

Genetics of Seed Colour and Pod Colour in Greengram (*Vigna radiata* L. Wilczek).

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ABSTRACT: An investigation was worked out at experimental Research Farm of Agricultural Research Station, Badnapur during *Kharif*, 2022 to study the genetic pattern of seed coat colour and pod colour and their joint segregation pattern in F₁, F₂, BC₁ and BC₂ of two crosses among three parents which differed for these traits. The seed colour determines the seed quality as well as market value. The analysis for inheritance studies for crosses having green x yellow seedcoat and black x yellow pod parental combination showed green seedcoat, black pod colour dominant over yellow seedcoat and yellow pod respectively. The joint segregation test for seedcoat colour and pod colour in F₂ and backcrosses revealed independent segregation to each trait and may advances to use as morphological markers individually for different genetic studies as well as to estimate rate outcrossing in greengram. The seedcoat colour and pod colour exhibited monogenic control which can be further used to exploit in mungbean improvement programme.

Keywords: Mungbean, inheritance, seedcoat colour, monogenic, dominance, joint segregation.

INTRODUCTION

Greengram (*Vigna radiata* (L.) Wilczek.) is an important daily diet based legume crop, usually consumed for sprouting purpose constituting (25%) protein. Polymorphic monogenic traits were the most prolific earlier markers employed for scientific investigations and seedcoat colour is one of the important morphological marker being used for genetic studies and varietal identification. Although morphological marker has limitation in nature but many exhibit genetic associations with economically valuable and agronomically relevant traits which facilitates the streamline for development of new varieties Chesnokova *et al.* (2020) and their assays still assisted in unadorned manner, rapid and inexpensive to score in genetic, breeding programmes and plant germplasm management. (Ghafoor, 1999; Singh and Singh, 1992). Now a days, in various varietal development programme, the identification of different genetic markers by a breeder has become an interest and accessing inheritance pattern have superabundant significance in hybridization. Furthermore, in the Philippines, only the shining yellow seedcoat varieties command at higher price than green seeded one. However, Indian consumers usually prefer green smooth shining seeds. Many authors (Chhabra *et al.* 1990; Khattak *et al.* 1998; Akhtar *et al.* 1988; Chen and

Liu 2001; Lambridges *et al.* 2004; Wang *et al.* 2013, Singh *et al.* 2016; Mau *et al.* 2023) have previously reported the inheritance studies in greengram for various qualitative traits including seedcoat colour. However, in contrast, information on genetic basis of seed coat colours is limited, contradictory and not fulfilled wisdom. Keeping the above facts in mind, the present investigation was attempted to examine the mode of inheritance of seedcoat and pod colour and linkage between these two traits. The information obtained may facility to use these morphological markers for various breeding programme in greengram

MATERIALS AND METHODS

Two mungbean cultivated varieties *viz.* BM 4 and Kopergaon as female parent and pure homozygous breeding line BM 2019-12 as male parent (Table 1) and their two crosses were used in the present study. The material consisting of F₁, F₂ and backcross population was grown at Research farm of Agricultural Research Station, Badnapur during *kharif* 2022. The material was planted 45 cm apart and planted to plant 10 cm. Visual observations of F₁, backcrosses and segregating population for seedcoat colour and pod color was recorded at plant maturity stage. For the linkage studies of seedcoat colour and pod colour, plants were counted on the basis of green seedcoat with black pod, (GSBP), green seed with yellow pod (GSYP), yellow seed with

black pod (YSBP) and yellow seed with yellow pod (YSYP). Statistical distribution of phenotypic classes of contrast cross combinations were subjected to test goodness of fit in F₂ (Panse and Sukhatme 1985) and tested in different gene pair model hypotheses. The confirmation of ratios obtained in F₂ segregating populations was done by the ratios obtained in backcrosses. While applying χ^2 test correction was made as suggested by Yates (1934).

$$\chi^2 = \sum \frac{(O - E)^2}{E}$$

$$X^2_{\text{Yates}} = \sum \frac{(|O - E| - 0.5)^2}{E}$$

Where,
O = Observed value
E = Expected value

Table 1: Botanical descriptors of parents used for inheritance study.

