

GENETIC VARIATION IN OUTCROSSING RATES IN JUTE  
(*CORCHORUS OLITORIUS* L.)

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ABSTRACT

Rate of outcrossing was estimated in  $F_2$  generation of 5-parent half diallel including parents as well as in  $F_2$  of  $5 \times 5$  line  $\times$  tester crosses of jute (*Corchorus olitorius* L.). The nature of variability among different crosses of two mating designs suggested polygenic control for the rates of outcrossing. Heritabilities in broad sense for this character were 19.1% and 22.1% in diallel and line  $\times$  tester mating designs, respectively.

Key words: Outcrossing, polygenic control, heritability, jute, *Corchorus olitorius*.

*Corchorus olitorius* L., one of the cultivated species of jute, is partially cross-pollinated [1]. Detailed floral biology of this species is described in [2]. Variable amount of cross pollination in this species was reported by several workers [3-5]. Quantitative studies on mating system of this species of jute has revealed extremely variable outcrossing among different loci, crosses and samples within a single locus suggesting a possible genotypic control on outcrossing rate [6]. Genetic variation in outcrossing rates in jute (*Corchorus olitorius*) is elucidated in this study.

MATERIALS AND METHODS

The dominant gene  $A^D$  produces anthocyanin pigment on stem and the recessive gene  $a^o$  produces anthocyaninless green stem of *Corchorus olitorius*.

The  $F_2$  generations of 5 nonpigmented parent  $a^o a^o$  half diallel crosses including parents and of line  $\times$  tester crosses between five nonpigmented  $a^o a^o$  and five pigmented  $A^D A^D$  parents formed the basic experimental materials. The names of the parents, lines and testers are given in Table 1. twenty five  $F_2$  of line  $\times$  tester were sown in the field. The parents and  $F_2$  of diallel crosses were nonpigmented hence alternate rows in  $F_2$  and homozygous dominant genotype  $A^D A^D$  were sown in the field. Randomized block design with three replications was adopted for both the mating designs. Standard space for jute was allowed between and within rows. The proportion of pigmented and nonpigmented plants in the field in diallel and in line  $\times$  tester were maintained at 1:1 and 3:1 ratios, respectively, assuming the frequency of the gene for anthocyanin pigment of equal order. Seed from randomly selected 10 recessive plants of each of the crosses and the parents over three replications were collected. About 250 seedlings were raised out of the seeds collected

from each randomly selected plant in Petri dishes in dark to facilitate identification of anthocyanin development at the epicotyl of heterozygotes according to the procedure suggested by Basak [7]. The number of pigmented seedlings among the nonpigmented ones was the basis of calculating outcrossing rate. The extent of outcrossing was estimated by the method of Harding and Tucker [8] and the frequency of recessive gene was assumed to be, 0.5. The grand mean and variance of outcrossing rates clearly indicated that they were normally distributed and hence used as such in analysis of variance.

Table 1. Number of heterozygotes (a) observed in total progeny (N) and estimates of outcrossing ( $\hat{\alpha}$ ) in the five parents and in their diallel crosses

Parent/cross	a	N	$\hat{\alpha}$
<b>Parents:</b>			
JRO 632	260	6335	0.082
C.G.	301	8146	0.074
Bangkok	436	7223	0.121
Tanganyika	238	6302	0.075
Russian Green	214	7409	0.058
Total	1449	35415	0.082
<b>Crosses:</b>			
JRO 632 × C.G.	292	6677	0.087
JRO 632 × Bangkok	211	7368	0.057
JRO 632 × Tanganyika	261	7194	0.073
JRO 632 × Russian Green	326	7069	0.092
C. G. × Bangkok	353	7754	0.091
C. G. × Tanganyika	282	6942	0.081
C.G. × Russian Green	190	7581	0.050
Bangkok × Tanganyika	220	6954	0.063
Bangkok × Russian Green	193	8033	0.048
Tanganyika × Russian Green	341	7403	0.092
Total	2669	72975	0.073
Grand Total	4118	108390	0.076

Heritability in broad sense for the two mating designs was estimated following Becker [9]. The procedure was essentially similar to that suggested by Jain [10] but no attempt was made to obtain a joint estimate of the two heritabilities as suggested by him.

