

INHERITANCE OF SOME CHARACTERS IN JUTE

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(Accepted: 14-i-71)

IN *Corchorus capsularis* inheritance of anthocyanin, branching habit, leaf taste, stipule character, petal and anther colour and pod shape and in *C. olitorius* anthocyanin and seed coat colour have so far been reported (Finlow and Burkill, 1912; Ghose, 1942; Ghose, Rao and Kundu, 1948; Patel, Ghose and Dasgupta, 1944; Patel, Ghose and Sanyal, 1945; Dasgupta and Sarma, 1954). This brief review indicates how scanty is the knowledge of individual traits of jute and their inheritance.

MATERIALS AND METHODS

In the present study, some standard varieties and synthesized stocks possessing contrasting phenotypes have been used in both the species of jute—*C. olitorius* and *C. capsularis*. Names of varieties and stocks used as parents are shown in the respective tables.

RESULTS AND DISCUSSION

C. olitorius

Inheritance of leaf surface.— F_1 's between Palmate (PM) with glossy leaf surface and JRO 632 and CG with nonglossy leaf surface produced glossy leaf. F_2 population from these two crosses showed glossy and nonglossy phenotypes. The observed frequencies of these classes are shown in Table 1. All the observed ratios fitted well to a ratio of 9:7. Thus glossy and nonglossy leaf surface are under digenic complementary gene action. The gene symbols **GL** for glossy and **gl** for nonglossy are proposed.

Inheritance of rolled leaf.— F_1 's between PM with rolled leaf and JRO 632 and CG with flat leaf produced flat leaf. The observed ratio in F_2 's fitted well to 9 : 7 ratio. In the F_2 of the first cross the ratio of flat leaf to rolled leaf was 192 : 120 ($P=0.01-0.05$) and in the second cross 176 : 121 ($P=0.8-0.7$). This leaf morphology is under the control of digenic complementary gene action. The gene symbols **MR** for flat and **mr** for rolled leaf phenotypes are proposed.

Inheritance of normal and crumpled leaf.—Cross between normal leaf parent and crumpled leaf parent produced normal F_1 's. F_2 population segregated

TABLE 1

Showing segregation of glossy, nonglossy leaf (*C. olitorius*)

Parents		F ₁	F ₂		χ ²	P.
Glossy	Nonglossy		Glossy	Nonglossy		
PM	JRO 632	Glossy	176	124	0.7126	.50-.30
PM	C.G.	„	264	171	0.4840	.10-.05
PM	C.G.	„	165	106	2.3670	.20-.10
PM	C.G.	„	191	128	1.7031	.20-.10
Pooled			796	529	8.0851	05-.02

into 3 (358) normal and 1 (97) crumpled indicating that this character is monogenically controlled, normal being dominant over crumpled. The gene symbols proposed for normal and crumpled are **Cr** and **cr**.

Inheritance of leaf size.—F₁'s of the crosses between narrow leaf parent, WO, and intermediate leaf parents, JRO 632 and TM, produced narrow leaf. F₂'s segregated into two phenotypic classes such as narrow and intermediate leaf. The results are presented in Table 2 and fit well to the expected 3 : 1 ratio indicating single gene difference between narrow and intermediate leaf types.

F₁'s between broad leaf parent, GE and intermediate leaf parents, JRO 620 and TM, produced intermediate leaf. F₂'s segregated into 3 intermediate and 1 broad leaf (Table 2). The observed ratio showed a good fit to a 3 : 1 ratio, indicating a simple monogenic difference between intermediate and broad leaf.

A third type of cross between narrow leaf parent, WO and broad leaf parent GE, produced F₁'s with narrow leaf. The observed frequency of segregating classes in F₂ are in Table 2. In F₂, three types of leaf, narrow, intermediate and broad were observed in a modified trihybrid ratio which fitted well a ratio of 36 : 15 : 13.