Parents	Source	Seed colour	Pod colour
Female			
BM 4	ARS, Badnapur	Green	Black
Kopergaon	MPKV, Rahuri	Green	Black
Male			
BM 2019-12	ARS, Badnapur	Yellow	Yellow

RESULTS AND DISCUSSION

Under the investigation for seed coat colour, female parents *viz.* BM 4 and Kopergaon showed green seed coat while male parent BM 2019-12 had yellow seedcoat. As a result seedcoat colour of all F₁ plants of both crosses (BM 4 × BM 2019-12 and Kopergaon × BM 2019-12) having green × yellow parent cross combinations produced green seedcoat indicated dominant behavior of green over yellow seedcoat (Table 2 and Fig. 1). The result showed two phenotypic classes of seedcoat colour in F₂ and backcross population. Thus two hypotheses of inheritance of seedcoat colour trait were proposed in which the one gene pair hypothesis was 3:1 followed segregation ratio of 9:7, 15:1, 13:1 for green and yellow seedcoat colour. The X² analysis results showed that for the crosses *viz.* BM 4 × BM 2019-12 and Kopergaon × BM 2019-12, the calculated chi square was (X²=2.25, P=0.13; X²=0.15, P=0.69) which was not significantly different from the 3:1 segregation ratio. In contrast the calculated X² for the two gene pair segregation ratio i.e. 11.23, 151.30, 13.32 and 16.50, 96.06, 5.37 respectively, were significantly different from the seed coat colour segregation pattern hypothesis of 9:7, 15:1 and 13:1 in both the crosses. Thus, the result revealed that the seedcoat colour segregation pattern in the F₂ and BC² population of cross BM 4 × BM 2019-12 and Kopergaon × BM 2019-12 score also fit the expected 3:1 and 1:1 seed colour revealed monogenic control for this trait and could be easily exploited in mungbean improvement. Similar dominance nature of green over yellow in mungbean have been earlier addressed by Murty and Patel (1973); Chen *et al.* (2001); Khattak (1998); Wang *et al.* (2013); Han *et al.* (2017) and Singh *et al.* (2016). Similarly, inheritance for crosses having

contrast black × yellow pod combination (BM 4 × BM 2019-12 and Kopergaon × BM 2019-12) exhibited black pod colour in F₁ plants revealed dominance for black pod colour, whereas yellow pods being recessive in mungbean ((Table 3). The F₂ population segregated in a 3:1 and 1:1 ratio of cross BM 4 × BM 2019-12 (X²=0.14, P=0.70; X²=0.15, P=0.69) and Kopergaon × BM 2019-12 (X²=1.41, P=0.23; X²=1.63, P=0.20) in both the crosses which fit for goodness by X² method indicated monogenic inheritance for this character. Khattak (2002) and Arshad *et al.* (2005) reported similar monogenic pattern in black × brown pod colour of blackgram while, Han *et al.* (2017) noted two dominant genes with suppressive action for black pod in brown × black pod colour in greengram.

Joint segregation of seedcoat colour and pod colour in mungbean:

The F₁ and backcross data of BM 4 × BM 2019-12 and Kopergaon × BM 2019-12 crosses have been summarized for linkage study of seedcoat and pod colour in (Table 4). The F₂ population of crosses *viz.* BM 4 × BM 2019-12 and Kopergaon × BM 2019-12 gave ratio of 9-green seed Black pod: 3 green seed yellow pod:3 yellow seed black pod: 1 yellow seed yellow pod for seedcoat and pod colour. The backcross of the same cross involving BM 2019-12 segregated in the ration 1:1:1:1 for the same four phenotypic classes as mentioned f₂ population of same crosses. The results obtained from BM 4 × BM 2019-12 and Kopergaon × BM 2019-12. gave a good fit to the expectation of and 9:3: 3:1 ratio in F₂ 1:1:1: in backcrosses clearly indicated that seedcoat colour and pod colour had no linkage and deviated from linked genes manifesting both characters assorted/segregated independently.

Table 2: Breeding behavior of F₁, F₂ and backcross population in green x yellow seedcoat cross combinations.

