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ARCHITECTURE OF SEED YIELD IN JUTE

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ABSTRACT

Combining ability analysis from five-parent diallel sets without reciprocals involving F_1 and F_2 generations of *Corchorus olitorius* L. and *C. capsularis* L. revealed that both additive and nonadditive types of gene actions were operating in the inheritance of plant height, days to flower, fruits/plant, fruit size, seeds/fruit, 100-seed weight, seed weight/fruit and seed yield/plant. Partitioning of dominance variance indicated that a considerable part of dominance gene action was due to the asymmetry of dominant gene distribution among the parents. The results also pointed out that additive variance was the major genetic component for days to flower, pod length, 100-seed weight and seed yield/plant in *C. olitorius* and for plant height as well as seeds/capsule in *C. capsularis*. Narrow sense heritability estimates for these traits were high except in one case. Among all the parents, JRO 7835 was identified as a promising general combiner for seed yield and its components.

Key words: Combining ability, *Corchorus olitorius, Corchorus capsularis.*

The jute fibre is extracted from the stem of two cultivated species, *Corchorus olitorius* L. and *C. capsularis* L. and hence major emphasis has so far been laid on selection of fibre yield and other related vegetative aspects. Several important studies have been carried out on the nature of inheritance of fibre yield [1–4]. In view of this type of selection pressure exerted on vegetative characters exclusively, no deliberate selection pressure by the breeders has been applied to improve seed size and yield. Only a few reports on the inheritance of seed yield and its components are available [5, 6]. Under such circumstances, it is imperative to understand the nature of inheritance of seed yield and its components to formulate an effective breeding strategy for improving these characters without loss of fibre yield. The present study aims to understand the nature of inheritance of seed yield and its components in jute.

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MATERIALS AND METHODS

Two sets of five-parent diallel crosses without reciprocals among the varieties of *C. olitorius* (JRO 620, JRO 524, JRO 632, JRO 878 and JRO 7835) and among those of *C. capsularis* (JRC 7447, JRC 4444, D 154, JRC 321 and JRC 212) were made. In each set, the five parents along with F_1 and F_2 generations were grown, respectively, in 1989 and 1990 in randomized block design with three replications. The distances between lines and plants within the lines were 30 cm and 10 cm, respectively. Three rows each of 1.5 m length constituted a plot for each parent and F_1 hybrid and five rows for each F_2 population. Fertilizers were applied at the rate of $N_{40}P_{20}K_{20}$ per ha for *C. olitorius* and $N_{60}P_{20}K_{20}$ per ha for *C. capsularis*.

Observations were recorded on five random plants from each plot of parents and F_1 and ten random plants from each F_2 for eight quantitative traits (Table 1). Ten random fruits of each plant were used to record observations.

ANOVA was performed separately for F_1 and F_2 generations. Combining ability analysis was undertaken following Griffing Model I, Method II [7] and Jones [8] after recording significant variation among the varieties.

RESULTS AND DISCUSSION

Analysis of variances for combining ability showed that the mean squares due to general and specific combining ability (gca, sca) were highly significant for all the characters in both the F_1 and F_2 generations of *C. olitorius* and *C. capsularis*, except for seed yield in *C. olitorius* and seeds/capsule in *C. capsularis* for which the mean squares due to sca was nonsignificant in F_1. Among the components of b, b_1, measuring midparental deviation, increased significantly in F_2 for seed weight/pod and seed yield/plant in *C. olitorius* and for capsule diameter, seeds/capsule, 100-seed weight and seed weight/capsule in *C. capsularis* probably due to dominance or segregation and recombination of genes. The b_2 component was significant in both F_1 and F_2 for most of the characters under study, indicating that the parents had a symmetrical distribution of dominant genes responsible for a particular character in both generations. The component b_3 (residual dominance) was also significant for most of the traits in both species.

The estimated additive variance was larger than the corresponding nonadditive or dominance variance in both generations for days to flower, pod length, 100-seed weight and seed yield/plant in *C. olitorius* but only for plant height and seeds/capsule in *C. capsularis*, resulting in higher estimates of narrow sense heritability except for 100-seed weight in F_2 of *C. olitorius*. The estimated dominance variance was high in both F_1 and F_2 for 100-seed