## RESULTS

The number of offsprings of the parents and crosses of 5 × 5 diallel set, number of heterozygotes observed among them, and estimates of outcrossing are presented in Table 1. Among the outcrossing rates of parents, those of Russian Green and Bangkok were the lowest and the highest, respectively. Binomial  $\chi^2$  test showed significant heterogeneity of mean outcrossing rates of the parents ( $\chi^2_{4df} = 212.4$ ,  $P < 0.05$ ). The mean rates of outcrossing in different crosses varied considerably and the test showed significant heterogeneity among them ( $\chi^2_{9df} = 321.8$ ;  $P < 0.05$ ).

The analysis of variance of the estimated rates of outcrossing in the parents and crosses is presented in Table 2. The significance of the parents and crosses indicates existence of variation in outcrossing rates among the parents and crosses. Error component in this case represents the residual variability among the parents and  $F_2$  segregants. When mean sum of squares for parents and crosses were tested against these errors, they turned out to be significant, indicating genotypic difference in the extent of outcrossing. Parent vs. hybrid component was, however, nonsignificant. The interaction between lines and replications representing genotype-environmental interaction was equal to error, suggesting absence of genotype-environment interaction in the limited sense. Binomial  $\chi^2$  tests revealed heterogeneity among the parental array mean rates of outcrossing ( $\chi^2_{4df} = 39.1$ ;  $P < 0.05$ ), and the parents within each of the parental arrays were\*found heterogeneous but in different order, as follows: JRO 632 ( $\chi^2_{4df} = 129.4$ ;  $P < 0.05$ ); C.G ( $\chi^2_{4df} = 114.3$ ;  $P < 0.05$ ); Bangkok ( $\chi^2_{4df} = 449.1$ ;  $P < 0.05$ ); Tanganyika ( $\chi^2_{4df} = 45.9$ ;  $P < 0.05$ ) and Russian Green ( $\chi^2_{4df} = 236.0$ ;  $P < 0.05$ ).

Table 2. Analysis of variance for outcrossing rates in 5-parent diallel crosses

Source	d.f.	MSS	F
Replications	2	0.0004	
Lines	14	0.0098	2.51*
Parents	4	0.0139	3.57**
Hybrids	9	0.0082	2.10*
Parents vs. hybrids	1	0.0073	
Replication $\times$ lines	28	0.0039	
Residual	405	0.0039	

\* $P < 0.05$ ; \*\* $P < 0.01$ .

Number of offsprings of the crosses of line  $\times$  tester, number of heterozygotes observed among them and estimates of outcrossing are presented in Table 3. Crosses exhibited considerable variation among them for the rate of outcrossing. Analysis of variance of the estimated rates of outcrossing in crosses are presented in Table 4. Mean outcrossing rates of the parents used as lines were significant against general error and those of testers were not significant. Line  $\times$  tester component was also found significant. When lines, testers and line  $\times$  tester were tested against their respective first order interactions only line  $\times$  tester component was significant and line missed narrowly the significant value. Again, when these interactions were tested against the general error, only line  $\times$  replication interaction turned out to be significant. In general this ANOVA indicated the presence of considerable interaction of lines, tester and line  $\times$  tester with replication.

Binomial  $\chi^2$  test further confirmed the existence of heterogeneity of mean outcrossing rates of parents used as lines ( $\chi^2_{4df} = 256.2$ ,  $P < 0.05$ ). Outcrossing rates of the crosses within line arrays were also found to be heterogeneous but in different order, were as follows: JRO 632 ( $\chi^2_{4df} = 52.0$ ,  $P < 0.05$ ); C.G. ( $\chi^2_{4df} = 146.2$ ;  $P < 0.05$ ), Bangkok ( $\chi^2_{4df} = 85.9$ ,  $P < 0.05$ ), Tanganyika ( $\chi^2_{4df} = 100.5$ ;  $P < 0.05$ ) and Russian Green ( $\chi^2_{4df} = 34.6$ ;  $P < 0.05$ ). Though the mean outcrossing rates of

different parents used as testers were of equal order, the crosses within the testers except those of JRO 620 were heterogeneous as follows: TM ( $\chi^2_{4df} = 208.2$ ;  $P < 0.05$ ), R-26 ( $\chi^2_{4df} = 62.4$ ;  $P < 0.05$ ), Russian Red ( $\chi^2_{4df} = 318.5$ ;  $P < 0.05$ ), and Peking ( $\chi^2_{4df} = 61.7$ ;  $P < 0.05$ ).

The estimates of heritability in broad sense from diallel and line  $\times$  tester crosses were 19.1% and 22.1%, respectively. General inspection of the genetic components revealed that dominance variance in both the designs was the major component.

