva Rao MJ. Germplasm Management in Commercial Plant Breeding Programs. In: Tiwari A, Tikoo SK, Angadi SP, Kadaru SB, Ajanahalli SR, Vasudeva Rao MJ, editors. *Market-Driven Plant Breeding for Practicing Breeders*. Singapore: Springer Nature; 2023. p. 33–68.

https://doi.org/10.1007/978-981-19-5434-4_2

15. Hazra S, Gorai S, Roy S, Bose S, Hazra P, Chattopadhyay A, et al. Isolation of yellow vein mosaic virus (YVMV)-resistant mutants of okra (*Abelmoschus esculentus* L.) through applied mutagenesis. *Plant Breed.* 2024;143(2):232–45. <https://doi.org/10.1111/pbr.13151>
16. Alhariri A, Behera TK, Jat GS, Devi MB, Boopalakrishnan G, Hemeda NF, et al. Analysis of Genetic Diversity and Population Structure in Bitter Melon (*Momordica charantia* L.) Using Morphological and SSR Markers. *Plants.* 2021;10:1860. <https://doi.org/10.3390/plants10091860>
17. Khatun R, Sarker RH, Sobhan MA. Combining ability for yield and yield contributing characters of white jute (*Corchorus capsularis* L.). *Bangladesh J Bot.* 2010;39(1):79–85. <https://doi.org/10.3329/bjb.v39i1.5530>
18. Roy A, Dasgupta K, Hazari S, Bhattacharya S, Das A. Heterosis and combining ability for yield and yield attributing traits in tossa jute (*Corchorus olitorius* L.). *Curr Appl Sci Technol.* 2020;39(46):41–9. <https://doi.org/10.9734/cjast/2020/v39i4631170>
19. Seye AI, Bauland C, Charcosset A, Moreau L. Revisiting hybrid breeding designs using genomic predictions: simulations highlight the superiority of incomplete factorials between segregating families over topcross designs. *Theor Appl Genet.* 2020;133:1995–2010. <https://doi.org/10.1007/s00122-020-03573-5>
20. Bhutia ND, Seth T, Shende VD, Dutta S, Chattopadhyay A. Estimation of heterosis, dominance effect and genetic control of fresh fruit yield, quality and leaf curl disease severity traits of chilli pepper (*Capsicum annuum* L.). *Sci Hort.* 2015;182:47–55. <https://doi.org/10.1016/j.scienta.2014.11.017>
21. Das A, Yadav RK, Choudhary H, Singh S, Khade YP, Chandel R. Determining genetic combining ability, heterotic potential and gene action for yield contributing traits and Yellow Vein Mosaic Virus (YVMV) resistance in Okra (*Abelmoschus esculentus* (L.) Monech.). *Plant Genet Resour.* 2020;18(5):316–29. <https://doi.org/10.1017/S1479262120000337>
22. Sengupta D, Nandy S, Mitra S, Dutta P, Sinha MK, Kole PC, et al. Genetical study on tossa jute (*Corchorus olitorius* L.) for yield and quality parameters. *Indian J Genet Plant Breed.* 2005;65(1):29–32.
23. Nayak BK, Baisakh B, Bastia D. Genetic divergence among the genotypes of tossa jute (*Corchorus olitorius* L.). *Environ Ecol.* 2009;27(1):86–8.
24. Kumar AA, Sharma HK, Choudhary SB, Maruthi RT. Combining ability and heterosis study for fibre yield and yield attributing characters in tossa jute (*Corchorus olitorius* L.). *Vegetos.* 2016;29:3. <https://doi.org/10.5958/2229-4473.2016.00083.5>
25. Rana MS, Rasu MG, Islam AKMA, Hossain MM. Diallel Analysis of Quality and Yield Contributing Traits of Pumpkin (*Cucurbita moschata* Duch. ex Poir.). *The Agri.* 2016;14(1):15–32. <https://doi.org/10.3329/agric.v14i1.29097>
26. Boeven PHG, Zhao Y, Thorwarth P, Liu F, Maurer HP, Gils M. Negative dominance and dominance-by-dominance epistatic effects reduce grain-yield heterosis in wide crosses in wheat. *Sci Adv.* 2020;6:24. <https://doi.org/10.1126/sciadv.aay4897>
27. Rai S, Hossain F, Hossain M. Studies on the combining ability and heterosis in Okra [*Abelmoschus esculentus* (L.) (Moench)] for bast fiber yield. *J Crop Weed.* 2011;7(2):64–6.
28. Chozin M, Sudjamiko S, Barchia MF. Genetic variability and traits association analyses on F2 generations for determination of selection criteria in Indonesian inland swamp rice breeding. *Aust J Crop Sci.* 2017;11(5):535–41. <https://doi.org/10.21475/ajcs.17.11.05.p317>
29. Dutta P, Hazra P, Hazra S, Maji A, Chattopadhyay A. Genetic expression of reproductive and fruit quality traits in snap melon (*Cucumis melo* var. *momordica* L.). *Euphytica.* 2023. <https://doi.org/10.1007/s10681-022-03146-1>
30. Wu X, Liu Y, Zhang Y, Gu R. Advances in research on the mechanism of heterosis in plants. *Front Plant Sci.* 2021;12:745726. <https://doi.org/10.3389/fpls.2021.745726>
31. Usatov AV, Klimenko AI, Azarin KV, Gorbachenko OF, Markin NV, Tikhobaeva VE. The relationship between heterosis and genetic distances based on SSR markers in *Helianthus annuus*. *Am J Agric Biol Sci.* 2014;9:270–76. <https://doi.org/10.3844/ajabssp.2014.270.276>
32. Palve SM, Kumar D. Combining ability for fibre strength in white jute (*Corchorus capsularis* L.). *Phytobreedon.* 1991;7(1&2):4–8.
33. Senapati S, Ali MN, Sasmal BG. Genetic variability, heritability and genetic advance in *Corchorus* sp. *Environ Ecol.* 2006;24:1–3.

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonpublishing.com/journals/index.php/PST/open_access_policy

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc. See https://horizonpublishing.com/journals/index.php/PST/indexing_abstracting

Copyright: © The Author(s). This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited (<https://creativecommons.org/licenses/by/4.0/>)

Publisher information: Plant Science Today is published by HORIZON e-Publishing Group with support from Empirion Publishers Private Limited, Thiruvananthapuram, India.