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Inheritance of Seed Coat Colour in Mung Bean[1]

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ABSTRACT

The action of the genes governing the mosaic seed coat colour of mung bean *Vigna radiata* (L) Wilczek has been worked out by using five sets of crosses involving parents having black, green, dark green mosaic, light green mosaic and dark yellow mosaic seeds. Four gene pairs (B, M, Br and G) were involved, B–M–brbr G– and bbM–Br–G genotypes produced dark green mosaic and light green mosaic seed coat colours respectively, whereas genotypes B–M–brbrgg and bbM–Br–gg produced dark yellow mosaic and light yellow mosaic seed coat colours respectively.

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INTRODUCTION

Mung bean (*Vigna radiata* (L.) Wilczek is a short duration pulse crop of Indian sub-continent valuable for its protein rich grain and also as a rich fodder. Murty and Patel (1972) investigated the inheritance of seed coat colour of mung and hypothesized four (**B, M, Br** and **G**) gene pairs. Factors **B–M–Br** or **B–G–** interacted to produce black seeds, while factor **B** in absence of **M, Br** and **G** also produced black seed coat colour. Factors **B** and **M** in absence of **Br**; and factors **Br** and **M** in absence of **B** interacted to produce mosaic seed coat, it being green mosaic with **G–** genetic background and yellow mosaic with **gg** genetic background with respect to **G** locus. Factors **B** and **Br** in absence of **M** interacted and produced brown seeds in presence of **G–** and amber colour in **gg** genetic background. **G–** and **gg** produced green and yellow seed coats respectively in absence of **B, M** and **Br**. Individually factors **M** and **Br** had no effect. Variation in the intensity of masaic colour though observed by these workers, was not taken into consideration. The present study was taken-up to investigate further the genetics of mosaic seed coat colour intensities.

MATERIALS AND METHODS

Five strains A.101-4, T.44, S.293-3, S.293-1 and S.62 having black, green, dark green mosaic (DGM), light green mosaic (LGM) and dark yellow mosaic (DYM) seed coat colours respectively were used in this study. The first two strains are common between previous

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TABLE 1

The parentage and the genetic constitution of the crosses used in the present study.

Cross No.	*Parentage*	*Presumed genotypes of the parents*
1	S. 293-3 × A. 101-4	*BBMMbrbrGG × BBMMBrBrGG*
2	S. 293-3 × T. 44	*BBMMbrbrGG × bbmmbrbrGG*
3	S. 293-3 × S. 293-1	*BBMMbrbrGG × bbMMBrBrGG*
4	S. 293-3 × S. 62	*BBMMbrbrGG × BBMMbrbrgg*
5	S. 293-1 × S. 62	*bbMMBrBrGG × BBMMbrbrgg*

(Murty and Patel, 1972) and present studies, the third and fourth strain are the derivatives of A.101-4×T.44 cross, and S.62 is the true breeding derivative of A.101-4×Sonamung cross selected from the previous study. The mature dry seeds of individual plants of the parents, F_1, F_2 and backcross populations of various crosses mentioned in Table 1 were visually examined for this purpose.

The experimental material was grouped into five sets each comprising of six entries of an individual cross in different generations. Each set was grown in a randomized block design replicated four times. A single replication had one row each of parents, F_1 and backcross generations, and three rows of F_2 population. There were 10 dibbles in a row, the inter and intra-row spacing being 60 cm. The study was conducted during monsoon 1971.

RESULTS AND DISCUSSION

The data pertaining the F_1, F_2 and backcrosses of the five crosses presented in Table 2 revealed that four gene pairs (**B,M,Br** and **G**) hypothesized by Murty and Patel (1972) were involved in the expression of seed coat colour. According to their hypothesis described earlier, factors **B** and **M** in presence of **brbr**, or factors **M** and **Br** in presence of **bb** interacted to produce mosaic seeds, the intensity of mosaic, however, was not differentiated by them. The present findings revealed that the **B–M–brbr** genotype produced dark mosaic seeds, while the **bbM–Br–** genotype produced light mosaic seed coat colour plants, they being green and yellow respectively in **G–** and **gg** genetic backgrounds.

According to the above hypothesis, the F_1 plants of the cross involving DGM (**BBMMbrbrGG**) and black (**BBMM BrBrGG**) seeded parents, will have black (**BBMMBrbrGG**) seed coat colour, while the F_2 population will segregate into two classes in the proportion of 3 black (**BBMMBr–GG**) : 1 DGM (**BBMM brbrGG**) seeded plants. The BC_1 population of the above cross involving DGM as the recurrent parent will have equal proportion of black (**BBMMBrbrGG**) and DGM (**BBMMbrbrGG**) seeded plants, while BC_1 population involving A.101-4 (black) as the recurrent parent will comprise only black (**BBMMBr–GG**) seeded plants. The data presented in Table 2 support this assumption.

The second cross involving DGM (**BBMMbrbrGG**) and green (**bbmm

brbrGG) seed coat colour lines as the parents will have DGM (**BbMmbrbrGG**) seeded F_1 plants. The F_2 generation will segregate into DGM (**B–M–brbrGG**), black (**B–mmbrbrGG**) and green (**bb M–brbrGG/bbmmbrbrGG**) seeded plants in the proportion of 9:3:4 respectively. The BC_1' population involving T.44 (green) as the recurrent parent will segregate into 1 DGM (**BbMmbrbrGG**), 1 black (**BbmmbrbrGG**) and 2 green (**bbMmbrbrGG** and **bbmmbrbrGG**) seeded plants, while the BC_1 population having S.293-3 (DGM) as the recurrent parent will comprise DGM (**B–M–brbr GG**) seeded plants only. This hypothesis is also supported by the data presented in Table 2.

