

(0)	(0)	(1)	(1)	(2)	(2)	(3)	(3)	(1-3)	(1-3)	(2-3)	(2-3)
Rg	rg	Rg	rg	Rg	rg	Rg	rg	Rg	rg	Rg	rg
gl	Gl	Gl	gl	gl	Gl	gl	Gl	Gl	gl	gl	Gl
lg	Lg	Lg	lg	Lg	lg	lg	Lg	Lg	lg	Lg	lg
<u>a</u>	<u>A</u>	<u>A</u>	<u>a</u>	<u>A</u>	<u>a</u>	<u>A</u>	<u>a</u>	<u>a</u>	<u>A</u>	<u>a</u>	<u>A</u>
87	97	1	3	19	34	45	38	0	1	6	10

Total = 341

Recombination: Rg-gl = 1.5%
 gl-lg = 20.2%
 lg-a = 29.3%

Backcross data from structurally normal chromosomes 3 came from the following cross:

<u>Gl Lg A Et</u>	X	<u>gl lg a et *</u>						Total
(0)	(0)	(1)	(1)	(2)	(2)	(1-2)	(1-2)	
Gl	gl	Gl	gl	Gl	gl	Gl	gl	
Lg	lg	lg	Lg	Lg	lg	lg	Lg	
<u>A</u>	<u>a</u>	<u>a</u>	<u>A</u>	<u>a</u>	<u>A</u>	<u>A</u>	<u>a</u>	
329	215	86	122	108	209	40	12	1121

Recombination: Gl-Lg = 23.2%
 Lg-A = 33.0%

* No classification was made for et since it was not well expressed. The marked deficiency of the a class is due to the semi-lethal effect of the et allele.

2. Preferential pairing in structurally heterozygous triploids.

A triploid plant found in the progeny of the cross of In 3b X In 3a came from a diploid egg with two In 3b chromosomes. One In 3a chromosome was contributed by the pollen parent. (For information about the extent of these inversions see the 1956 News Letter). Both In 3b chromosomes carried the A₁ allele and the recessive a₁ allele was in the In 3a chromosome. Although a large progeny from triploid plants is rather difficult to obtain, reciprocal crosses were made with a₁ testers and the ensuing kernels classified for the A and a phenotypes. Using the triploid as the female parent there was a ratio of 225 colored:43 colorless kernels (83.9% A) in the backcross. The reciprocal crosses gave 405 colored:75 colorless kernels (84.4% A). Control data were available from backcrosses of triploids with three structurally normal chromosomes 3, two with the A allele and one with the a allele. When these structurally homozygous triploids were used as the female parent in backcrosses there was a ratio of 874 colored:276 colorless kernels (76.0% A). The

$$\begin{array}{r}
 5.4 : 1 \\
 75 \overline{) 405} \\
 \underline{375} \\
 300 \\
 \underline{300} \\
 0
 \end{array}$$

$$\begin{array}{r}
 3 : \\
 276 \overline{) 874} \\
 \underline{828} \\
 46
 \end{array}$$

$$\begin{array}{r}
 3.19 \\
 276 \overline{) 874} \\
 \underline{828} \\
 46
 \end{array}$$

$$\begin{array}{r}
 460 \\
 276 \\
 \hline
 1840
 \end{array}$$

reciprocal mating gave 225 colored:80 colorless (73.8% A). These data, limited though they are, suggest that pairing was not at random in the structurally heterozygous triploid but tended to occur preferentially between the two In 3b chromosomes. If these two chromosomes always formed a bivalent and disjoined normally, only colored kernels would be found in backcrosses. If pairing between the three chromosomes were at random, then the ratio of colored: colorless kernels should be that found in the control matings with structurally identical chromosomes. The observed data fall between these two extremes and are indicative of some degree of preferential pairing. These data are of interest in connection with the problem of pairing in allopolyploids with partially homologous chromosomes.

M. M. Rhoades

3. Further studies on the Li pericentric inversion in chromosome 9.

Li reported (M. N. L. 1950) that the break points in In 9a were at 0.7 in 9S and 0.9 in 9L. The sh locus was distal to the break point in 9S while wx was included in the inverted segment. Crossovers within the inversion loop give rise to two kinds of deficient-duplicate chromosomes. One is a Dp 9S Df 9L chromatid which has in duplicate the distal .3 of 9S and is deficient for the terminal .1 of 9L. The complementary duplicate-deficient strand is Df 9S Dp 9L. This chromatid is deficient for the distal .3 of 9S and has the distal .1 of 9L in duplicate. Li found that 2.4 percent of the functioning megaspores had the Df 9S Dp 9L chromosome. No statement was made about the functioning of the Dp 9S Df 9L megaspores. The following data afford additional information on the cytogenetics of this inversion:

<u>Sh Bz In Wx</u>		X		sh bz wx pollen					
sh	bz	N	wx						
Sh	sh	Sh	sh	Sh	sh	sh	Sh		
Bz	bz	bz	Bz	bz	Bz	bz	Bz		
<u>Wx</u>	<u>wx</u>	<u>Wx</u>	<u>wx</u>	<u>wx</u>	<u>Wx</u>	<u>Wx</u>	<u>wx</u>	Total	
1104	1099	0	2	10	11	142	720	3088	
1834 Sh:1254 sh				1837 Bz:1251 bz			1257 Wx:1831 wx		

The greater number of Sh and Bz kernels compared to those homozygous for the sh and bz alleles is due to the large Sh Bz wx class which comes in large part from Dp 9S Df 9L gametes produced by crossing over within the inversion. It is evident that the Bz locus is distal to the break point in 9S. However the Sh Bz wx can also come from single exchanges between bz and the In and from 2- and 2-strand doubles within the inversion where one exchange is between wx and the break point in 9L. These should be relatively infrequent. The complementary class,