

2. Inheritance of target spot.

In 1951, an F_2 population grown for class aleurone color studies segregated for plants with peculiar lesions and subsequent necrosis of the leaves. These lesions begin as tiny dots and enlarge into large concentric spots an inch or more in diameter with alternately light and dark rings within. Coalescence of these spots leads to necrosis of the leaves which may become so severe on the bottom leaves that they die. This character is expressed when the corn is about two months old and continues to maturity. It is so similar to the description of "target spot" diseases of other plant species that it was tentatively given that name. Isolations were made from the lesions to determine if some micro-organism were responsible. An *Alternaria* species was repeatedly isolated but it lacked pathogenicity on unrelated corn. The reason for this became apparent when it was shown that susceptibility is heritable.

In 1952 The Plant Disease Reporter contained two articles describing the occurrence of a corn disease which closely fits the above description. McKeen (April 15, 1952) described its occurrence on a Guatemalan strain grown in Ontario, while Semeniuk and Vestal (May 15, 1952) found it on a Congo corn grown in Iowa. In both instances the disease killed the plants before maturity; in our cultures this is not the case and there is little obvious reduction in vigor.

Reciprocal crosses were made between the original target spot plants and a limited number of marker strains. All F_1 populations in 1952 were normal, while plants from selfed seed all showed target spots. Large F_2 and backcross populations were grown in 1953. Segregation was typical of that expected on a monohybrid basis except that in most cultures there was a deficiency of target spot plants which could be ascribed to lack of infection. Translocations 1-9a and 2-9a had been included as markers. Results in the accompanying table indicate that the recessive gene for susceptibility to target spot (*ta*) is located on chromosome 9.

Crosses	Testcross progeny			
x + ta	S.S. +	S.S. ta	+ +	+ ta
T 1-9a + + ta	218	72	154	159
T 2-9a + + ta	37	1	38	13

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