

Further studies on crossing over in inversion 3a.

Backcross data from plants heterozygous for Lg₂ and A₁. In every combination listed in column one, the A allele is in the left-most chromosome. The first 8 entries are from Rhoades and Dempsey (1953).

Chromosome structure	Linkage phase		Heterozygous parents		Lg A	lg a				
	Lg a	lg A	Total	Recomb. %			S.E.			
N/N C	m	and h	522	568	203	219	1512	27.8	1.16	
In/N C	m		3015	2142	24	84	5605	1.9	.18	
In/N C	h		1410	1215	6	8	2639	0.5	.14	
In/In C	m		514	420	401	356	1691	44.8	1.21	
In/In R	m		393	340	610	592	1935	37.9	1.11	
In/In R	h		333	311	606	566	181	6	35.5	1.12
In Df-Dp/In R	h		823	68	1335	229	2455	36.3	.97	
In Df-Dp/In R	m		192	18	255	34	499	42.1	2.21	
N Df-Dp/N R	R		564	1045	2052	1031	4692	34.3	.69	
N Df-Dp/N R	R	h	32	399	1773	86	2790	33.4	.89	
N/N* R	m		738	767	1522	1485	4512	33.4	.70	
In/In C	m		1087	988	880	922	3877	46.5	.80	
In/In C	h		350	385	341	334	1410	47.9	1.33	
In/In R	m		307	365	509	475	1656	40.5	1.20	
In/In R	h		302	311	422	462	1497	41.0	1.27	

*The LgA chromosome was derived from a double exchange from an In/N plant.

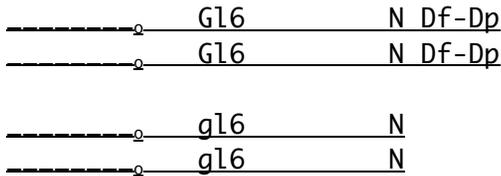
The average unweighted percentage of recombination between Lg₂ and A₁ in N/N plants is 30.6 while in the homozygous inversion plants where A is nearer the centromere and Lg is more distal the percentages of recombination varied from 35.5 to 47.9 with an unweighted mean of 42.0 percent. The difference in recombination percentages in N/N and In/In plants can be accounted for by a centromere effect on crossing over. Since both Lg and A are in the inverted segment it can be argued, on the basis that closer proximity to the centromere results in a decrease in exchange frequency and conversely an increase in crossing over when further removed, that the physical distance of the proximal break of the inversion from Lg is less than the distance of the second break from A.

The Df-Dp chromosomes derived from In 3a/N plants have varying portions of the proximal part of the long arm of chromosome 3 in duplicate. One of these Df-Dp chromosomes was tested to determine whether or not the gl₆ locus, which is proximal to Lg₂, was included in the duplicated segment of the Df-Dp chromosome. The following crosses were made:

-----○-----	GL6	A	N Df-Dp	
-----○-----	gl6	a	N	x gl6 a
(0)	(x)	(x)	(0)	
Gl A	gl A	Gl a	gl a	A:a ratio on ear
290	255	600	597	585:1250 (31.9% A)

Sum = 1841
 Gl6-A recombination = 49.1%
 % Gl6 in seedlings = 51.1
 % A in seedlings = 31.2

Since earlier studies showed that approximately 26% of Df-Dp ovules function, is [sic] clear from the Gl:gl ratio that Gl₆ is not included in the duplicated piece of 3L for if it were there would be approximately 50 percent more Gl than gl seedlings and a 1:1 ratio was obtained. This argument is based on the following table. It is clear from the 49.1 percent recombination between Gl₆ and A that at least one crossover occurred between Gl₆ and the Df in all, or nearly all, megasporocytes so we can eliminate the products of no exchange bivalents and consider only single and double exchanges.



Type of exchange	Gl not in duplication				Gl in duplication			
	N gl	N Gl	Dp-Df gl	Dp-Df Gl	N gl	N Gl	Dp-Df gl	Dp-Df Gl
singles	1	1	1	1	1	1	0	2
2 strand doubles	2	0	0	2	2	0	0	2
3 strand doubles	2	2	2	2	2	2	0	4
4 strand doubles	0	2	2	0	0	2	0	2
	5	5	5	5	5	5	0	10

If Gl₆ is not in duplication a 1:1 ratio is expected. This was found, [sic]

If Gl₆ were in duplication, a ratio of approximately 1.5:1.0 should occur. The observed ratio of Gl:gl deviates significantly from 1.5:1.0 but is very close to a 1:1.

2. Ears from crosses of Bt₁/bt₁ plants with sh₃ showed a 1:1 segregation for shrunken kernel type. Although the phenotypes of sh₃ and bt₁ are quite dissimilar, they are allelic.

3. A new gl₁ was found on chromosome 5. Its linkage relations with A₂ and Bt₁ are shown below. Only colored seeds (A₂) were used since another aleurone factor was segregating.

(1)	(2)		
gl	A ₂	Bt ₁	x gl a ₂ bt ₁
Gl	a ₂	bt ₁	
(0)	(1)	(2)	(1-2)
gl	Gl	gl	Gl
A ₂	A ₂	A ₂	A ₂

Bt	Bt	bt	bt
1281	15	69	0

$$\Sigma = 1365$$

$$\text{Region (1) } gl-A_2 = 15 \div 1365 = 1.1\%$$

$$\text{Region (2) } A_2-Bt = 69 \div 1365 = 5.1\%$$

The order is:

$gl A_2$	Bt
1	5

On the basis of negative allelism tests with unplaced glossies, the new gl was designated gl_{17} .

M. M. Rhoades and
Ellen Dempsey