# Inheritance of Flower Color in Chickpea

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Flower color is a useful morphological marker in chickpea (Cicer arietinum L.). Inheritance of this trait was studied using two white-flowered chickpea genotypes, P 9623 and RS 11, and one blue-flowered genotype, T 39-1. The genetic constitutions of the white flower colors of P 9623 and RS 11 were different, for in an earlier study their $F_1$ produced pink flowers. The two $F_1$s of the crosses P 9623 × T 39-1 and RS 11 × T 39-1 also produced pink flowers. Each of the two $F_2$ populations segregated in 9 pink:3 blue:4 white-flowered plants. These results can be explained by a three-gene model. These three independently segregating genes are probably the same as C, B, and P reported in the literature earlier. Allelic tests could not be undertaken, as the genetic stocks used in the earlier studies are not available. The genetic constitutions of the three parents and their $F_1$s are proposed. These accessions should be useful for conducting allelic tests for determining flower color loci in chickpea and for comparative studies with field pea. The seeds of these genetic stocks are maintained at the Genetic Resources and Enhancement Program at ICRISAT and are available for research purposes on request.

Chickpea or garbanzo (Cicer arietinum L.) is the third most important food legume worldwide and the most important in South Asia, the Middle East, and Eastern Africa. It is the premier pulse crop of India, accounting for 28% of the total pulse crop area and 38% of its production (FAO 1998). In chickpea, three major and distinct flower colors are identified, namely pink, blue, and white. About two-thirds of the world germplasm accessions at ICRISAT are pink flowered and nearly one-third have white flowers. Those with blue flowers are rare (Pundir et al. 1988).

Kumar (1997) reported complementary gene action for pink flower color in a cross of two white-flowered germplasm accessions, P 9623 (ICC 4854) and RS 11 (ICC 4992). Khan and Akhtar (1934) and Ayyar and Balasubramanian (1936) also reported such complementation. However, the genetic stocks available with the same names as those used by Khan and Akhtar do not correspond with the names in the world chickpea germplasm collection maintained at ICRISAT. In their study, stocks T 9, T 11, and T 39, all with white flower color, have accession numbers ICC 5870, ICC 5874, and ICC 5861, respectively, whereas the listed flower colors of these stocks are pink, blue, and pink, respectively. Thus these do not correspond with the original testers used by Khan and Akhtar (1934) and Ayyar and Balasubramanian (1936). It is highly improbable that those stocks can be traced. Therefore allelic tests are not possible with the original genetic stocks.

Kumar (1997) suggested the need for flower color and genetic studies with P 9623 and RS 11 as two different white flower color testers. Therefore our study was conducted to establish new genetic stocks for flower color in chickpea.

## Materials and Methods

An experiment was conducted with three chickpea genotypes: P 9623 (ICC 4854), RS 11 (ICC 4992), and T 39-1 (ICC 5912). Stock T 39-1 is blue flowered and was used as the common male parent in both crosses. Stocks P 9623 and RS 11 are both white flowered and were used as female parents. The crosses P 9623 × T 39-1 and RS 11 × T 39-1 were made in the Rabi season 1995 to provide the $F_1$ generations. The hybrid seeds were grown during the Rabi season 1996 to obtain the $F_2$ seeds. Reciprocal crosses produced in 1996 showed similar results for flower color as those in 1995. Therefore only the first set of crosses made in 1995 was studied further.

The parental, $F_1$, and $F_2$ generation seeds of the two crosses were sown on 14 October 1997 on 60 cm ridges on a deep Vertisol under conserved soil moisture conditions at the ICRISAT center. The plot sizes were 10 rows, 4 m long, 60 cm apart for each $F_2$, and one row each for parents and $F_1$s. The seeds were planted at a 20 cm spacing within the row. Normal crop management practices were followed. Plants were classified into pink-, blue-, and white-flowered types based on the color of the corolla. Observations on corolla color of freshly opened flowers were recorded on 160 random competitive plants in the $F_2$ generation of the cross P 9623 × T 39-1 and on 150 plants in the cross RS 11 × T 39-1. For each of the parental and $F_1$ generations, all 20 plants were observed. The chi-square test was applied to the observed segregation in the two $F_2$ generations.

## Results and Discussion

In both crosses between the white-flowered female parents P 9623 and RS 11 and the blue-flowered male parent T 39-1, the $F_1$s were pink, suggesting interaction of blue and white flower colors. The data for the three flower colors fit well to the ratio of 9 pink:3 blue:4 white in the $F_2$ generations of both the crosses, P 9623 × T 39-1 and RS 11 × T 39-1 (Table 1). Results for both crosses showed a supplementary type of gene action for flower color based on segregation for two independent loci.

