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Full Length Research Paper

Segregation of genes controlling seed colour in sesame (*Sesamum indicum* linn.) from Nigeria

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Genetic analysis of seed colour was carried out on crosses involving nine accessions of Sesame (*Sesamum indicum* L.) from Nigeria. Inheritance studies showed that different gene actions were responsible for the expression of this important character. In three of the crosses, single gene action was observed, while in two others, the trait was under the control of two genes. In the sixth cross, involving white and black parents, an array of white, black, brownish white and brown colours were observed in the F_2. The variation in gene systems controlling seed colour expression observed in this study revealed the complex nature of the expression of this trait. Results also indicated that plants with the same seed colour might be under different genotype constitution.

Key words: Genetic *analysis,* Sesamum indicum*, accessions, genesystems, genotype constitution.*

INTRODUCTION

Sesame (*Sesamum indicum* L.) is an important oil-seed crop grown in Nigeria. It is commonly known as beniseed. The plant belongs to the family Pedaliaceae and genus *Sesamum*. It originated from tropical Africa and was taken at an early stage to India where it was domesticated and became a crop of the New World (Ashri, 1995). The seeds are rich in high-grade edible oil, which is used for many different purposes. Traditionally, the seeds are roasted and mixed together with roasted groundnut or used as soup-thickening condiment (Falusi and Salako, 2001). Sesame is an annual herbaceous food and oil-seed crop of international importance (Raw Materials Update, 2001). The crop is widely grown in northern and central Nigeria between latitudes 7 – 14°N and an annual rainfall of about 1000 – 1500 mm (Iwo, et al., 2005).

Critical investigations on the inheritance pattern of the crop have been few. Van Rheenen (1970) studied the inheritance of colour of petiole and colour of nectary in local *S. indicum* L. and reported that the mode of inheritance of these characters was monogenic. Falusi (2000) also reported a similar monogenic inheritance in hairiness of stem and petiole in interspecific cross between *S. indicum* L, and *S. prostratum* L. The seed colour is a major trait that affects consumer's acceptability. Paltak and Dixit (1992) reported that the consumer's preference for this trait differs from region to region. This present study is therefore aimed at understanding the gene systems operating in the expression of seed colour in Nigerian sesame.

MATERIALS AND METHODS

The materials used in this study were collected by Falusi and Salako (2001) and maintained by several generations of selfing at National Cereals Research Institute Badeggi, Nigeria. To confirm that they were homozygous lines, a greenhouse evaluation was done and no segregation was observed in each line. The lines in relation to the characters studied are as follows: -

NSG -01	-	white Seeds
NSG-02	-	Black Seeds
NSG-03	-	Brown Seeds
NSG-04	-	Brown Seeds
NSG-05	-	White Seeds
NSG-06	-	Brownish Black Seeds
NSG-07	-	Brown Seeds
NSG-08	-	Brownish White Seeds
NSG-09	-	Yellowish white Seeds

They were combined in the following crosses

NSG-01	X	NSG-02
NSG-01	X	NSG-06
NSG-01	X	NSG-08
NSG-01	X	NSG-07
NSG-03	X	NSG-09
NSG-04	X	NSG-05

Table 1. NGS-01 X NGS -02.Observed no. of plants.

Generation	Black	White	Brownish black	Brown	Total
NGS-01	0	25	0	0	25
NGS -02	40	0	0	0	40
F1	35	0	0	0	35
NGS -01 X F1	80	70	0	0	150
NGS -02XF1	60	0	0	0	60
F2	140	60	5	10	215

Table 2. Observed number of plants in NGS-01 X NGS-06.

Generation	Brownish black	White	Total	Expected ratio	X^2
NGS-01	0	25	25		
NGS -06	50	0	50		
F1	70	0	70		
NGS -01 X F1	75	65	140	1:1	0.714
NGS -06XF1	60	0	60		
F2	120	32	152	3:1	1.263

Table 3. Observed number of plants in NGS-01 X NGS-08.

Generation	White	Brown	Brownish white	Total	Expected ratio	X^2
NGS-01	30	0	0	30		
NGS -08	0	0	45	45		
F1	0	0	50	50		
NGS -01 X F1	65	10	41	116		
NGS -08XF1	0	0	55	55		
F2	70	10	85	165	6:1:9	1.733

Crosses to produce F1 and backcross seeds were made in the green house. To produce F2 seeds, a proportion of F1 seeds were sown in the field. They were maintained to maturity and capsules were harvested from them. Field evaluation was carried out for different generations. The design used for the planting was a randomized complete block with four replications. Spacing was 50 cm within row and 80 cm between rows. Each row has 10 m long. Visual observation was used to classify seeds into alternate classes. The chi-square method was used to test for the goodness of fit to the proposed segregation ratio.

