Indian J. Genet., **66**(3): 243-244 (2006)

Short Communication

Genetics of anthocyanin pigmentation in blackgram (*Vigna mungo* L. Hepper)

Sanjeev Gupta, Shiv Kumar, B. B. Singh and Subhash Chandra

Division of Crop Improvement, Indian Institute of Pulses Research, Kanpur 208 024

(Received: July 2005; Revised: July 2006; Accepted: July 2006)

The blue-red purple coloration in hypocotyle, petiole, immature pods and adjacent plant parts in blackgram (*Vigna mungo* L. Hepper) usually results from the presence of a class of water soluble pigments i.e. anthocyanins. The genes controlling the production and distribution of anthocyanin pigments are useful marker genes. The flavonoid pathway leading to anthocyanins has been well-characterized in a number of model systems, including, maize, petunia, snapdragon and, more recently, *Arabidopsis*. Genetic characterization has been made for expression of this important plant pigment in many crops. Various workers have reported that a single dominant gene conditioned inheritance of anthocyanin pigmentation in different crops like, cowpea, mungbean, linseed etc. However, the anthocyanin in hypocotyls of mungbean was found to be controlled by two supplementary genes with recessive epistatic interaction [1]. The present study aims at study of inheritance of anthocyanin pigmentation on different plant parts of blackgram.

The experimental material comprised, two accessions of blackgram showing high anthocyanin expression , i.e. PLU 710 and NP 21 and one accession IC 8219 with light green foliage having no expression of anthocyanin pigmentation. Crosses were made among different types during rainy season of year 2001. F_1 seeds along with those of parents were grown in 2002, and seeds for F_2 population were obtained. These seeds were grown again to get F_3 population during rainy season of 2003. The observations were made in F_3 population during rainy season of year 2004. The chi-square test (χ^2) was used to study the genetics of anthocyanin pigmentation, as suggested by Snedecor and Cochran [2], as follows:

$$\chi^2 = \frac{(F_0 - F_E)^2}{F_E}$$

Where, F_0 = Observed Frequency and F_E = Expected Frequency.

The heterogeneity test was applied to the results of the chi-square test for the different populations studied to check the consistency of the results for each population as suggested by Mather [3].

The results showed that from the crosses involving parents with and without anthocyanin pigmentation expressed anthocyanin pigmentation on hypocotyls, petiole, peduncle and immature pods in F_1 plants. The absence of deviants in the F_1s during *kharif* 2002 indicated either possible absence of natural crosses or dominant expression of anthocyanin pigmentation which was likely governed by a dominant allele. The observed and expected data on segregation of the F_2 population for presence or absence of pigmentation were shown in Table 1. The segregation data indicates that there is complete dominance of expression of anthocyanin pigmentation in most of the parts studied except on immature pods only in a cross involving PLU 710 as a parent. The dominance expression in the population was so because the supposed heterozygotes segregated in the F_2 generation in a ratio that is consistent with monogenic ratio of 3:1. The F_3 progenies of crosses showed 1 homozygous with anthocyanin expression : 2 segregating: 1 homozygous without anthocyanin expression (Table 2). The chi-squares were non-significant for F_2 (Table 1) as well as F_3 (Table 2) populations except for immature pods in a cross PLU 710/ IC 8219 only, where chi-square value for F_2 was significant. This indicates that the proposed null hypothesis was accepted for all cases except in one case. All the F_2 plants from a cross, NP 21 × PLU 710, where both the parents having anthocyanin pigmentation on all the parts, expressed presence of anthocyanin pigmentation. The absence of segregation for without pigmentation in this cross, both in F_2 and F_3 families indicated that the anthocyanin gene in both the parents are allelic and at the same locus.

