

<u>Bt</u> <sub>1</sub> <u>Bt</u> <sub>1</sub> <u>Bt</u> <sub>1</sub>	Normal
<u>Bt</u> <sub>1</sub> <u>Bt</u> <sub>1</sub> <u>bt</u> <sub>1</sub>	Normal
<u>Bt</u> <sub>1</sub> <u>bt</u> <sub>1</sub> <u>bt</u> <sub>1</sub>	Brittle *(unusual class)
<u>bt</u> <sub>1</sub> <u>bt</u> <sub>1</sub> <u>bt</u> <sub>1</sub>	Brittle

Work is planned to determine the frequency of this aberrant ratio in the population in an attempt to clarify further this unusual segregation ratio.

R. J. Lambert

3. Location of glossy-4 in relation to cytological breakpoints of paracentric inversions in chromosome 4L.

A series of paracentric inversions obtained from Dr. Gregory Doyle was crossed to su gl<sub>4</sub> stocks in order to determine the location of glossy-4 in relation to the proximal breakpoints of six different paracentric inversions of 4L. The recombination value between sugary-1 and glossy-4 was used as a measure of the location of glossy-4 in relation to the cytological breakpoints. The following table gives the results for the testcross data:

Testcross	Parent Types		Cross-overs		% Recombination
	<u>Su</u> <sub>1</sub> Gl <sub>4</sub>	<u>su</u> <sub>1</sub> gl <sub>4</sub>	<u>Su</u> <sub>1</sub> gl <sub>4</sub>	<u>su</u> <sub>1</sub> Gl <sub>4</sub>	
<u>Inv. 4e (.16L-.81L) x su gl</u> <sub>4</sub> <u>su gl</u> <sub>4</sub>	463	400	5	5	1.16
<u>Inv. 4f (.17L-.63L) x su gl</u> <sub>4</sub> <u>su gl</u> <sub>4</sub>	604	622	7	9	1.30
<u>Inv. 4i (.19L-.66L) x su gl</u> <sub>4</sub> <u>su gl</u> <sub>4</sub>	576	555	6	2	0.07
<u>Inv. 4j (.24L-.66L) x su gl</u> <sub>4</sub> <u>su gl</u> <sub>4</sub>	682	688	87	75	11.82
<u>Inv. 4a (.30L-.90L) x su gl</u> <sub>4</sub> <u>su gl</u> <sub>4</sub>	634	649	45	36	6.31
<u>Inv. 4d (.40L-.96L) x su gl</u> <sub>4</sub> <u>su gl</u> <sub>4</sub>	618	619	71	60	10.59

Cytological breakpoints determined by D. Morgan, R. Morris and A. E. Longley.

Based on normal recombination values (15%) between su<sub>1</sub> and gl<sub>4</sub>, the data indicate that glossy-4 is proximal to the breakpoint in inversions 4j, 4d and probably 4a. Glossy-4 is probably distal to the proximal breakpoint in inversion 4e, 4f and 4i. The recombination value between su-gl<sub>4</sub> (6.31%) for inversion 4a is lower than expected. This may be the result of the proximal breakpoint reducing crossing-over in the su-gl<sub>4</sub> region. Additional material will be analyzed to determine the frequency of the inversion in the crossover classes to obtain a more precise location of glossy-4 in relation to the inversions.

R. J. Lambert

#### 4. Inheritance of linoleic acid in corn.

Gas-liquid chromatographic analyses were made on individual kernels of R84, Illinois High Oil, and the F<sub>1</sub>, F<sub>2</sub> and backcross progenies. Oil was extracted with petroleum ether, esterified and then dissolved in approximately 1 ml petroleum ether. Three  $\mu$ l of the solution was injected into the chromatograph. All analyses were made on an Aerograph Hi-Fi 600 using the standard diethyleneglycol succinate-chromosorb W Column. A flame ionization detector was used.

The frequency distributions in the backcross populations strongly suggest monohybrid inheritance for oleic and linoleic acids, i.e., low linoleic is dominant to high, and low oleic is recessive to high. The F<sub>2</sub> data were less convincing, although individual F<sub>2</sub> ear analyses revealed that the ratio in only one ear out of six was quite deviate, presumably because Illinois High Oil was heterogeneous with respect to the alleles in the system. Segregation in only one of the six F<sub>2</sub> ears is shown in Figure 1.

Table 1  
Mean Linoleic and Oleic Acid Content of Individual  
Kernels of Parents, F<sub>1</sub>, F<sub>2</sub> and Backcross Generations

Population	Percent of Total Oil		
	Linoleic <sup>1</sup>	Oleic <sup>2</sup>	Sum
R84 ♂	61.3	24.5	85.8
IHO ♂	48.8	35.3	84.1
F <sub>1</sub> (R84 ♀)	52.2	31.3	83.5
F <sub>1</sub> (IHO ♀)	47.6	36.1	83.7
BC R84	54.3	29.1	83.4
BC IHO	51.2	32.5	83.7
F <sub>2</sub>	51.5	32.3	83.8

<sup>1</sup>Standard deviation =  $\pm 1.32\%$

<sup>2</sup>Standard deviation =  $\pm 0.78\%$