Table 3. Number of heterozygotes (a) observed, total progeny (N), and estimates of outcrossing ( $\hat{\alpha}$ ) in the crosses, lines and testers

Lines	Parameter	JRO 620	Values in crosses with different testers				
			TM	R 26	Russian Red	Peking	total
JRO 632	$\bar{a}$	212	283	286	293	320	1394
	N	6552	7316	2615	6551	6834	33468
	$\hat{\alpha}$	0.065	0.077	0.092	0.089	0.094	0.083
C.G.	$\bar{a}$	245	378	272	392	246	1533
	N	7507	7552	7244	6539	7025	35867
	$\hat{\alpha}$	0.065	0.100	0.075	0.109	0.070	0.085
Bangkok	$\bar{a}$	238	220	221	134	236	1049
	N	6850	7682	6362	6847	6728	34469
	$\hat{\alpha}$	0.069	0.057	0.069	0.039	0.072	0.061
Tanganyika	$\bar{a}$	206	302	263	159	190	1120
	N	6547	6743	6624	6259	6368	32541
	$\hat{\alpha}$	0.063	0.090	0.079	0.051	0.060	0.069
Russian Green	$\bar{a}$	247	184	211	257	250	1149
	N	6991	6934	7313	7254	7056	35548
	$\hat{\alpha}$	0.071	0.053	0.058	0.071	0.071	0.065
Total	$\bar{a}$	1148	1367	1253	1253	1242	6245
	N	34447	36227	33758	33450	34011	171893
	$\hat{\alpha}$	0.067	0.075	0.074	0.074	0.073	0.073

## DISCUSSION

The present results exhibit significant difference in the degree of outcrossing among the parents, crosses, and among the crosses within parental arrays of diallel set. The lines of the line  $\times$  testers set, which happened to be the same as the parents of the diallel set, also exhibited significant difference among themselves for the degree of outcrossing. Though mean outcrossing rates of the testers were not significantly different among themselves, the crosses within most of the testers exhibited significant difference in outcrossing. In an earlier study in the same species with a number of different marker loci, Basak and Gupta [5] observed variation not only in the outcrossing rates for several marker loci but also for a common locus,  $A^D/a^o$  in different genotypic backgrounds. They observed continuous distribution of outcrossing rates for different loci and concluded polygenic control of outcrossing,

as suggested in [11]. Harding and Tucker [8] found variation in outcrossing among different loci in lima beans. The four barely genotypes with different awn characters differed among themselves with respect to outcrossing as female parents, and the homozygotes and heterozygotes had consistently different outcrossing rates over the years [12].

Table 4. Analysis of variance of outcrossing rates in 5 × 5 line × tester crosses

Source	d.f.	MSS	F
Replications	2	0.0013	
Lines	4	0.0225	7.34**
Testers	4	0.0010	<1
Lines × testers	16	0.0090	2.64**
Replications × lines	8	0.0109	3.19
Replications × testers	8	0.0026	
Replications × lines × testers	32	0.0043	
Residual	675	0.0034	

\*\* P < 0.01.

Response to selection of a particular phenotype is also an alternative evidence of existence of quantitative genetic control. Response to selection for outcrossing rates in *Amaranthus cruentus* L. [13], *Nicotiana rustica* [14], and field beans [15] proves polygenic control of outcrossing rates. Jain [16] has cited other examples supporting this contention.

The observed genetic variability in *C. olitorius* for outcrossing is assumed to have generated from the existing genotypic variability in floral morphology and related characteristics which predispose the flowers of different genotypes to bee pollination in differential manner. Basak and Chaudhuri [17] distinguished the floral characters of two cultivated jute species (*C. olitorius* and *C. capsularis*) due to which the former species outcrossed more frequently than the latter. Jain [16] demonstrated that differences in fertility and outcrossing in *Limnanthes alba* and *L. gracilis* were associated with floral characteristics of these species in different directions and reviewed the known examples of genetic variation in the factors regulating breeding systems in different plant species.

Though the heritability estimates were low in both the mating designs, they nevertheless confirmed that outcrossing or autofertility in this jute species is under polygenic control. In general, outcrossing rates are under the control of numerous nongenetic factors and, consequently, weakly heritable. Also, Jain [16] found variation in floral biology and degree of selfing among five different races of the inbreeding species *Limnanthes floccosa* under polygenic control with low heritability.

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