Indian J. Genet., 58(2) 143-147 (1998)

INHERITANCE AND LINKAGE RELATIONS OF GENES FOR YELLOW SEEDLING IN COTTON (*GOSSYPIUM SPP.*)

MUNSHI SINGH, R. P. SINGH AND V. P. SINGH

Division of Genetics, Indian Agricultural Research Institute, New Delhi 110 012

(Received: August 14, 1996; accepted: May 5, 1998)

ABSTRACT

Genetical studies of chlorophyll deficient lethal seedling were undertaken in two *G. hirsutum* progenies, viz., N-3-19-18-3-5-7-1-20 and N-3-19-27-7-12-1-27. Digenic segregation in the ratio of 15:1 for normal green and pale yellow lethal seedlings indicated that the lethal trait was controlled by duplicate recessive genes. In F_2 populations of five interspecific crosses, similar segregational pattern was observed. In the *G. hirsutum* progeny N-3-19-27-7-12-1-27 cinus colour (red vs. green) was controlled by the dominant genes segregating in the ratio of 11 red : 5 green, while in F_2 populations obtained from interspecific cross 188-26-7-3- × 21-4-4, this character segregated in the ratio of 13 red: 3 green, showing inhibitory action of genes. Hypocotyle colour (red vs. green) was caused by two dominant genes behaving in complementary manner (7:9) in the *G. hirsutum* progeny, while it showed duplicate epistasis with segregation ratio of 15 red: 1 green in F_2 population derived from *G. hirsutum* × *G. hirsutum* cross. The loci controlling normal vs. pale yellow lethal seedlings, cinus and hypocotyle (red vs. green) were found to be linked. The crossover values estimated to be 18.92% between genes for seedling colour and cinus colour, 34.07% between genes for seedling colour and hypocotyle colour, and 29.06% between loci for cinus and hypocotyle colour.

Key words: Cotton, lethality, cinus, hypocotyle, segregation, genes, inheritance, linkage, yellow seedlings.

Occurrence of pale yellow, lethal seedlings have been reported in segregating populations of interspecific crosses of tetraploid cottons, controlled by digenic complementary epistatic gene action. These genes have been designated as le_1 and le_2. Lee [1] and Rooney and Stelly [2] have also reported lethal genes Le^{dav} in the wild species *Gossypium davidsonii* Kell. and transferred this lethal gene Le^{dav} into a rare genotype le_1le_1 le_2le_2 of *G. barbadense* L/ le_2 le_2 L. [3]. The resulting stock $le_1le_1le_2le_2Le^{dav}Le^{dav}$ was incompatible with cultivars of both *G. barbadense* and *G. hirsutum*. However, the compatibility of le_1le_2 with Le_2^{dav} is being used to determine the frequency of le_1 and le_2 in a representative samples of *G. hirsutum* cultivars developed in USA [2]. Butany and Singh [4] reported spontaneous occurrence of lethal yellow seedlings in breeding lines derived from an intra-*hirsutum* cross for the

first time. Similar yellow lethal seedlings were observed during 1991-92 in two progenies from a variable strain Pusa 595B derived from an intra-*hirsutum* cross. The present investigation reports the inheritance of yellow lethal seedlings in *G. hirsutum* and interspecific crosses of *G. hirsutum* × *G. badbadense*. Linkage between loci for lethal yellow seedlings, cinus colour and hypocotyle colour have also been studied.

MATERIALS AND METHODS

Out of 30 progenies derived from Pusa 595B two progenies showed chlorophyll deficient lethal seedlings both in March and July, 1991 sown crop. These plants survived only for 7-8 days after germination. In some of the progenies cotyledonary leaves also showed yellow patches on otherwise normal green seedlings. The number of normal green and yellow lethal seedlings in the entire population was recorded during 1991 and 1992. Segregation for green and yellow seedlings was also followed in the F_2 generation obtained from five interspecific crosses involving three *G. hirsutum* and four *G. barbadense* parental lines. In March sown crop during 1992, the data was also recorded for cinus and hypocotyle pigmentation segregating for green red cinus, red pigmented vs. green hypocotyle in both *G. hirsutum* and the F_2s of interspecific crosses. The segregation ratios for individual trait as well as joint segregation for different traits were worked out. The simple X^2 test was applied to test the goodness of fit of different genetic ratios and for detecting linkage.

