Linkage tests of *waxy1* marked T3-9 reciprocal translocations.

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In the collection of A-A translocation stocks maintained at MGCSC is a series of *waxy1*-marked translocations that are used for mapping unplaced mutants. Over the last decade, new *wx1*-marked translocations have been introduced into this series and are in a conversion program to convert each translocation to the inbred backgrounds M14 and W23. These inbred conversions are then crossed together to produce vigorous F1's to fill seed requests. Below is a summary of the linkage results for some of these stocks. Additional translocation stocks will be tested as time allows.

We report here the positive results of two- and three-point linkage tests for two of these translocations: *wx1 T3-9(034-11)* (Tables 1-3) and *wx1 T3-9g* (Tables 4 and 5). The linkage tests were set up as modified backcrosses as indicated. A Findley source of *wx1 T3-9g* showed no linkage with its appropriate markers and was discarded.

The data reported here were compiled by Janet Day Jackson before her sudden and untimely death.

Table 1. *wx1 T3-9(034-11)* (3L.46; 9S.36), E. G. Anderson source #1.

Two-point linkage data for *gl6 - wx1 T3-9(034-11)*.
Testcross: *gl6 wx1* X [*Gl6 wx1 T3-9(034-11)* X *gl6 Wx1 N*]

Region	Phenotype	No.	Totals
0	Wx gl	391	
	wx Gl	471	862
1	Wx Gl	76	
	wx gl	90	166
Total			1028

% recombination *gl6 – wx1* = 16.1 +/- 1.1%

Table 2. *wx1 T3-9(034-11)* (3L.46; 9S.36), E. G. Anderson source #1.

Three-point linkage data for *gl6 – lg2 - wx1 T3-9(034-11)*.
Testcross: [*Gl6 Lg2 wx1 T3-9(034-11)* X *gl6 lg2 Wx1 N*] X *gl6 lg2 wx1 N*

Region	Phenotype	No.	Totals
0	gl lg Wx	183	
	Gl Lg wx	189	372
1	gl Lg wx	71	
	Gl lg Wx	68	139
2	Gl Lg Wx	24	
	gl lg wx	32	56
1 + 2	gl Lg Wx	3	
	Gl lg wx	16	19
Total			586

% recombination *gl6 – lg2* = 27.0 +/- 1.8
% recombination *lg2 – wx1* = 12.8 +/- 1.4
% recombination *gl6 – wx1* = 39.8 +/- 2.0

Table 3. *wx1 T3-9(034-11)* (3L.46; 9S.36), E. G. Anderson source #2.

Note: This source of *wx1 T3-9(034-11)* was maintained independently of the source tested in Tables 1 and 2 due to a pedigree error labeling it as *T8-9(034-11)*.

Three-point linkage data for *gl6 – lg2 - wx1 T3-9(034-11)*.
Testcross: [*Gl6 Lg2 wx1 T3-9(034-11)* X *gl6 lg2 Wx1 N*] X *gl6 lg2 wx1 N*

Region	Phenotype	No.	Totals
0	gl lg Wx	557	
	Gl Lg wx	580	1137
1	gl Lg wx	73	
	Gl lg Wx	63	136
2	Gl Lg Wx	48	
	gl lg wx	53	101
1 + 2	gl Lg Wx	0	
	Gl lg wx	10	10
Total			1384

% recombination *gl6 – lg2* = 10.5 +/- 0.8
% recombination *lg2 – wx1* = 8.0 +/- 0.7
% recombination *gl6 – wx1* = 18.6 +/- 1.0

Table 4. *wx1 T3-9g(F-24)* (3L.40; 9L.14), Robertson source.

Three-point point linkage data for *gl6 - lg2 - wx1 T3-9g*.
Testcross: [*Gl6 Lg2 wx1 T3-9g* X *gl6 lg2 Wx1 N*] X *gl6 lg2 wx1 N*

Region	Phenotype	No.	Totals
0	gl lg Wx	69	
	Gl Lg wx	49	118
1	gl Lg wx	4	
	Gl lg Wx	2	6
2	Gl Lg Wx	13	
	gl lg wx	2	15
1 + 2	gl Lg Wx	0	
	Gl lg wx	3	3
Total			142

% recombination *gl6 – lg2* = 6.3 +/- 2.0
% recombination *lg2 – wx1* = 12.7 +/- 2.8
% recombination *gl6 – wx1* = 19.0 +/- 3.3

Table 5. *wx1 T3-9g(F-24)* (3L.40; 9L.14), Robertson source.

Two-point linkage data for *lg2 - wx1 T3-9g*.
Testcross: [*Lg2 wx1* T3-9g X *lg2 Wx1* N] X *lg2 wx1* N

Region	Phenotype	No.	Totals
0	Wx lg	400	
	wx Lg	394	794
1	Wx Lg	56	
	wx lg	17	73
Total			867

% recombination *lg2 – wx1* = 8.4 +/- 0.9