

## Inheritance of Resistance to Brown Blotch Disease of Cowpea

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### Abstract

The inheritance pattern of resistance to brown blotch disease of cowpea was investigated by using crosses involving two resistant (Hope, Crimson) and two susceptible (Ife Brown, Ife Branched Peduncle) parents. The  $F_1$  data indicated that resistance was dominant over susceptibility. Segregation patterns in the  $F_2$  and backcross generations of all crosses showed a good fit to a 15 resistant: 1 susceptible ratio suggesting that two duplicate dominant genes condition resistance to brown blotch disease. Furthermore, since segregating populations of reciprocal as well as non-reciprocal crosses gave similar ratios, it was concluded that the two dominant genes which condition resistance were nuclear genes.

### Introduction

In a previous study, Obisesan et al (1988) reported the sources of resistance to the brown blotch disease caused by a fungus, *Colletotricum truncatum* (Schw). As a result of the devastating effect of brown blotch disease on general performance and grain yield, fungicide has been widely employed to curtail its spread in cowpea fields. Control of plant diseases through host plant resistance has been considered to be the safest, most effective and economical when compared to other methods (Meiners, 1981). Breeding cowpea plants for resistance to brown blotch disease should therefore be more germane particularly since it has been documented that the disease is seedborne (Emechebe, 1981; Kelani, 1984).

In any quest to breed crops for resistance to diseases, the first step is usually to identify the genes and understand the mode of inheritance of the resistant character. This information becomes very helpful in deciding on the most appropriate breeding methodology to adopt in incorporating the resistant gene(s) to the crop/variety. The objective of this study was to determine the mode of inheritance of resistance to the brown blotch disease in cowpea.

### Materials and Methods

The study was conducted using two resistant (Crimson, Hope) and two susceptible (Ife brown and Ife Branched peduncle (Ife-BPC) pure lines of cowpea. Crimson and Hope pure lines were obtained from IITA. Ife Brown was developed at the Obafemi Awolowo University and obtained from the Department of Plant Science of the University. Ife-BPC is a mutant selection from Ife Brown (Fawole et al, 1985). Reciprocal crosses were made between each of the resistant and susceptible parents. The parents,  $F_1$  and reciprocal crosses were planted in 10 litre plastic buckets

arranged in the green house. Some  $F_2$  plants of each cross were advanced to  $F_2$  generation. Another set of  $F_1$  plants from each cross and reciprocal cross were backcrossed to each of their respective parents to obtain the backcross generations. The parents and all generations ( $F_1$ ,  $F_2$ , backcross to each parent and their respective reciprocals) within a cross were inoculated with 5 day old pure culture of *Collectrichum truncatum*, the incitant of brown blotch disease.

A spore suspension was prepared by blending the pure culture in a warring blender. The suspension was strained through cheese cloth and diluted serially until a spore concentration of  $5.5 \times 10^5$  spores/ml was obtained. A Neubar Hemacytometer was used to ascertain spore concentration.

Clean seeds of parents,  $F_1$ , including reciprocals,  $F_2$  and backcrosses were planted in 4 litre buckets filled with sterilized soil. On the eighth day of planting, the soil in the pots were lightly watered and the seedlings inoculated by pouring 100 ml of spore suspension on the surface of the soil in each of the buckets containing the seedlings in the evening. There were 20 seedlings per bucket. Control pots containing the susceptible parents were not inoculated. Inoculated and control plants were placed on wet floor under the greenhouse bench for 48 hours after which they were placed on top of the greenhouse bench. Ten days after inoculation seedlings were rated usually according to the severity of symptoms as follows:-

Disease Reaction	Length of Lesion at base of stem	Disease Rating
No symptom	0 cm	Resistant
Very mild symptoms > 0.0	1.0 cm	
Mild symptoms > 1.0	2.0 cm	
Severe symptoms > 2.0	≤ 3.0 cm	Susceptible
Very severe symptoms > 3.0	≤	
	≤	

### Results and Discussion

All parents were true-breeding for resistance/susceptibility. The  $F_1$  of all crosses including reciprocals were resistant to brown blotch (Table 1). This indicates that the resistant trait is dominant over susceptibility. The  $F_2$  segregation ratios in all crosses (including their reciprocals) conformed to a 15 resistant: 1 susceptible ratio which suggests digenic inheritance. If the genotypes of the resistant parents are designated as  $R_1R_1R_2R_2$  and the susceptible ones as  $r_1r_1r_2r_2$ , then genotypes of the  $F_1$  is  $R_1r_1R_2r_2$ . The  $F_2$  generation should be made up of  $9R_1-R_2-: 3R_1-r_2r_2: 3r_1r_1R_2-: 1r_1r_1r_2r_2$ . The observed 15 resistant: 1 susceptible ratio in the  $F_2$  suggests that two duplicate dominant genes condition to the expression of the resistant character; thus  $R_1-R_2-$ ,  $R_1-r_2r_2$  and  $r_1r_1R_2-$  genotypes all exhibit the resistant phenotype.