From the present study it is concluded that inheritance of anthocyanin pigmentation on different

Table 1. Segregation for anthocyanin pigmentation in F_2 population of inter-varietal crosses of blackgram observed in different plant parts

Tested population	Observation	Values
Hypocotyl		
NP 21 / IC 8219	Anthocyanin pigmentation	116
	No Expression	34
	χ^2 value (3:1)	0.434
	Probability	0.50-0.70
PLU 710/ IC 8219	Anthocyanin pigmentation	86
	No expression	28
	χ^2 value (3:1)	0.012
	Probability	0.90-0.95
Petiole		
NP 21 / IC 8219	Anthocyanin pigmentation	122
	No expression	28
	χ^2 value (3:1)	3.20
	Probability	0.05-0.10
PLU 710/ IC 8219	Anthocyanin pigmentation	91
	No expression	23
	χ^2 value (3:1)	1.414
	Probability	0.20-0.30
Immature Pods		
NP 21 / IC 8219	Anthocyanin pigmentation	117
	No expression	33
	χ^2 value (3:1)	0.720
	Probability	0.30-0.50
PLU 710/ IC 8219	Anthocyanin pigmentation	100
	No expression	14
	χ^2 value (3:1)	9.836*
	Probability	0.005-0.01
Peduncle		
NP 21 / IC 8219	Anthocyanin pigmentation	106
	No expression	44
	χ^2 value (3:1)	1.501
	Probability	0.20-0.30
PU 710/ IC 8219	Anthocyanin pigmentation	92
	No expression	22
	χ^2 value (3:1)	1.976
	Probability	0.10-0.20

*value for significance of p = 0.05 is 3.84

plant parts of blackgram appeared to be monogenic, with anthocyanin presence dominant over absence. In a report the anthocyanin pigmentation on hypocotyls, stem, petiole and peduncle of blackgram was reported to be controlled by a dominant gene [4]. The present finding is an agreement with this report. Further, various reports revealed that the expression of anthocyanin pigmentation was found dominant over absence in mungbean [5, 6].

The exception to above conclusion occurred in one of the eight cases with different parent PLU 710, where there was an excess of plants in F_2 progeny

Table 2. Frequencies of F_3 lines in response groups for anthocyanin pigmentation in various crosses of blackgram

Cross	Number of F_3 lines			χ^2 (1:2:1)	
	Homozygous with Anthocyanin expression	Segregating	Homozygous with no expression	Value*	Prob.
Hypocotyl					
NP 21/ IC 8219	10	28	12	0.880	0.50-0.70
PLU 710/ IC 8219	10	21	12	0.209	0.90-0.95
Petiole					
NP 21/ IC 8219	13	28	9	1.360	0.50-0.70
PLU 710/ IC 8219	9	23	11	0.395	0.80-0.90
Immature pods					
NP 21/ IC 8219	10	27	6	3.558	0.10-0.20
PLU 710/ IC 8219	11	32	7	4.560	0.10-0.20
Peduncle					
NP 21/ IC 8219	11	30	9	2.160	0.30-0.50
PLU 710/ IC 8219	11	23	9	0.395	0.80-0.90

*value for significance of p = 0.05 is 5.99

with anthocyanin pigments on immature pods. This may be due to rare occurrence of a second major dominant gene for anthocyanin expression, or meiotic irregularity in this particular cross. On further analysis of F_3 population of this particular cross revealed that homozygous lines with anthocyanin expression were 1.5 times excess than homozygous lines with no expression. However, segregating lines were having the composition of plants with and without anthocyanin expression very close to the ratio of 3:1. This supports the hypothesis that anthocyanin production is controlled by a single dominant gene. In order to conform to *Vigna* gene nomenclature rules, the gene symbol *Ant* is proposed for anthocyanin expression in blackgram.

References

1. **Mukherjee A. and Pradhan K.** 2002. Genetics of mungbean: I. Anthocyanin pigment in hypocotyl. J. Interacad, **6**: 434-437.
2. **Snedecor G. W. and Cochran W. G.** 1989. Statistical Methods. 8th Edition Ames Iowa State University Press, USA, 107-130.
3. **Mather J.** 1957. The measurement of linkage in heredity. Butler and Tanner Ltd., London, pp. 149.
4. **Apparao S. and Jana M. K.** 1973. Inheritance of anthocyanin coloration in *Phaseolus* mutants. Proceedings of Indian Science Congress Association, **60**: 302.
5. **Dwivedi S. and Singh D. P.** 1986. Inheritance of purple pigmentation and seed colour in greengram. Crop Improv., **13**: 63-66.
6. **Virk D. S. and Sharma M. M.** 1977. A dominant mutation in *Vigna radiata* var. *radiata*. Crop Improv., **4**: 115-116.