RESULTS AND DISCUSSION

Segregation data for green vs. yellow seedling colour in *hirsutum* and interspecific crosses are given in Table 1. Out of the 30 progenies studied during March 1991, two *hirsutum* progenies viz., N-3-19-27-7-12-1-27 and N-3-19- 18-3-5-2-1-20 segregated in the ratio of 15 normal green to 1 yellow seedlings indicating the presence of two recessive genes for pale yellow lethal seedlings. Similar segregation ratios were observed for yellow seedlings in the F_2 populations of inter- specific crosses. In 1992 also, progenies segregated in a 15 normal green to 1 yellow seedling. One to two genes with varying degree of epistatic interactions for pale yellow seedlings have been, reported previously by different workers [4-10]. In a series of papers Lee [1, 3, 11-12] and Rooney and Stelly [2] have reported complementary nature of these genes.

Segregation for cinus and hypocotyle colour red vs. green from one *G. hirsutum* (N-3-19-27-7-12-1-27) progeny and 5 interspecific crosses is given in Table 2. The segregational ratio of 11 red to 5 green was observed which is a threshold effect of gene action with the modification of dominance. Such type of epistasis has already

Table 1. Segregation for normal green and lethal, pale yellow seedling in the selfed progenies of heterozygotes derived from intra- *hirsutum* cross and in the F_2 populations of five interspecific crosses (*G. hirsutum* x *G. barbadense* L.)

Year	Intra-*hirsutum*						Interspecific *G. hirsutum* L. × *G. barbadense*					
	Progenies	Normal	Yellow	Total	Exp. ratio	X^2-value	Cross	Normal	Green	Total	Exp. ratio	X^2-value
1991	N-3-19-27-7-12-1-27	137	15	152	15:1	3.43	188-26-7-3 x 17-6-1	14	1	15	15:1	.0042
							188-26-7-3 x 16-14-6	88	6	94	15:1	.0210
	N-3-19-18-3-5-2-1-20	43	5	48	15:1	1.4221	188-26-7-3 x 21-4-4	180	11	191	15:1	.0750
							188-6-3 x 19-18-4	89	4	93	15:1	.5800
1992	B-3-19-27-7-12-1-27	850	62	912	15:1	0.469	700-5-3 x 17-6-1	104	4	108	15:1	1.17
	Pooled	1030	82	1112	15:1	2.45	Pooled	475	26	501	15:1	0.95

Table 2. Segregation for cinus and hypocotyle colour in an intra-*hirsutum* progeny and in an interspecific cross

Progeny	Intra-*hirsutum* progeny						Interspecific cross *G. hirsutum* × *G. barbadense*						
	Colour of	Red	Green	Total	Exp. ratio	X^2-value	Cross	Color of	Red	Green	Total	Exp. ratio	X^2-value
N-3-19-27-7-12-1-27	Cinus	640	272	912	11:5	0.85	188-26-7-3 ×21-4-4	Cinus	360	67	427	13:3	2.36
	Hypocotyle	405	507	912	7:9	0.16		Hypocotyle	407	20	427	15:1	1.66

been reported in cotton for glandular pattern [13]. Hypotocyle green colour was dominant over red with a complementary gene action. In the F_2 generation from interspecific cross (*G. hirsutum* 188-26-7-3 × *G. barbadense* 21-4-4) cinus colour segregated in a ratio of 13 red to 3 green indicating the presence of dominant and recessive epistasis. In the same interspecific cross, segregation for hypocotyle colour in ratio of 15 red to 1 green was observed showing duplicate epistasis. The segregation for seedling (green vs. yellow), leaf cinus (red vs. green) and hypocotyle (green vs. red) is shown in Table 3. The X^2-test gave significant values for association among the three traits. Endrizzi and Taylor [14] and Endrizzi and Stitch [15] reported that genes R_2-Yg_2 are located on chromosome 7 (A-genome) while genesR_1-Yg_1 are situated on chromosome 16 (D. genome).