RESULTS AND DISCUSSION

When NGS-O1 (a white seeded line) was crossed to NGS-02 (a black seeded line), the F1 progenies produced seeds, which were black (Table 1). The backcross progenies of the F1 to NGS- 02 parents produced black seeds. However, when the F1 were backcrossed to NGS-01 parent, they produced progenies with black seeds and white seeds in a 1:1 ratio. The F2 progenies on the other hand produced four classes of brownish black. The cross between NGS-01 (a white seeded line) and NGS-06 (a brownish black seeded line) produced F1 seeds, which were brownish black in colour (Table 2). In the F2, the Chi-square value obtained showed a good fit to support the observed 3 brownish black : 1 white ratio suggesting single gene inheritance of the brownish black seed colour. For the cross between NGS-01 (a white seeded line) and NGS-08 (a brownish white seeded line), the F1 offsprings produced brownish white seeds like NGS -08 parent. The backcross progenies of the F1 to the white seeded parent gave three classes of seed colours, white, brown and brownish white (Table 3). These three classes were also obtained in the F2 in the ratio that fit the 9 brownish white : 6 white : 1 brown epistatic ratio.

In the cross between NGS-01 (a white seeded parent) and NGS-07 (a brown seeded parent), the F1 progenies were brown seeds (Table 4). The chi-square test of goodness of fit of both backcross and F2 progenies gave satisfactory fit to the 1 brown : 1 white and 3 brown : 1 white ratios respectively suggesting single gene inheritance with brown colour dominant over white colour. For the cross between NGS-03 (a brown seeded parent) and NGS-09 (a yellowish white seeded parent) the F1 progenies produced seeds, which are yellowish white like

Table 4. Observed number of plants in NGS -01 X NGS-07.

Generation	Brown	White	Total	Expected ratio	X^2
NGS-01	0	25	25		
NGS -07	60	0	60		
F1	82	0	82		
NGS -01 X F1	107	85	192	1:1	2.530
NGS -07XF1	122	0	122		
F2	130	45	175	3:1	0.054

Table 5. Observed number of plants in NGS -03 X NGS-09.

Generation	Brown	Yellowish white	Total	Expected ratio	X^2
NGS-03	42	0	42		
NGS -09	0	38	38		
F1	0	65	65		
NGS -03 X F1	70	22	92	3:1	
NGS -09XF1	0	62	62		
F2	85	115	200	7:9	0.126

Table 6. Observed number of plants in NGS -04 X NGS-05.

Generation	Brown	White	Total	Expected ratio	X^2
NGS-04	40	0	40		
NGS -05	0	36	36		
F1	45	0	45		
NGS -04 X F1	75	0	75		
NGS -05XF1	60	64	124	1:1	0.129
F2	115	35	150	3:1	0.222

NGS-09 parent (Table 5). When the F1 were back-crossed to NG-03 (brown seeded parent), a good fit was obtained to the 3 brown : 1 yellowish white ratio. The F2 data also gave a good fit to the 9 yellowish white : 7 brown degenic epistatic ratio with yellowish white being dominant over brown. In the cross between NGS-04 (a brown seeded parent) and NGS-05 (a white seeded parent) the F1 plants produced seeds, which had brown colour like NGS -04 Parent (Table 6).

When the F1 was backcrossed to the white seeded parent, a 1 brown : 1 white ratio was obtained. In the F2, a good fit was obtained to the 3 brown : 1 white ratio indicating a single gene inheritance of the brown seed colour, which is dominant over the white seed colour. This study revealed the existence of a wide variation in gene systems ontrolling seed colour in sesame. In three of the crosses, NGS-01 X NGS-06, NGS-01 X NGS-07 and NGS-04 X NGS-05, a single gene was found to control the trait in each cross. There was an indication that NGS-01 did not have colour genes since it would always allow any genotype crossed against it to express all their colour genes.

In the crosses NGS-01 x NGS-08 and NGS-03 X NGS-09, two complementary genes were found to be operating. In the cross NGS-01 X NGS -08, the brownish white seed colour was dominant over white colour while brown seed colour expressed in the F2 implies that the gene for brown colour was in the brownish white genotype. For NGS-01 X NGS-02 cross, four classes of colors (that is, black, white, brown, and brownish black) were recovered from the F2 generation. Since NGS-01 appeared not to carry colour gene, then it means that the brownish black and brown colour genes were present in the black genotype of NGS-02 parent, but were masked. The fact that the white colour gene was recessive to other colour genes crossed to it showed that the white colour genes occured in homozygous recessive form. The use of NGS-01 line therefore, has enabled a better understanding of seed colour inheritance in sesame.

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