The same segregation ratio in the $F_2$ generation of both crosses in this study suggested similar genetic constitutions for the two white-flowered parents P 9623 and RS 11. However, Kumar (1997) reported a pink-flowered $F_1$ between the two white-flowered parents. This suggested that these parents had different genetic constitutions for their white flower colors. Therefore the trigenic model of inheritance is found appropriate to explain this flower color segregation. Such segregation has been implied or reported earlier (Ayyar and Balasubramanian 1936; D'Cruz

**Table 1.** Segregation for flower color in the $F_2$ generation of two crosses of chickpea, Rabi season 1997–1998

| Cross | Parent/generation | Flower color | Expected ratio ($F_2$) | No. of plants Observed | No. of plants Expected | $\chi^2$ | P |
|---|---|---|---|---|---|---|---|
| P 9623 × T 39-1 | P 9623 | White | | | | | |
| | T 39-1 | Blue | | | | | |
| | $F_1$ | Pink | | | | | |
| | $F_2$ | Pink | 9 | 77 | 90.00 | 4.44[NS] | .10–.25 |
| | | Blue | 3 | 34 | 30.00 | | |
| | | White | 4 | 49 | 40.00 | | |
| RS 11 × T 39-1 | RS 11 | White | | | | | |
| | T 39-1 | Blue | | | | | |
| | $F_1$ | Pink | | | | | |
| | $F_2$ | Pink | 9 | 88 | 84.38 | 1.18[NS] | .50–.75 |
| | | Blue | 3 | 30 | 28.12 | | |
| | | White | 4 | 32 | 37.50 | | |

NS = not significant.

and Tendulkar 1970; Phadnis 1976). It would be ideal if allelic tests could be done using the earlier genetic stocks. As pointed out above, those genetic stocks are unlikely to be traced after such a long time. Therefore we suggest that P 9623, RS 11, and T 39-1 be used as new genetic stocks for chickpea flower color studies in the future.

Ayyar and Balasubramanian (1936) used the gene symbols P, C, and B to indicate flower colors. The symbols $Pco_a$, $Pco_{b1}$, and $Pco_{b2}$ used by D'Cruz and Tendulkar (1970) and A, B, and C used by Phadnis (1976) could be the same as P, B, and C, respectively. These workers used different gene symbols for flower color without conducting allelic tests with the genetic stocks used in earlier studies. Since the original genetic stocks used in earlier studies are unavailable, a fresh look at the flower color genes and their symbols is necessary.

Assuming the model of Ayyar and Balasubramanian (1936), the flower color in the present study was controlled by three genes: C, B, and P. All three genes in the dominant condition produced pink color. The pink color of the $F_1$ would have the genetic constitution of C-B-P-. The gene B imparted blue color to the petals in association with C. Therefore the genetic constitution of the blue-flowered parent, T 39-1, could be CCBBpp. The white-flowered parents, P 9623 and RS 11, could have any of six possible genotypes for white flower color; namely CCbbPP, CCbbpp, ccBBPP, ccBBpp, ccbbPP, and ccbbpp. However, as the two parents produce a pink $F_1$, between them they must have all three dominant alleles. This suggests only three possible genotypes, namely, CCbbPP, ccBBPP, and ccbbPP. The absence of trihybrid ratio in the $F_2$ ruled out the possibility of ccbbPP. Kumar (1997) suggested the genetic constitution for P 9623 to be CCbbPP. This is based on the observation that this genotype produces white flower color when crossed with most other white flower color lines (Kumar J, unpublished data). Therefore the genetic constitution for RS 11 could be ccBBPP. The genetic constitutions of the two pink flower-colored $F_1$s of these parents with T 39-1 would be CCBbPp or CcBBPp, as segregation was observed only for two genes in their $F_2$ generations. Therefore the proposed genetic constitutions and resulting phenotypes of the three parents and $F_1$s are P 9623, CCbbPP (white); RS 11, ccBBPP (white); T 39-1, CCBBpp (blue); $F_1$(P 9623 × T 39-1), CCBbPp (pink); $F_1$(RS 11 × T 39-1), CcBBPp (pink).

Thus genes B and C complement each other in the absence of P resulting in the appearance of blue color but individually impart white color to the petals. The gene P showed supplementary action converting blue to pink color, but without any effect by itself, thus imparting white color to the petals when present singly or in combination with either C or B. The recessive alleles of all three genes together also produce white petal color.

These results were further confirmed by observing crosses between white-flowered $F_2$ segregants obtained from P 9623 × T 39-1 and those from RS 11 × T 39-1 (Kumar J, unpublished data). As expected, only pink and blue flowers were obtained from these crosses. This further confirms the genetic constitutions postulated for these genetic stocks in this article.

In our study, flower color was controlled by three independent genes. The study confirmed that white-flowered phenotypes could have different genetic constitutions (Ayyar and Balasubramanian 1936; Davis 1991).

Twenty-two genes are known to govern flower color in the related genus Pisum. In another related genus, Lens, only two genes have been identified thus far. Muehlbauer et al. (1995) believe that more genes for flower color may exist in Lens also. Therefore more than three loci may govern flower color in chickpea (Kumar 1997). Further studies are warranted to investigate this character and determine the evolutionary relationships between chickpea and related genera. Flower color, as a phenotypic marker, will also be useful in molecular marker studies in this crop.

The genetic stocks used and the results obtained in this investigation should be useful in conducting further studies on flower color in chickpea. The seeds of these genetic stocks are maintained at the Genetic Resources and Enhancement Program at ICRISAT and are available for research purposes on request.

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