Table 3. Frequency distribution of the progenies of Self heterozygote N-3-19-27-7-12-1-27 in different phenotypic classes

Phenotypic class	Observed frequency	Chisquare for testing independent inheritance
1. Green plant, Red cinus, Green hypo.	286	X^2-value for plant seedling colour and cinus colour = 97.39**
2. Green plant, Red cinus, Red hypo.	344	
3. Green plant, Green cinus, Green hypo.	203	X^2-value for seedling colour and hypocotyle colour = 20.70**
4. Green plant, Green cinus, Red hypo.	17	
5. Yellow plant, Red cinus, Green hypo.	4	X^2-value for cinus colour and hypocotyle colour = 89.99**
6. Yellow plant, Green cinus, Red hypo	38	
7. Yellow plant, Red cinus, Red hypo.	6	
8. Yellow plant, Green cinus, Green hypo	14	
Total	912	

**Significant at P = 0.01

The occurrence of yellow lethal seedlings in a single plant progeny of an intra-*hirsutum* population as a result of inbreeding during the fourth and fifth cycle of pedigree selection [4] and in the present study indicated that the recessive genes controlling- yellow lethal seedling character have been carried in a population in the form of genetic load for several generations which get eliminated through inbreeding by the process of segregation at a particular stage. The dominant duplicate genes located on both A and D genome chromosomes controlling normal green seedling characters have mutated to recessive lethal genes which remained hidden in the heterozygous population for 4-5 generations. The association of yellow lethal seedling character with genes controlling green hypocotyle and cinus colour suggest

occurrence of spontaneous mutations for the entire linkage group i.e. gene block controlling cotyledonary leaf colour, hypotocyle and cinus colour. The occurrence of yellow lethal seedling (i.e. yellow cotyledonary leaves), green hypotocyle and green cinus colour in the original parental populations of normal green cotyledonary leaves, red pigmented hypocotyle and red cinus colour in *G. hirsutum* have clearly established that the mutation to lethality might have triggered mutability of other linked genes controlling hypocotyle and cinus pigmentation in *G. hirsutum*

REFERENCES

1. J. A. Lee. 1981 a. Genetics of D_3 complementary lethality in *Gossypium hirsutum* and *G. barbadense* L. J. Heredity., **72**: 299-300.
2. W. L. Rooney and D. M. Stelly. 1989. Allelic composition of cotton at the Le_1 and Le_2 loci. Crop Sci., **29**: 707-712.
3. J. A. Lee. 1981 b. A genetical scheme for isolating cotton cultivar. Crop Sci., **214**: 339-341.
4. W. T. Butany and M. Singh. 1965. The inheritance of chlorophyll deficiencies in cotton. Indian J. Genet., **25(1)**: 59-90.
5. G. N. Stroman and C. H. Mahoney. 1925. Heritable chlorophyll deficiencies in seedling cotton. Bull. Tex. Agric. Ex. Sta., 333.
6. C. P. Yu. 1939. The inheritance and linkage relations of yellow seedling, a lethal gene in Asiatic cotton. J. Genet., **39**: 61-68.
7. R. Balasubrahmanyam. 1947. The inheritance of two chlorophyll deficients in Asiatic cottons. Proc. 3rd Conf. Cott. Gr. Prob., India, (I.C.C., Bombay). 97-99.
8. N. R. Bhat and K. B. Desai. 1958. Genetic studies on the yellow green and green yellow mutants in *Gossypium hirsutum*. Indian J. Genet., **18**: 54-56.
9. G. B. Patel, Z. A. Munshi and G. T. Patel. 1947. Genetics of some mutations in *herbaceum* cotton of Gujarat (Bombay Province). Proc. 3rd Conf. Cotto. Gr. Prob., India (I.C.C., Bombay): 87-97.
10. C. L. Rhybne. 1958. Linkage studies in *Gossypium* I. Altered recombination in allo-tetraploid *G. hirsutum* L. following linkage transference from related diploid species. Genetics., **43**: 822-834.
11. J. A. Lee. 1986. Registration of NC-D_3 compatible 1 and NC-D_3 compatible 1 and NC-D_3 incompatible 1 germplasm lines of cotton. Crop Sci., **26**(1): 1260-1261.
12. J. A. Lee. 1982. Linkage relationship between Le and G1 alleles in cotton. Crop Sci., **22**: 1211-1213.
13. J. A. Fuchs, J. D. Smith and L. S. Bird. 1972. Genetic bases for an 11:5 dihybrid ratio observed in *Gossypium hirsutum* L. J. Hered., **63**: 300-303.
14. J. E. Endrizzi and T. Taylor. 1968. Cytogenetic studies of $NLC_{1Y}JR_2$ marker genes and chromosome deficiencies in cotton. Genet. Res., **12**: 295-304.
15. J. E. Endrizzi and L. S. Stitch. 1970. Association of two marker genes with chromosomes I of cotton. Agron. Abstr. Am. Soc. of Agron., Madison, Wis., p. 9.