Three interacting genes each with two alleles (**Bl/bl**, **I/i** and **N/n**) are postulated. A heterozygote for all these genes (**Bl bl Ii Nn**) was narrow leaved and upon selfing produced 27 **Bl-I-N-** and 9 **bl bl I-N-** (a total of 36) narrow leaf, 9 **Bl-I-nn**, 3 **Bl Bl ii nn**, 3 **bl bl I-nn** (a total of 15) intermediate leaf and 9 **Bl-ii N-**, 3 **bl bl ii N-** and 1 **bl bl ii nn** (a total of 13) broad leaf. It can be seen from the genotypic constitution that narrow leaf character is expressed in presence of dominant **I** and **N** irrespective of any allelic form of **Bl**. Dominant **Bl** in combination with recessive **n** irrespective of any allele of **I**, produces intermediate leaf. Broad leaf phenotype is produced when both the **Bl** and **I** loci are recessive or by the interaction of dominant **Bl** with dominant **N** in presence of recessive **i**,

TABLE 2

Showing segregation of narrow, intermediate and broad leaf (*C. olitorius*)

Parents			F ₁	F ₂			Expected ratio	χ ²	P.
Narrow	Interme- diate	Broad		Nar- row	Inter- medi- ate	Broad			
WO	JRO 632		Narrow	976	318		3:1	0.1247	.80-.70
WO	TM		,,	305	114		,,	1.0891	.30-.20
Pooled				1281	432		3:1	0.0339	.90-.80
	JRO 620	GE	Interme- diate		672	208	3:1	0.8727	.50-.30
	TM	GE	,,		729	283	,,	4.7430	.05-.02
Pooled					1401	491	3:1	0.8910	.50-.30
WO		GE	Narrow	602	263	212	36:15:13	1.1302	.70-.50

Inheritance of seed coat surface.—PM, a nonshiny seed coat parent was crossed with shiny seed coat parents, DRE and LRE respectively. F₁'s produced nonshiny seed coat. The observed frequencies of the phenotypic classes in F₂ were 234 : 104 in the first cross and 337 : 85 in the second. The observed ratio showed a good fit to a 3 : 1 ratio for in the first cross while F₂ of the cross LRE × PM showed a less satisfactory fit (P = .05-02). But the pooled χ₂ for all the families is non-significant and hence the observed ratio over all the crosses fitted well the expected one. This shows that shiny-nonshiny seed coat is under simple monogenic inheritance. The gene symbols proposed are **Sh** for nonshiny and **sh** for shiny.

F₁'s between a common parent GE with fuzzy seed coat and other parents CG, WO and JRO 632 with nonfuzzy seed coat respectively, showed nonfuzzy seed coat. F₂ segregations for different crosses are shown in Table 3. The observed ratios showed good fit to 15 : 1 ratio. This indicates that this character is governed by duplicate genes. The following gene symbols, **Fz₁**, **Fz₂** for nonfuzziness and **fz₁**, **fz₂** for fuzziness are proposed.

A phenotypic ratio of 45 nonfuzzy, nonshiny: 15 nonfuzzy shiny: 4 fuzzy was observed when the joint segregation of nonshiny-shiny (3 : 1) and non-fuzzy-fuzzy (15 : 1) was considered. The observed frequencies of each of these classes in F₂ of crosses GE × KT1 and JRO 632 × GE are shown in Table 4. In F₁'s of both the crosses seed coat was nonshiny and nonfuzzy. The observed ratio in F₂ showed a very good fit to the expected 45 : 15 : 4 ratio. Thus 3

TABLE 3

Showing segregation of nonfuzzy and fuzzy seed coat (C. olitorius)

Parents		F ₁	F ₂		Expect- ed ratio	χ ²	P.
Non-fuzzy	Fuzzy		Non- fuzzy	Fuzzy			
WO	GE	Nonfuzzy	302	18	15 : 1	0.2133	.70-.50
CG	GE	„	209	11	„	0.5868	.50-.30
JRO 632	GE	„	249	15	„	0.1454	.80-.70
CG	GE	„	198	14	„	0.4520	.70-.50
Pooled			958	58	15 : 1	0.5081	.95-.90

TABLE 4

Showing joint segregation of nonfuzzy, fuzzy and shiny seed coat (C. olitorius)

