9. <u>Inheritance of Reaction to the Chlamvdospores of Corn Smut, Ustilago zea</u> (Beckman) Unger Derived from a Single Cross.

Two compatible lines of corn smut (10A4 x 17D4) obtained from the Department of Plant Pathology, University of Minnesota, were inoculated into plants in the field. The chlamydospores from the galls obtained from this cross were stored and used for inoculation on the material tested for smut reaction. The spores were measured out, mixed in a given quantity of water and sprayed on the plants. A resistant inbred line derived from Minnesota 13, the same one used by Saboe in earlier studies, and a susceptible inbred, Baker 164, together with material from the backcrosses, were sprayed with this suspension just as the tassel emerged from the boot.

Sixteen chromosomal interchange stocks, which were susceptible to smut, were crossed with the resistant Minnesota 13 line and only semisterile F_1 plants were backcrossed both to the resistant and susceptible parents. These tested sixteen of the twenty arms of the ten chromosomes. The backcross progeny were inoculated. From the backcross to the resistant, there were 3.62 per cent of smutted plants and from the backcross to the susceptible parent, there were 29.13 per cent smutted plants. These results show that the resistance of this inbred is dominant for this one lot of chlamydospores. The inoculated Minnesota 13 showed no smutted plants while the susceptible Baker 164 showed 63.6 per cent. The uninoculated Baker 164 showed only 3.11 per cent of smutted plants.

Significant deviations from independence of smut reaction and semisterility, a P value less than .001 were observed with interchange 2-7c, 3-5a, 3-6a, 3-7b, 4-5c, 4-6 (57-31) and 5-9a and .05-.02 for 2-9a and .02-.01 for 1-4a for the progeny from backcrossing the semisterile F_1 's to the susceptible parent.

The associations indicate that the difference in reaction of these two inbreds to this corn smut inoculum is governed by at least 5 or possibly 6 factor pairs. The inferred location of these factor pairs (or linked groups of factors) is as follows: In the short arms of chromosomes 4 and 9, in the long arms of chromosomes 3, 5 and 7 and another possibly in the short arm of chromosome 3.

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