The third cross **BBMMbrbrGG** (DGM) × **bbMMBrBrGG** (LGM) will have the F_1 plants with black (**BbMM BrbrGG**) seed coat colour. The F_2 population will segregate into 9 black (**B–MMBr–GG**): 3 DGM (**B–MMbr brGG**): 3 LGM (**bbMMBr–GG**): 1 green (**bbMMbrbrGG**) seeded plants. The BC_1 population involving S.293-3 (DGM) as the recurrent parent will segregate into equal proportion of black (**B–MMBr–GG**) and DGM (**B–MMbr brGG**) seeded plants, while the BC_1' population having S.293-1 (LGM) as the recurrent parent will have equal proportion of black (**BbMMBr–GG**) and LGM (**bbMMBr–GG**) seeded plants. The data presented in Table 2 are in agreement with this hypothesis.

TABLE 2

Breeding behaviours of the F_1 F_2 and backcross generations of various crosses.

Cross No.	*Generation of crosses*	*Expected ratio*	*Observed value* Black	DGM	LGM	Green	DYM	LYM	Yellow	*Chi-square value*	*P-value*
1	F_1 (S. 293-3 × A. 101-4)		37								
	F_2 (S. 293-3 × A. 101-4)	3:1	66	20						0·139	0·50-0·75
	BC_1 (S. 293-3 × F_1)	1:1	20	17						0·243	0·50-0·75
	BC_1' (A. 101-4 × F_1)		33								
2	F_1 (S. 293-3 × T. 44)			33							
	F_2 (S. 293-3 × T. 44)	3:9:4	16	51		29				1·430	0·25-0·50
	BC_1 (S. 293-3 × F_1)			34							
	BC_1' (T. 44 × F_1)	1:1:2	12	10		17				0·846	0·50-0·75
3	F_1 (S. 293-3 × S. 293-1)		38								
	F_2 (S. 293-3 × S. 293-1)	9:3:3:1	61	22	24	5				1·111	0·75-0·90
	BC_1 (S. 293-3 × F_1)	1:1	21	16						0·676	0·25-0·50
	BC_1' (S. 293-1 × F_1)	1:1	19		16					0·257	0·50-0·75
4	F_1 (S. 293-3 × S. 62)			38							
	F_2 (S. 293-3 × S. 62)	3:1		83			32			0·490	0·25-0.50
	BC_1 (S. 293-3 × F_1)			38							
	BC_1' (S. 62 × F_1)	1:1		15			19			0·471	0·25-0·50
5	F_1 (S. 293-1 × S. 62)		37								
	F_2 (S. 291-1 × S. 62)	36:9:9:3:3:3:1	60	12	15	3	4	6	2	1·738	0·90-0·95
	BC_1 (S. 293-1 × F_1)	1:1	12		11					0·043	0·75-0·90
	BC_1' (S. 62 × F_1)	2:1:1	19	9			10			0·053	0·75-0·90

The F_1 plants of the fourth cross viz. S.293-3 (**BBMMbrbrGG**) × S.62 (**BBMM brbrgg**) will have DGM (**BBMMbrbr Gg**) seeds, whereas the F_2 population will segregate into two classes in the proportion of 3 DGM (**BBMMbrbrG–**): 1 DYM (**BBMMbrbrgg**) seeded plants. The BC_1 population involving S.293-3 (DGM) as the recurrent parent will have all plants with DGM (**BBMMbrbrG–**) seeds, while the BC_1' population involving S.62 (DYM) as the recurrent parent will have equal proportion of DGM (**BBMMbrbrGg**) and DYM (**BBMM brbrgg**) seeded plants. The observed data (Table 2) are in agreement with the proposed hypothesis.

The fifth cross **bbMMBrBrGG** (LGM) × **BBMMbrbrgg** (DYM) will have the F_1 plants with black (**BbMM BrbrGg**) seed coat colour. The F_2 population will segregate into 36 black (**B–MMBr–G–** and **B–MMBr–gg**): 9 DGM (**B–MMbrbrG–**): 9 LGM (**bb MMBr–G–**): 3 DYM (**B–MMbrbrgg**): 3 LYM (**bbMMBr–gg**): 3 green (**bb MMbrbrG–**): 1 yellow (**bbMMbrbr gg**) seeded plants (Table 2). The yellow mosaic seeds, like green mosaic seeds, were of dark and light intensities suggesting that the **B–M–brbr** interacted with **gg** to produce dark yellow mosaic, while the **bbM–Br–** interacted with **gg** to produce light yellow mosaic seed coat colour. These findings indicated that the genotypes **B–M–brbr** produced dark mosaic, while **bbM–Br–** genotype produced light mosaic seeds. In **G**–background **B–M–brbr** and **bbM–Br–** gene combinations produced dark and light green mosaic seeds respectively, while in **gg** background these genotypes produced dark and light yellow mosaic seed coat colour respectively. The data of BC_1 and BC_1' populations (Table 2) are in agreement with this hypothesis. The yellow mosaic seeds of the F_2 and BC_1' generations of the cross S.293-3 (DGM) × S.62 (DYM) were of dark intensity (**BBMMbrbrgg**). This finding is also in line with the proposed hypothesis.

The digenic inheritance of the mung seed coat colour has been reported by Bose (1939) and Rheenen (1965). Sen and Ghosh (1959) ascribed three gene pairs, while Murty and Patel (1972) assigned four gene pairs (B, M, Br and G) for the expression of this trait. The present findings are in confirmity with the findings of Murty and Patel (1972) and further revealed that gene combinations **B–M–brbr** and **bbMMBr–** had differential expression for mosaic intensity, the former combination produced dark mosaic, while the latter combination produced light mosaic seeds. The green base to mosaic intensities was provided by **G**–genotype, and yellow base was due to **gg** background.

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