Abstract

Almost all cotton fibers produced in the world are white; however some tetraploid cottons produce naturally colored lint ranging from brown to green which can help to reduce the use of toxic dyes in the textile industry. Fiber color is a genetically inherited feature resulting from the presence of pigments intermingled with cellulose in the cotton fiber. The present study was conducted at the Agricultural Research Station, Dharwad Farm during Kharif, 2018 and 2019 to understand the inheritance pattern of the brown color in color-cotton. The F₂ population was considered to study the gene action and to reconfirm the same, the F₂:3 populations were also investigated. The variation observed for the color was quite high with different shades of brown lint color in the two populations studied. According to the χ² test, the F₃ and F₂:3 populations segregated into colored fiber and white fiber lines which fit well into the expected 1:2:1 ratio, indicating incomplete dominant gene action.

Keywords
Color-cotton, Brown lint, χ² test, Gene action, Incompletely dominant gene action

Introduction

Cotton, the king of fibers is the largest natural textile material worldwide. The cotton fiber with the presence of pigments intermingled with cellulose produces what is called naturally colored cotton. Since time immemorial the color and white linted cotton are found in nature, as evidenced from the excavation of Huaca Prieta on the northern Peruvian Coast of South America which indicated the usage and cultivation of color-cotton since 2500 B.C., (Stephens, 1975, Apodaca, 1990). The lint exists in various hues and the brown and green colors are most common among them. The brown color, in turn, has many shades ranging from dark brown to mahogany red.

The textile industries artificially apply the dyes to the cotton to make it colored. This results in harmful industrial discharge from dyeing industries into water bodies that risk human health and the environment. The use of naturally colored cotton eliminates the dyeing process in textiles from which about one-half of the cost of preparing fabrics can be reduced (Pooja and Anita, 2018). Furthermore, fabrics made of naturally colored cotton are steadfast compared to
synthetically dyed clothes that do not fade quickly. Despite the economic and ecological benefits, commercial cultivation of naturally colored cotton is very limited by the farmers because of few drawbacks.

The fiber of low quality is most important among them. The fiber quality and yield are negatively associated with the fiber color which in turn makes the color-cotton less productive along with the lower quality of the fiber (Feng et al., 2015). In addition to low quality, the limited range of colors, the instability of lint color overexposure to sunlight, the need for isolated fields to avoid contamination of white cotton, and the lack of standard quality classification criteria have limited its cultivation (Matusiak and Frydrych, 2014).

The development of fiber color in cotton is genetically controlled. It was reported that the brown color has a dominant legacy (Wang et al., 2012). Kohel (1985) investigated the fiber color genes and reported six loci for brown color, namely Lc1 and Lc2 (medium brown), Lc3 (dark brown), Lc4, Lc5, and Lc6 (light brown). The inheritance study of fiber color will allow us to determine the gene action involved in lint color that could be used by crossing white linted with color linted lines in the development of more productive color-cotton varieties.

### Materials and Methods

A study was carried on in the early segregating generations’ viz., F2 and F2:3 to evaluate the segregation pattern for fiber color in a cross between Sahana (white lint) and DB-50-2 (dark brown lint). The crossed F1 seeds were selfed to generate the F2 population. Each F2 plant was selfed to advance the generation to F3. Both F2 and F2:3 populations were examined to know the inheritance pattern for lint color.

The experiment was conducted during Kharif, 2018 and Kharif, 2019 at Agricultural Research Station, Dharwad Farm, University of Agricultural Sciences, Dharwad. Plants of the F2 generation and F2:3 progenies were grown in a row of 4.2m length with a spacing of 90 cm between rows and 20 cm between plants. All the recommended measures were practiced to raise a healthy crop. The agronomical and plant protection measures were carried out from sowing to harvest as per the standard recommendation.

The F2 population and F2:3 populations under study were visually inspected and scored for the lint color from the completely opened boll. The brown color had segregated into many shades ranging from light to dark brown.

A Chi-square test was performed to assess the inheritance pattern for fiber color in F2 and F2:3 populations. The significance of the difference between observed and expected frequencies or ratios was studied using the method given by Klug and Cummings (1999). Chi-Square test ($\chi^2$ test) is the summation of the squared deviation of observed and expected frequencies divided by expected frequencies given by the formula,

$$\chi^2 = \sum \frac{(O - E)^2}{E} \text{ with (n - 1) d.f}$$

where,

- $O =$ observed frequencies
- $E =$ expected frequencies
- $n =$ number of classes

The chi-square values tested against table values with n-1 degrees of freedom (n is the number of classes).

The deviations were taken as significant wherever the calculated chi-square value was
over the table value at both levels, and the presumed ratio was not considered a fit, and vice-versa.

Results and Discussion

In the cross, the fiber color of each plant in F₁ was intermediate to that of the parents that confirmed the brown color of fiber had nuclear inheritance and exhibited partial dominance over white (Ware, 1932; Richmond, 1943 and Xianlong, 2004). On visual inspection of individual plants in F₂, the intensity of brown color varied showing five different shades (Fig. 1). Further, the F₂:₃ populations were studied to reconfirm the segregation pattern of fiber color. The dark brown and light brown shades did not segregate for the color trait. Hence, the progeny lines of the F₂:₃ populations that segregated for fiber color were only considered for fitting the ratio. Since discrete grouping of color was not possible, the plants with similar and slightly darker shades than brown were grouped under the brown category, and the rest with lighter shades of brown were grouped in the intermediate category.

Table 1 Chi-square test in the cross Sahana (white lint) x DB-50-2 (dark brown lint) for lint color segregation

| Generation | Total no. of plants | Color of lint | White | Observed ratio | χ² value |
|------------|---------------------|---------------|-------|----------------|----------|
| P₁         | 42                  | -             | -     | All            |          |
| P₂         | 41                  | All           | -     | -              |          |
| F₁         | 39                  | -             | All   | -              |          |
| F₂         | 345                 | 101           | 160   | 84             | 1:2:1    | 3.54     |
| F₃         | 2117                | 532           | 1048  | 537            | 1:2:1    | 0.23     |

Fig.1 Pictorial representation of the variability for fiber color of cross Sahana x DB-50-2
For the interpretation of results, the chi-square test of the cross indicated no significant deviation from the inheritance pattern of the 1:2:1 phenotypic ratio (Table 1). Among the 345 plants, 101 plants possessed brown color, 160 plants had intermediate color, and 84 plants were white. Further, the F2:3 populations were studied to reconfirm the segregation pattern of fiber color. Among the 2117 plants, 532 showed brown color, 1048 carried intermediate color, and 537 plants had white color. In the chi-square analysis, the p-value was more than 0.05 implying the acceptance of the null hypothesis. The F2 and F2:3 populations segregated into different shades of color and white that fit well into the expected ratio of 1:2:1. This portrayed that the brown color was controlled by a single incompletely dominant gene. A similar result was noticed by Nivedha et al., (2020), Shaohua et al., (2008), and Hinchliffe et al., (2016).

Even though the ratio supported single gene inheritance, the varying intensity of brown color in F2 and F2:3 rather than two discrete color phenotype classes paved the way for the possibility of more than one locus responsible for color as proposed by Kohel (1985). Wang et al., (2014) reported that the modification of minor genes could have accounted for variations in the F2 population. Therefore, further studies should be carried for judging the number of loci governing brown lint color trait in cotton.

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