The segregation patterns in the backcross generations were also similar in both crosses. Backcross to the susceptible parent segregated into a 3 resistant ( $R_1r_1R_2r_2; R_1r_1r_1r_2; r_1r_1R_2r_2$ ): 1 susceptible ( $r_1r_1r_2r_2$ ) ratio. All backcrosses to the

**TABLE 1: REACTIONS OF PARENET, F<sub>1</sub>S AND SEGREGATION PATTERNS OF CROSSES**

Parents/Crosses	Observed		Expected		Susceptible	X <sup>2</sup>
	Resistant	Susceptible	Resistant	Susceptible		
<b>Parents</b>						
1c Brown (P <sub>1</sub> )	0	30	0	30	0	0
1c BPC (P <sub>2</sub> )	0	30	0	30	0	0
Hope (P <sub>1</sub> )	30	0	30	0	0	0
Cinnamon (P <sub>2</sub> )	30	0	30	0	0	0
<b>F<sub>1</sub> &amp; Reciprocal F<sub>1</sub></b>						
P <sub>1</sub> x P <sub>2</sub>	30	0	30	0	0	0
P <sub>2</sub> x P <sub>1</sub>	30	0	30	0	0	0
P <sub>1</sub> x P <sub>1</sub>	30	0	30	0	0	0
P <sub>2</sub> x P <sub>2</sub>	30	0	30	0	0	0
P <sub>1</sub> x P <sub>2</sub>	30	0	30	0	0	0
P <sub>2</sub> x P <sub>1</sub>	30	0	30	0	0	0
P <sub>1</sub> x P <sub>1</sub>	30	0	30	0	0	0
P <sub>2</sub> x P <sub>2</sub>	30	0	30	0	0	0
<b>F<sub>2</sub> &amp; Reciprocal F<sub>2</sub></b>						
P <sub>1</sub> x P <sub>1</sub>	500	36	502	34	0.13a	0.13a
P <sub>2</sub> x P <sub>2</sub>	338	30	345	23	2.27a	2.27a
P <sub>1</sub> x P <sub>2</sub>	590	50	600	40	2.67a	2.67a
P <sub>2</sub> x P <sub>1</sub>	116	12	120	8	2.81a	2.81a
P <sub>1</sub> x P <sub>1</sub>	267	31	270	18	0.25a	0.25a
P <sub>2</sub> x P <sub>2</sub>	74	6	75	5	0.21a	0.21a
P <sub>1</sub> x P <sub>2</sub>	123	7	121	9	0.48a	0.48a
P <sub>2</sub> x P <sub>1</sub>	180	20	185	15	1.80a	1.80a
<b>Backcrosses &amp; Reciprocal Backcrosses</b>						
(P <sub>1</sub> x P <sub>2</sub> ) x P <sub>1</sub>	63	17	60	20	6.60b	6.60b
(P <sub>2</sub> x P <sub>1</sub> ) x P <sub>1</sub>	80	0	80	0	0.0	0.0
(P <sub>1</sub> x P <sub>2</sub> ) x P <sub>2</sub>	80	0	80	0	0.0	0.0
(P <sub>2</sub> x P <sub>1</sub> ) x P <sub>2</sub>	58	23	60	20	0.07b	0.07b
(P <sub>1</sub> x P <sub>2</sub> ) x P <sub>1</sub>	56	24	60	20	1.06b	1.06b
(P <sub>2</sub> x P <sub>1</sub> ) x P <sub>2</sub>	80	0	80	0	0.0	0.0
(P <sub>1</sub> x P <sub>2</sub> ) x P <sub>2</sub>	80	0	80	0	0.0	0.0
(P <sub>2</sub> x P <sub>1</sub> ) x P <sub>1</sub>	55	25	60	20	1.67b	1.67b
(P <sub>1</sub> x P <sub>2</sub> ) x P <sub>2</sub>	35	5	30	10	3.33b	3.33b
(P <sub>2</sub> x P <sub>1</sub> ) x P <sub>1</sub>	60	0	60	0	0.0	0.0
(P <sub>1</sub> x P <sub>2</sub> ) x P <sub>2</sub>	50	0	50	0	0.0	0.0
(P <sub>2</sub> x P <sub>1</sub> ) x P <sub>2</sub>	96	24	90	30	1.60b	1.60b
(P <sub>1</sub> x P <sub>2</sub> ) x P <sub>1</sub>	42	8	37	13	2.66b	2.66b
(P <sub>2</sub> x P <sub>1</sub> ) x P <sub>2</sub>	40	0	40	0	0.0	0.0
(P <sub>1</sub> x P <sub>2</sub> ) x P <sub>2</sub>	75	0	75	0	0.0	0.0
(P <sub>2</sub> x P <sub>1</sub> ) x P <sub>1</sub>	62	18	60	20	0.77b	0.77b

a = not significantly different when tested for 15:1 ratio at P = 0.05  
 a = not significantly different when tested for 3:1 ratio at P = 0.05

resistant parents were also resistant ( $R_1R_1R_2R_2$ ,  $R_1R_1R_2r_2$ ,  $R_1r_1R_2R_2$  and  $R_1r_1R_2r_2$ ). Segregation patterns observed in these backcrosses do corroborate digenic inheritance. In an earlier report it was stated that resistance to brown blotch was controlled by a pair of recessive genes (IITA, 1984). The disparity between their result and this may be attributable to use of different resistant lines of cowpea and/or different races of incitant of the brown blotch disease. While IITA used IT82E-16, pure lines crimson and Hope were used in the present study. However these two investigations and those of Fatunla and Ladipo (1980), as well as Arowolo and Obisesan (1986) who all worked on cowpea indicated that resistance to cowpea diseases is often conditioned by oligogenes.

It was concluded from this study that two dominant nuclear genes conditioned resistance to the brown blotch disease since no reciprocal differences in segregation ratios were observed.

### Acknowledgement

The author is grateful to Mrs. Popoola and Mr. Wole Osude for technical assistance received in the laboratory and greenhouse respectively.

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