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Genetic studies in F_2 population of naturally brown coloured upland cotton (*Gossypium hirsutum* L.)

N. PREMALATHA*, AMIT KUMAR MAZUMDER, A. ANBUSRIMATHI AND S. S. DEEPTI VARSHA

Depatment of Cotton, Tamil Nadu Agricultural University, Coimbatore -641 003

**Email: npremalatha@gmail.com*

Abstract : The present study aims to understand the inheritance of brown coloured lint in cotton. It is known that white coloured lint is governed by a recessive allele and it is obviously made clear that the coloured lint is a dominant character expecting the phenotypic ratio of 3:1 in the segregating population F_2. But when observing the lint colour of F_1s and F_2s of a cross between a coloured cotton variety and a white coloured cotton variety, the intensity of colour of F_1 was intermediate to both the parents of extreme phenotype and the phenotypic ratio of segregating population fits 1:2:1 (Brown, Intermediate and white) which was assessed using Chi square test. This indicates that the lint colour trait is governed by a single nuclear gene and the coloured lint phenotype is incompletely dominant over that of the white colour. Since the cotton lint varies extensively in the intensity of brown colour, there is a possibility that the trait is governed by polygenes supporting Multiple factor hypothesis. The varying intensity of colour observed among segregants might be due to more than one locus or modifiers which could be confirmed in F_3 generation.

Key words: Colour, cotton, fibre quality, inheritance, naturally coloured cotton

Cotton with naturally coloured lint, other than white, is commonly referred as coloured cotton. Cotton fiber color is a genetically inherited trait resulting from the presence of pigments intermingled with cellulose. Naturally colored cottons are mutants of white fiber and there are several lint colors such as brown, black, red, pink, blue, and green (Khan *et al.*, 2009). Brown is the most common color and has many shades ranging from dark brown and shades vary from light brown to mahogany red in the four cultivated as well as many of the wild species. Depending on the intensity it is named as light brown, *khaki*/camel colour, dark brown/chocolate colour, dirty grey, tan and red (Singh *et al.*, 2001). Fibre quality is the most important and limiting factor in the genetic improvement of colour cotton. The color of cotton fiber is the result of the presence of pigments intermingled with cellulose (Carvalho *et al.*, 2014). It is a genetically inherited characteristic resulting in different shades of green and brown (Dickerson *et al.*, 1999). Zhang and Wang (2000) reported that the intensity of brown colour showed negative correlation with fibre quality. Efe *et al.*, (2009) reported that fibre quality in naturally coloured cotton is inferior to white linted cotton. Kohel (1985) tested known genes for lint color for allelism and reported that the brown fiber color was controlled by six loci: Lc1 and Lc2 were responsible for medium brown color of lint, Lc3 was responsible for dark brown, and Lc4, Lc5 and Lc6 were responsible for light brown (Wang *et al.*, 2014). Murthy (2001) stated that the genes responsible for fiber color often had pleiotropic effects. The fiber color of brown cotton was reported to be controlled by incomplete dominance of a major gene and an extra, recessive minor gene (Wu *et al.*, 2010). Carvalho *et al.*, (2014) crossed *G. barbadense* accessions representing different shades of brown and white *G. hirsutum* cultivars and concluded that all fiber colors were governed by a single gene. Semizer- Cuming *et al.*, (2015) studied 94 F_2 individuals of a cross between green

Table 1. Details of cross combinations made with number of plants studied in each cross

S. No.	Crosses	Number of plants studied in F2
1.	MCU5 × Higgins Badham	234
2.	Higgins Badham × MCU 5	214
3.	Algerian Brown ×CO 14	220

coloured cotton and white linted cotton and observed that frequency distribution for each parameter showed typical quantitative variation. The association of colour and fibre quality traits help in understanding the relationship to improve the quality of naturally coloured cotton genotypes.

