



Short Communication

## Inheritance of anthocyanin pigmentation in flower and other plant parts in the genus *Cicer*

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(Received: October 2005; Revised: May 2006; Accepted: May 2006)

Chickpeas (*Cicer arietinum* L.) are often divided into two groups *desi* and *kabuli*. Besides the differences for seed characteristics, the former have purple anthocyanin pigmentation in most of the plant parts such as corolla, veins on the dorsal surface of the standard petal, floral pedicel, rachis, and stem. In contrast, *kabuli* does not show anthocyanin pigmentation in any plant part. Although both groups are cross compatible [1] and hybridization have been exploited between them to introgress the desirable traits from *kabuli* to *desi* and *vice versa*, yet the genetics of pigmentation in floral and other plant parts is not well understood. Many workers have reported a diversity of results in this regard [2-4]. Gene(s) involved in pigmentation have pleiotropic effects on various plant parts. However, Muehlbauer and Singh [5] reported that the relationship between corolla pigmentation and general plant pigmentation has not been established adequately. Moreover, information on genetics of anthocyanin pigmentation in inter-specific crosses between *C. arietinum* and *C. reticulatum* is lacking. The objectives of present studies were (i) to confirm the inheritance of floral pigmentation, and (ii) to correlate its expression in other plant parts for anthocyanin pigmentation in intra- and inter-specific crosses of chickpea.

The material comprised four cultivars of chickpea (*C. arietinum*) and one accession of its wild relative, *C. reticulatum*. The *desi* chickpea cultivars, GL 769 and ICC 1665 contain anthocyanin pigmentation in corolla, veins on the dorsal surface of the standard petal, floral pedicel, rachis, and stem, whereas the *kabuli* chickpea cultivars, L 550 and FGK 45, did not produce anthocyanin pigmentation in any plant part. Pigmentation was present in wild chickpea, *C. reticulatum*, accession No. 205. Two intra-specific single crosses of *C. arietinum*, L 550 × GL 769 and ICC 1665 × L 550 and their reciprocals and two inter-specific single crosses, L 550 × No. 205 and FGK 45 × No. 205, were generated. Observations for the presence or absence of pigmentation in corolla, veins on the dorsal surface of the standard petal, floral pedicel, rachis and stem were recorded visually in F<sub>1</sub>s and segregating populations. The gene interactions were tested by  $\chi^2$ .

The expression of anthocyanin pigmentation in corolla, veins, floral pedicel, rachis and stem in F<sub>1</sub> of crosses L 550 × GL 769 and L 550 × ICC 1665 and their reciprocals indicated that the trait is dominant and governed by nuclear gene(s). The F<sub>2</sub> of all four intra-specific crosses segregated in the ratio of 9 pigmented : 7 non-pigmented plants (Table 1). These results suggest that the anthocyanin pigmentation in corolla and other plant parts is produced by two complementary genes, *B* and *C* in the presence of third gene *P*, as proposed earlier [3]. It is further supported by segregation pattern in F<sub>3</sub> single plant progenies (Table 2). The epistatic action of two genes was also reported earlier [6]. However, some workers reported results contrary to our findings: a single dominant gene for corolla pigmentation in chickpea [7-8]. Genes for pigmentation have pleiotropic effect in veins, floral pedicel, rachis and stem, as no exceptional recombinants in F<sub>2</sub> or F<sub>3</sub> was found. Pleiotropy of genes causing pigmentation was reported for vein pigmentation [8], stem pigmentation [3] and for stem and pedicel pigmentation [6].

The F<sub>1</sub>s of two inter-specific crosses, L 550 × No. 205 and FGK 45 × No. 205, showed dominance of genes of *C. reticulatum* for anthocyanin pigmentation in corolla and other plant parts over the gene(s) of *C. arietinum* for non-pigmentation. F<sub>2</sub> populations of both the crosses segregated into the ratio of 15 pigmented : 1 non-pigmented plants (Table 1) indicating that anthocyanin pigmentation is produced by two duplicate genes. The presence of recessive alleles at both loci caused non-pigmentation. The results were confirmed by the data from F<sub>3</sub> single plant progenies (Table 2).

