

centages. We studied germination under the following conditions: three replications of 20 seeds each were planted in 5-6 cm deep soil (taken from a maize field). During the first ten days, the temperature was 8°C and from the eleventh day, 13-14°C. In Table 1, we have summarized the data from 29 maize genotypes with germination percentages of 70-90. We also calculated the sum of temperatures. It is probable that there are strong differences in the heat requirement, because all maize samples were able to germinate to an almost similar per cent, but the dynamics and final stage were very different in time. For the best types, 220°C was enough for complete germination, while others only began to germinate and finished above 400°C. Samples marked "oszv" are progenies of seeds overwintered in the breeding nursery in Martonvásár. These S₂ plants showed less heat requirement for good germination than any others.

We hope that by this technique we can select maize genotypes which have much less "time-loss" under low temperatures during a cool spring.

Márton Herczegh

ILLINOIS STATE UNIVERSITY
Normal, Illinois
Department of Biological Sciences

1. Screening for redundant segments in the *Zea mays* genome with monosomic maize plants.*

Reciprocal translocations are found in the progeny of monoploid X diploid crosses (Alexander, Nature 201:737-738, 1964). We (Weber and Alexander, Chromosoma 39:27-42, 1972) have recently identified break-points of 22 reciprocal translocations generated in this way. The points of translocation appear to be at points of interchromosomal redundancy because a) certain of the translocations were found repeatedly and b) my previous work (Weber, Genetics 60:235, 1968) indicated that illegitimate recombination between nonhomologously synapsed segments does not occur in

*Partially supported by A.E.C. Contract No. AT(11-1)-2121.

maize. It would obviously be desirable to catalog a larger number of translocations from monoploid X diploid crosses; however, recovery of translocations from these crosses is an extremely arduous procedure because: a) monoploids occur with a low frequency, b) the number of progeny per ovule is low (1/113 ovules), and c) the frequency of translocations found in monoploid X diploid crosses is also low (1.3% of the survivors of monoploid X diploid crosses had a reciprocal translocation).

As an extension of this work, translocations from monosomic X diploid crosses are being isolated and their breakpoints are being cataloged in a study to map additional points of redundancy in the Zea mays genome. Only a single chromosome is unpaired in a monosomic plant; thus, the frequency with which translocations are generated in crosses between monosomic and diploid plants would be lower than the frequency observed in monoploid X diploid crosses. However, more offspring are viable and large progenies have been produced from crosses between monosomics and diploids.

Crosses of known monosomics 2, 7, 8, 10, and their diploid sibs with normal diploid lines were made in the summer of 1969, and the resultant progeny were planted in the summer of 1970. All plants were grown to maturity and at least one open-pollinated ear from each plant was examined. Of the 17,359 plants scored, 212 expressed varying degrees of semisterility. A sample from each semisterile ear was planted in the summer of 1971, and plants were scored for pollen and ovule semisterility. Families segregating for semisterility were crossed with KYS and a series of known translocations. The progeny were grown in the summer of 1972, microsporocyte samples were taken, and they are currently being analyzed cytologically for the presence of reciprocal translocations.

The results from this material are as follows:

Cross	Number of progeny tested	Number of translocations confirmed cytologically	Frequency of translocations
2N X 2N	6980	1	0.01%
Monosomic 2 X 2N	241	1	0.41%
2N X Monosomic 7	4083	2*	0.05%
2N X Monosomic 8	2787	6	0.22%
2N X Monosomic 10	3268	6	0.18%

*One additional line which carries female and male semisterility from a 2N X monosomic 7 cross has not yet been analyzed cytologically; thus, it is likely that another member is in this class.

It is significant that a much higher frequency of reciprocal translocations is found in progeny of all monosomic X diploid crosses tested than in progeny of diploid X diploid crosses (control population). This strongly suggests that the unpaired monosomic chromosome can occasionally pair with homologous segments found in other regions of the genome, and recombination can occur between the paired regions.

18,992 additional progeny from monosomic by diploid crosses (monosomics 6, 8, and 10) as well as crosses involving a diploid control were screened in the summer of 1971, and 322 ears expressing some degree of semisterility were recovered. 12,203 progeny of monosomic X diploid crosses were screened this past summer.

David F. Weber

2. Fatty acid profiles from maize scutella: a new genetic tool.*

Introduction: Most research involving the genetics of fatty acids in Zea mays has been conducted by extracting the lipids from either whole kernels or entire embryos. Since the kernels are destroyed by these methods, siblings must be used in subsequent crosses and their fatty acid profiles can only be inferred. This article describes a technique to

*Partially funded by A.E.C. Contract No. AT(11-1)-2121.