In the present study, two naturally brown coloured cotton varieties Higgins Badham and Algerian Brown and two white coloured elite cotton varieties known for their fiber quality MCU 5 and CO 14 were selected and used as parents in hybridization. Three crosses were made between naturally colour cotton and white linted varieties, direct and reciprocal crosses between MCU 5 and Higgins Badham and a direct cross between Algerian Brown and CO 14. The F_1 generation of all the three crosses and parents were raised in the field for the comparison of the lint colour. The F_1 plants of each cross were selfed to obtain F_2 generation and the F_2 generation of each was studied in order to assess the inheritance pattern of lint colour. Selfing was carried out using wet clay method and thread method. This experiment was conducted during *kharif* 2019 at Department of Cotton, Tamil Nadu Agricultural University, Coimbatore. The experimental field was kept under isolation in order to avoid contamination of white cotton. Each cross was raised in 20 rows with the spacing of 90 × 45 cm and all recommended crop management practices were followed. Segregation for lint colour was recorded on each plant where nearly 70 per cent bolls were open in F_2. The F_2 populations of three crosses under study were visually inspected and scored for lint colour. The colour grades for different shades were given by matching with the universally accepted colour chart of the Royal Horticultural Society (2001). Chi square test was used to assess the Mendelian inheritance pattern for lint colour in F_2 segregating population.

The significance of difference between the observed and expected frequencies or ratios was studied using the method given by Klug and Cummings (1999).

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$$\chi 2 = \Sigma(O-E)2 / E$$

Where,
O = Observed frequencies
E = Expected frequencies

The chi square values tested against table values with n-1 degrees of freedom (n is the number of classes) or the probability value were taken into consideration for rejection or acceptance of Null hypothesis.

The colour of naturally coloured cotton is genetically controlled. The observations of the F1s obtained by crossing coloured and white linted varieties revealed that the colour intensity is intermediate of both the parents involved in each cross. This indicates that brown colour is incompletely dominant over white with respect to lint colour. Reciprocal crosses did not exhibit significant difference with respect to lint colour. This indicates that the cytoplasmic differences have little or no bearing on lint colour, thus lint colour is governed only by nuclear genes. The segregants for lint colour in F_2 populations had brown colour of varying colour intensity. Since discrete grouping of colour was not possible, the plants having similar and slightly darker shades than brown parent were grouped under brown and those with lighter shades than brown parent were taken under intermediate category.

Table 2. Chi square test of different crosses in F_2 population for lint colour

1. MCU 5 × Higgins Badham

Phenotype	Degrees of freedom	Observed	Expected	X2 Value	Value
Brown	1	55	58.5	0.27	0.60
Intermediate	2	114	117		
White	1	65	58.5		
Total	**4**	**234**	**234**		
2. Higgins Badham × MCU 5					
Brown	1	59	53.5	0.22	0.64
Intermediate	2	101	107		
White	1	54	53.5		
Total	**4**	**214**	**214**		
3. Algerian Brown × CO 14					
Brown	1	45	51.5	0.76	0.38
Intermediate	2	102	103		
White	1	59	51.5		
Total	**4**	**220**	**220**		

The chi square test of all the crosses for the segregation of lint colour in F_2 also did not deviate significantly from the expected 1:2:1 phenotypic ratio of the mendelian inheritance pattern for incomplete dominance.

In the first cross, MCU 5 × Higgins Badham, among 234 F_2 plants, 55 plants possessed brown fibre, 114 plants had intermediate phenotype and 65 plants were found to have white fibre (Table 2). In the corresponding reciprocal cross (Higgins Badham × MCU 5), among 214 F_2 plants studied, 59 plants had brown fibre, 107 plants were found to have intermediate fibre and 54 plants possessed white fibre (Table 2). In the third cross Algerian Brown × CO 14, among 206 F_2 populations, 45 plants possessed brown fibre, 102 plants had intermediate phenotype and 59 plants had white fibre (Table 2).

In the chi square analysis of all the crosses, indicated that all theses crosses fit 1:2:1 expected phenotypic ratio at a significant level of $\alpha = 0.05$ and brown colour fibre of naturally coloured cotton is governed by a single incompletely dominant gene action. These results were in agreement with the reports of Shaohua *et al.*, (2008), Hinchliffe *et al.*, (2016), Wen *et al.*, (2018), Nivedha *et al.*, (2020) and Keerthi *et al.*, (2021). Even though the ratio supported single gene inheritance, the varying intensity of brown colour in F_2 rather than discrete two phenotypes paved way for the possibility of more than one locus responsible for colour as proposed by Kohel (1985) and Murthy (2001).

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