

of the same chromosome is ruled out because of their distinct features at pachytene. From the known history of their pedigree, these B chromosomes seem to have originated from the A's. But their continued presence, without loss, if they are acentric fragments or the origin of separate centromeres for those that are centric and form bivalents regularly is difficult to explain.

P. Chandravadana
B. G. S. Rao
W. C. Galinat

MICHIGAN STATE UNIVERSITY
East Lansing, Michigan
MSU/AEC Plant Research Laboratory

1. Peroxidase isozymes of maize: Genetic, ontogenetic and specificity studies.

Genetic variants of peroxidase have been found in pollen and endosperm extracts of several inbred maize strains. The two variants most easily discernible in the pollen extracts appear to follow simple Mendelian rules and are apparently regulated by codominant alleles at one locus. The genetic evidence supports a monomeric structure for the peroxidase products of this locus. In addition to these variants, five other zones of peroxidase activity are present in zymograms of pollen extracts which segregate in a manner suggesting other gene loci. Examination of the liquid endosperm of these strains shows a total of 7-8 peroxidases.

Differential distribution of these peroxidases in specific tissues or organs of the maize sporophyte was reported previously (Scandalios, 1964). Experiments done to determine the subcellular distribution of these peroxidases indicate that most, if not all, are probably associated with cell wall components. Chloroplasts, isolated intact and purified, show no peroxidase activity when such activity is measured both qualitatively and quantitatively. Chloroplasts have been isolated from five

different inbred maize strains and from several pea mutants, and all gave negative peroxidase activity.

John G. Scandalios
Elmer C. Rossman*
Luci G. Espiritu**

*Department of Crop Science, Michigan State University, East Lansing, Michigan.

**Present address: Botany Department, Laguna, Philippines.

2. The genetics of amylases in maize.

Amylases of maize were separated into two zones by acrylamide gel electrophoresis, at pH 8.2. The fast (Zone-1) and slow (Zone-2) anodal zones are tentatively identified as alpha- and beta-amylase, respectively. Genetic variants were found in both Zone-1 and Zone-2. Genetic analysis of the Zone-2 amylase showed that the variants at this zone are under the control of two alleles acting without dominance. The resolution of Zone-1 amylase was found to be best by assaying endosperm extracts from 10-day old seedlings. Preliminary genetic analysis of 220 F₂ seedlings indicates that Zone-1 amylase is controlled by two alleles independently from the Zone-2 amylase.

The possibility of genetic linkage between Zone-2 amylase and several other genetically well-defined isozyme systems in maize was examined in our efforts to assign the amylase genes on specific chromosomes. Genetic linkage was assessed through backcross and F₂ progeny by electrophoretically assaying individual kernels, 16-20 days after pollination. The data from such experiments are summarized in the table below. It appears that Amy-2 and Ct (catalase) are linked on a chromosome within 5 map units of each other. No linkage was detected between AcP (acid phosphatase) and Amy-2 or Ct.