Parents		F ₁	F ₂			Expect- ed ratio	χ ²	P.
Non- fuzzy Non- shiny	Fuzzy		Non- fuzzy Non- shiny	Non- fuzzy shiny	Fuzzy			
KT-1	GE	Nonfuzzy Nonshiny	626	220	68	45:15:4	2.1251	.50-.30
JRO 632	GE	„	696	206	68	„	2.7259	.30-.20
Polled			1322	426	128	45:15:4	1.4151	.30-.20

nonshiny-fuzzy and 1 shiny-fuzzy classes merged into 4 fuzzy phenotypes. It is not very clear whether difficulties in identification of nonshiny and shiny seed coat is due to presence of fuzziness or due to interaction of **Sh** or **sh** gene with **fz**₁ or **fz**₂ which modified 45 : 15 : 3 : 1 into 45 : 15 : 4 ratio.

Inheritance of seed coat colour.—All the F₁'s between parents with black seed coat and parents with green seed coat had black seed coat. The observed F₂ ratio showed a good fit to an expected ratio of 3 black and 1 green seed coat. The results are presented in Table 5. Crosses between green parent and chocolate seed coat parent produced green seed coat in F₁'s and in F₂'s green and chocolate segregated into 3 : 1 ratio. But when black seed coat parent was crossed to chocolate seed coat parent, F₁'s produced from them were of black

TABLE 5

Showing segregation of seed coat colour (*C. olitorius*)

Parents			F ₁	F ₂			Expected ratio	χ ²	P.
Black	Green	Chocolate		Black	Green	Chocolate			
JRO 632	DRE		Black	526	180		3:1	0.0927	.80-.70
JRO 632	TM		„	80	27		„	0.0031	.95-.90
GE	PM		„	57	16		„	0.3698	.70-.50
JRO 632	PM		„	657	213		„	0.1108	.80-.70
Pooled				1319	436		3:1	0.0229	.99
	WO	GE	Green		229	77	3:1	0.0043	.95-.90
	KT-1	GE	„		584	207	„	0.5769	.50-.30
	CG	GE	„		183	79	„	3.7099	.10-.05
Polled					996	363	3:1	2.1214	.50-.30
JRO 632		GE	Black	324	220	159	27:21:16	4.61	.10-.05

seed coat. F₂'s of this cross segregated into 27 black : 21 green : 16 chocolate coloured seed coat which is a modified trihybrid ratio. Hence three interacting genes with two alleles of each (**S/s**, **C/c** and **B/b**) may be proposed for seed coat colour. A heterozygote for each of these three genes (**Ss Cc Bb**) produced black seed coat. Upon selfing this individual produced genotypes, of which 27 **C-B-S** - black seed coat colour, 9 **C-B-ss**, 9 **C-bb S-**, 3 **C-bb ss** (a total of 21) green seed coat colour and the rest 9 **cc B-S-**, 3 **cc bb S-**, 3 **cc B-ss**, 1 **cc bb ss** (a total of 16) produced phenotype of chocolate seed coat colour. Since **cc bb ss** individuals produce chocolate seed coat, none of these three dominant genes are necessary for this phenotype. Individuals dominant for **C** but not for **B** and **S** are green in colour, that is, chocolate colour turns to green in presence of dominant **C**, whatever might be the other allelic constitution of the other two loci excepting the simultaneous presence of dominant **B** and **S**. Production of black colour necessitates the presence of dominant alleles of all the three genes. Dominant **S** produces a colourless precursor which by action of dominant **C** gene alone and **C** and **B** in combination produces green and black seed coat colour respectively. Patel, Ghose and Sanyal (1945) reported single factor with two alleles, **Gr** (dull black) and **gr** (green) for seed coat colour. The chocolate shiny seed coat colour in *C. olitorius* is of special importance here. Chocolate shiny seed coat colour of *C. capsularis* has so far been considered to be unique and one of the distinguishing characters between *C. capsularis* and

C. olitorius, since such phenotype in the latter species was not known earlier. Hence the observation of chocolate shiny seed coat colour in *C. olitorius* in the present study removes one of the specific differences between these two species.