Table 1. Estimates of gca effects for eight characters of *C. olitorius*

Parent	Generation	Plant height ($x10^{-2}$)	Days to flower	Capsule per plant	Capsule length ($x10^{-2}$)	Seeds per capsule	100-seed wt. ($x10^{-4}$)	Seed wt. per pod ($x10^{-4}$)	Seed yield per plant
JRO 620	F_1	- 0.91	- 3.80**	- 0.83**	19.66**	- 0.12	25.70**	29.40**	0.22*
	F_2	- 7.68**	- 2.22**	- 0.56**	35.28**	0.45	- 2.0	- 31.40**	- 0.26**
JRO 524	F_1	- 1.48	1.50**	- 0.55**	- 16.20**	- 2.21**	- 27.10**	- 46.20**	- 0.62**
	F_2	- 0.40	0.70**	0.19	-16.57**	- 2.32**	- 29.10**	- 50.0**	0.11
JRO 632	F_1	0.94	- 4.35**	- 0.26	28.94**	- 2.85**	27.10**	- 22.0*	- 0.24**
	F_2	3.03	- 1.53**	- 1.37**	22.43**	2.98**	20.80**	81.40**	- 0.59**
JRO 878	F_1	7.80**	2.81**	0.72**	- 18.20**	1.36**	- 34.20**	- 10.50	0.40**
	F_2	3.46**	1.25**	0.03	- 49.14**	- 4.49**	- 22.0**	- 72.80**	- 0.12
JRO 7835	F_1	- 6.34**	3.84**	0.93**	- 14.20**	3.82**	8.60	49.40**	0.23**
	F_2	1.60	1.80**	1.71**	8.0	3.38**	32.30**	72.80**	0.86**
SE (g_i)	F_1	± 1.84	± 0.46	± 0.23	± 3.39	± 0.42	± 6.28	± 10.66	± 0.10
	F_2	± 1.64	± 0.24	± 0.25	± 5.29	± 0.97	± 6.47	± 12.37	± 0.11
SE (g_i–g_j)	F_1	± 2.91	± 0.74	± 0.37	± 5.36	± 0.67	± 9.94	± 16.86	± 0.17
	F_2	± 2.59	± 0.38	± 0.39	± 8.35	± 1.53	± 10.23	± 19.56	± 0.18

*,**Significant at 0.05 and 0.01 levels, respectively.

weight, seed weight/capsule and seed yield/plant in *C. capsularis*. Unlike *C. capsularis*, none of the traits in *C. olitorius* exhibited dominance variance of consistent nature from F_1 to F_2. As regards fruits/plant of both species, the major role of dominance in F_1 reversed rendering additive component in comparison to the former increased in F_2, as a result quite appreciable increase in narrow sense heritability in F_2 was observed.

Therefore, the results suggest that the estimated additive variances are likely to show an upward bias due to the presence of significant asymmetry in gene distribution among the parents as *a* or gca according to Hayman [9] is composed of $D - F + H_1 - H_2$.

The estimates of gca of the parents belonging to *C. olitorius* (Table 1) revealed that only JRO 7835 had significantly positive gca effects for seed yield and its components in F_1 which further increased in F_2, indicating reinforcement of additive effects of genes and their breeding value. On the contrary, none of the *C. capsularis* varieties showed consistency in gca effects in either of the two generations (Table 2).

Table 2. Estimates of gca effects for eight characters of *C. capsularis*

Parent	Generation	Plant height ($\times 10^{-2}$)	Days to flower	Capsules per plant	Capsule diameter ($\times 10^{-2}$)	Seeds per capsule	100-seed wt. ($\times 10^{-4}$)	Seed wt. per capsules ($\times 10^{-4}$)	Seed yield per plant
JRC 7447	F_1	13.17**	0.57	0.30	-0.46**	-0.57**	-0.85	-0.57	0.46**
	F_2	3.20**	1.63**	0.73	0.03	0.34	-26.0**	-2.0	0.14
JRC 4444	F_1	-3.68**	1.57**	-0.99**	0.32**	0.21	-0.86	-2.0	-0.40**
	F_2	4.20**	-0.61**	-8.15**	-0.06	0.49**	29.71**	15.10**	-0.77**
D 154	F_1	-5.26**	0.74**	3.48**	0.32**	0.74**	16.28**	18.0**	0.58**
	F_2	-0.94	0.49**	0.52	-1.11**	-0.50**	11.14**	-7.70	0.21
JRC 321	F_1	-2.54**	-4.83**	-1.76**	0.21**	-0.03	-28.30**	-14.86**	-0.55**
	F_2	-0.23	-5.58**	1.98**	2.16**	0.80**	5.43	18.0**	0.27
JRC 212	F_1	-1.68**	1.93**	-1.02**	-0.40**	-0.35**	13.43**	-0.57	-0.08
	F_2	-6.23**	4.06**	4.91**	-1.02**	-1.13**	-20.28**	-33.40**	0.15
SE (g_i)	F_1	±0.64	±0.32	±0.45	±0.03	±0.15	±3.22	±2.34	±0.18
	F_2	±1.15	±0.22	+0.64	±0.41	±0.19	±5.10	±4.17	±0.15
SE (g_i–g_j)	F_1	±1.02	±0.51	±0.71	±0.06	±0.24	±5.09	±3.70	±0.29
	F_2	±1.81	±0.36	±1.01	±0.65	±0.31	±8.06	+6.59	±0.23

*,**Significant at 0.05 and 0.01 levels, respectively.

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