Hypotheses	Generation	Observed		Expected		Total Plants	X ²	P
		Green seed	Yellow seed	Green seed	Yellow seed			
BM 4 x BM 2019-12	F ₁	All	-	-	-	14	-	-
One gene								
3:1	F ₂	106	46	114	38	152	2.25 ^{ns}	0.13
Two genes								
9:7	F ₂	106	46	85.42	66.42	152	11.23*	0.00
15:1	F ₂	106	46	142.5	9.42	152	151.30*	8.98
13:3	F ₂	106	46	123.42	28.42	152	13.32*	0.00
Test crosses								
1:1								
(F ₁) x BM 4	BC ₁	All	00	-	-	20	-	-
(F ₁) x BM 2019-12	BC ₂	16	10	13	13	26	1.38 ^{ns}	0.23
Kopergaon x BM 2019-12	F ₁	All	-	-	-	18	-	-
One gene								
3:1	F ₂	100	36	102	34	136	0.15^{ns}	0.69
Two genes								
9:7	F ₂	100	36	76.43	59.43	136	16.50*	4.85
15:1	F ₂	100	36	127.5	8.43	136	96.06*	1.11
13:3	F ₂	100	36	110.43	25.43	136	5.37*	0.02
Test cross								
1:1								
(F ₁) x Kopergaon	BC ₁	All	00	-	-	24	-	-
(F ₁) x BM 2019-12	BC ₂	12	10	11	11	22	0.18^{ns}	0.66

Table 3: Breeding behavior of F₁, F₂ and backcross population in black x yellow pod colour cross combinations.

Hypotheses	Generation	Observed		Expected		Total Plants	X ²	P
		Black pod	Yellow pod	Black pod	Yellow pod			
BM 4 x BM 2019-12	F ₁	All	-	-	-	14	-	-
One gene								
3:1	F ₂	112	40	114	38	152	0.14 ^{ns}	0.70
Two genes								
9:7	F ₂	112	40	85.42	66.42	152	18.77*	1.46
15:1	F ₂	112	40	142.5	9.42	152	105.73*	8.44
13:3	F ₂	112	40	123.42	28.42	152	5.77*	0.01
Test crosses								
1:1								
(F ₁) x BM 4	BC ₁	All	00	-	-	20	-	-
(F ₁) x BM 2019-12	BC ₂	14	12	13	13	26	0.15 ^{ns}	0.69
Kopergaon x BM 2019-12	F ₁	All	-	-	-	18	-	-
One gene								
3:1	F ₂	96	40	102	34	136	1.41^{ns}	0.23
Two genes								
9:7	F ₂	96	40	76.43	59.43	136	11.36*	0.00
15:1	F ₂	96	40	127.5	8.43	136	125.96*	3.12
13:3	F ₂	96	40	110.43	25.43	136	10.237*	0.00
Test cross								
1:1								
(F ₁) x Kopergaon	BC ₁	All	00	-	-	24	-	-
(F ₁) x BM 2019-12	BC ₂	14	8	11	11	22	1.63^{ns}	0.20

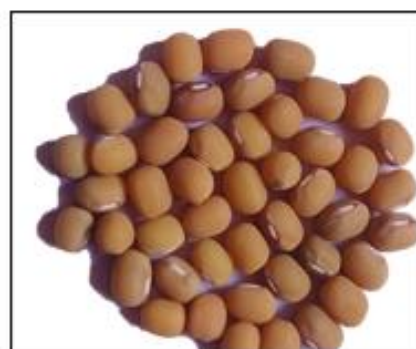
Table 4: Joint segregation of seedcoat colour and pod colour in mungbean using F₂ and backcross generation.

Cross combinations	Generation	Expected ratio	GSBP	GSYP	YSBP	YSYP	Total Plants	X ²	P
BM 4 x BM 2019-12	F ₂	9:3:3:1	78	28	34	12	152	2.44	0.48
(F ₁) x BM 2019-12	BC ₂	1:1:1:1	8	8	6	4	26	1.69	0.63
Kopergaon x BM 2019-12	F ₂	9:3:3:1	70	30	26	10	136	1.66	0.64
(F ₁) x BM 2019-12	BC ₂	1:1:1:1	7	5	7	3	22	2.00	0.57

GSBP-Green seed Black pod, GSYP -Green seed Yellow pod, YSBP -Yellow seed Black pod, YSYP -Yellow seed Yellow pod.



BM 4



BM 2019-12



F₁
(BM 4 x BM 21-21)



F₂



F₂

Fig. 1. Representative examples illustrating degree of expression of BM 4 x BM 2019-12 for seedcoat colour in mungbean

CONCLUSION

In conclusion the seedcoat and pod colour in cross BM 4 x BM 2019-12 and Kopergaon x BM 2019-12 was found under control of dominant gene with monogenic gene action. The monogenic control of these traits can be used to exploit in mungbean improvement programme.

FUTURE SCOPE

Information based on this investigation would facilitate to incorporate these traits for genetical studies, to estimate rate of outcrossing in mungbean and use as genetic/morphological markers individually for identification of varieties/F₁ hybrid in mungbean breeding programmes.

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Conflict of Interest. None.

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