C. capsularis

Inheritance of greenness of leaf.—Cross between deep green leaf parent, *Mogra* and pale green leaf parent, Canning, JRC 13, JRC 212 and *Fanduk*, produced F_1 's with pale green leaf indicating pale green to be simply dominant over deep green colour of leaf. F_2 segregation in all these crosses filled well with a 3 (1087) pale and 1 (349) deep green. This again confirms the simple monogenic inheritance of this character. The gene symbols proposed for pale green and deep green are g^D and g^d respectively.

Inheritance of leaf serration.—Crosses between deep serrated parent, *Tripura* and shallow serrated parents, JRC 321 and JRC 212, produced F_1 's with shallow serrated leaf; shallow serration is simply dominant over deep serration. Phenotypic frequencies in the F_2 , agreed with 3 (1206) shallow serrated: 1 (372) deep serrated leaf indicating simple monogenic inheritance for this character. The gene symbols proposed for deep serration and shallow serration are **Sr** and **sr** respectively.

Inheritance of fasciation of stem.—Crosses between fasciated stem parent, JRC 918, and non fasciated stem parent, *Maniksari*, produced F_1 with non-fasciated stem indicating nonfasciation was simply dominant over fasciation of

TABLE 6

Showing joint segregation of fasciation and branching of stem and their recombination fraction (*C. capsularis*)

Parents		F_1	F_2				\hat{p}	SE. \hat{p}
Nonfasciated Branched	Fasciated Nonbranched		Nonfasciated		Fasciated			
			Branched	Non-Branched	Branched	Non-Branched		
Maniksari	JRC 918	Nonfasciated Branched	267	85	38	75	0.2881	0.0256
		χ^2	P.					
		(Fasciation)	0.1211	.80-.70				
		(Branching)	2.1953	.20-.10				
		(Linkage)	51.0021	<.05				

stem. The F_2 segregation (1246 nonfasciated : 386 fasciated) shows the simple monogenic control of the character. Similar crosses examined for the joint segregation of nonfasciation—fasciation and branched—nonbranched stem, gave F_1 which was nonfasciated and branched. Joint segregations in F_2 are shown in Table 6. It can be seen that when a single character pair such as nonfasciation vs. fasciation or branched vs. nonbranched is considered, each of them satisfactorily fit to a 3 : 1 ratio. This indicates further that besides nonfasciation—fasciation, branching is simply dominant over nonbranching and monogenically inherited. This confirms the observation of Patel, Ghose and Sanyal (1945) regarding branching. The joint segregation of these characters shows an indication of linkage between them, since χ^2 for linkage is highly significant. After the detection of linkage, maximum likelihood estimate of the recombination fraction was found to be 0.2881 ± 0.0256 . So the linkage between these two loci is neither very tight nor very loose. The gene symbols proposed for nonfasciation and fasciation are **Fs** and **fs**. The gene symbols for branching and non-branching, **Br** and **br** proposed by Patel, Ghose and Sanyal (1945) may be retained.

SUMMARY

Inheritance of 7 different characters in *Corchorus olitorius* was investigated, of which crumpled/normal leaf and nonshiny/shiny seed coat are monogenically controlled, glossy/nonglossy leaf and flat/rolled leaf are governed by two pairs of complementary genes, nonfuzzy/fuzzy seed coat is controlled by duplicate genes, and seed coat colour (black, green and chocolate) and leaf size (narrow, intermediate and broad) showed modified trigenic ratios (27 : 21 : 16 and 36 : 15 : 13).

Pale green/deep green leaf, shallow serrated/deep serrated leaf and nonfasciated/fasciated stem in *C. capsularis* were found to be inherited monogenically.

Fasciation of stem and branching in *C. capsularis* were found to be linked genetically, the M. L. estimate of linkage being $28.81\% \pm 2.56\%$.

ACKNOWLEDGEMENTS

The authors are grateful to the Head of the Department of Genetics and Plant Breeding, Kalyani University for provision of laboratory and field facilities and to Dr. S. Dana for his interest in this study. Two of them are grateful to I.C.A.R. (M.K.J.) and Kalyani University (P.P.) respectively for the grant of predoctoral fellowships.

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