The gene symbols *B/b*, *C/c* and *P/p* were proposed earlier [9] for corolla pigmentation in *C. arietinum*. We propose gene symbols, *B<sup>r</sup>* and *C<sup>r</sup>*, for anthocyanin pigmentation in *C. reticulatum*. Both genes are duplicate to each other. The third gene, *P* being in homozygous state, is silent. The overall dominance relationship would be *B<sup>r</sup>* > *B* > *b* and *C<sup>r</sup>* > *C* > *c*. Ladizinsky and Adler [10, 11] suggested that either the *C. reticulatum* is a wild progenitor of *C. arietinum*, or both species originated

**Table 1.** Inheritance of anthocyanin pigmentation in corolla and other plant parts in F<sub>1</sub> and F<sub>2</sub> of intra-specific (*C. arietinum*) and inter-specific (*C. arietinum* × *C. reticulatum*) crosses in *Cicer*

| Cross                         | F <sub>1</sub> | Number of F <sub>2</sub> plants |     | Expected ratio | χ <sup>2</sup> | Probability |
|-------------------------------|----------------|---------------------------------|-----|----------------|----------------|-------------|
|                               |                | P*                              | NP* |                |                |             |
| <b>Intra-specific crosses</b> |                |                                 |     |                |                |             |
| L 550 (NP) × GL 769 (P)       | P              | 115                             | 98  | 9:7            | 0.44           | 0.50-0.70   |
| GL 769 (P) × L 550 (NP)       | P              | 111                             | 74  | 9:7            | 1.06           | 0.30-0.50   |
| L 550 (NP) × ICC 1665 (P)     | P              | 148                             | 126 | 9:7            | 0.56           | 0.30-0.50   |
| ICC 1665 (P) × L 550 (NP)     | P              | 142                             | 99  | 9:7            | 0.70           | 0.30-0.50   |
| <b>Inter-specific crosses</b> |                |                                 |     |                |                |             |
| L 550 (NP) × No. 205 (P)      | P              | 237                             | 20  | 15:1           | 1.03           | 0.30-0.50   |
| FGK 45 (NP) × No. 205 (P)     | P              | 225                             | 19  | 15:1           | 0.98           | 0.30-0.50   |

**Table 2.** Segregation for anthocyanin pigmentation in corolla and other plant parts in F<sub>3</sub> single plant progenies and expected genotypes of the respective F<sub>2</sub> plants in different crosses in *Cicer*

| F <sub>2</sub> phenotype                      | No. of progenies | F <sub>3</sub> phenotype  | Genotype of F <sub>2</sub> plants           |
|-----------------------------------------------|------------------|---------------------------|---------------------------------------------|
| <b>L 550 × GL 769 (Intra-specific cross)</b>  |                  |                           |                                             |
| Pigmented corolla                             | 12(1/16)         | Did not segregate-P*      | PPBBCC                                      |
| -do-                                          | 51(4/16)         | Segregated in 9 P : 7 NP* | PPBbCc                                      |
| -do-                                          | 52(4/16)         | Segregated in 3 P : 1 NP  | PPBBcc/PPBbCC                               |
| Non-pigmented corolla                         | 98(7/16)         | Did not segregate-NP      | PPB_cc/PP bbC_/PPbbcc                       |
| <b>L 550 × No. 205 (Inter-specific cross)</b> |                  |                           |                                             |
| Pigmented corolla                             | 110(7/16)        | Did not segregate-P       | PPB'B'C'/PPB'B'C'/PPB'bC'/PPB'B'cc/PPbbC'C' |
| -do-                                          | 62(4/16)         | Segregated in 15 P : 1 NP | PPB'bC'                                     |
| -do-                                          | 65(4/16)         | Segregated in 3 P : 1 NP  | PPB'bcc/PPbbC'                              |
| Non-pigmented corolla                         | 20(1/16)         | Did not segregate-NP      | PPbbcc                                      |

\*P: Anthocyanin pigmented plants; NP: Non-pigmented plants

from common ancestors. Based on the above fact, one can assume that the genes for anthocyanin pigmentation in both species were initially the same, but mutated spontaneously during the process of evolution that occurred under domestication of *C. arietinum*. The probable mutations of *B<sup>r</sup>* and *C<sup>r</sup>* alleles to *B* and *C* alleles might have occurred at different muton positions. The interaction and complementation among sub-products of mutant alleles leads to the production of anthocyanin pigmentation. The interpretation of complementation can be explained in such a way that each mutant allele produce a sub-product which alone is insufficient to produce anthocyanin pigmentation, but when these two sub-products interact in a common background, they complement each other to produce anthocyanin pigmentation. In both intra- and inter-specific crosses, pleiotropic action of the genes for anthocyanin pigmentation in corolla and other plant parts gave additional evidences to support the occurrence of multiple alleles for anthocyanin pigmentation in the genus *Cicer*.

Our study suggested that anthocyanin pigmentation is produced by two complementary genes in intra-specific crosses and by two duplicate genes in inter-specific crosses in the genus *Cicer*. In both cases the third gene, *P*, is present in homozygous dominant state. Further, the genes for anthocyanin pigmentation in corolla have pleiotropic effects on anthocyanin pigmentation in other plant parts, giving additional evidence of multiple alleles for both loci.

## References

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