A SCAFFOLD FOR A NEW LINKAGE GROUP (VII)

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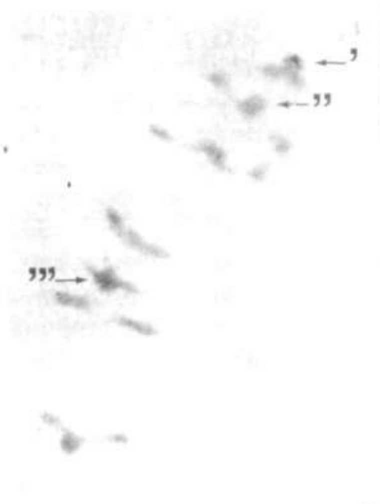
•I. Cytological notes for L-lll, L-21, and L-112

In an earlier paper (5), evidence was presented for including the linkage segment r-tl-bt in the linkage segment V (gp), i.e. only six linkage segments for the seven chromosomes of the pea. This leaves a new Linkage group to be found. In previous reports by Folkeson and Lamm the chromosome lacking localized markers was indicated to be a satellite chromosome .

A revision in progress of Lamm's tester set using BSG-staining shows that L-lll and L-112 share the same satellite chromosome in their interchange systems (4). These interchange lines are then suitable for linkage studies to define the missing linkage group. L-lll has, in the latest paper (12), been interpreted as a T(4-5) interchange. The present investigation reveals that the long arm, rather than the short arm, is involved in the satellite chromosome concerned, i.e. T(4L-5L) (Figs. 1, 2).

In a < ross between L-112 and L-21, seven bivalents were found with complete (100%) fertility (Lamm unpub., cf. 10) indicating identical chromosome structure (cf. 7). This made it possible to compile the cytological results of L-112 and L-21.

In a cytological investigation by Blixt (2), L-21 was interpreted as T(1S-4S/7S). However, by plotting analysis, Blixt's cytological measurements can also be interpreted as a T(3S-4S/7S). This interpretation has recently been supported by Lamm (10) and Folkeson (4) and is also supported by unpublished data from work with L-112 in the ongoing revision.



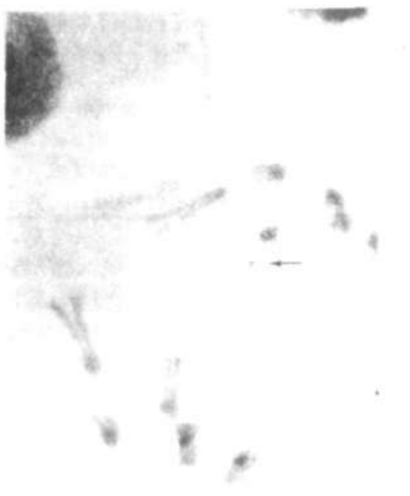


Fig. 1. (Ml) Arrows I and III indicate the bivalents originating from the split quadrivalent. Two BSG spots in each of the bivalents concerned indicate that the interchange point is in the long arm of the involved SAT-chromosome of L–111. Arrow II points to the bivalent of the second SAT-chromosome.

Fig. 2. (A1) Arrow indicates chromosome with unequal chromatids, one with a BSG spot (cf. 18).

II. Ambiguous linkage for wsp and 6pgd-p

The linkage wsp-r previously established (14), which locates these genes in the same linkage group, occurs only in crosses with lines L-21 and L-112 which are of known structure (2,8) and L-25 and 1,-794 of unknown structure. Linkage for wsp-r was, on the other hand, not detectable in crosses no. 429, 607, 999, and 1229 (16, 17). A compilation of H. Lamprecht's results of cross no. 1062 (L-25 x L-998) places the interchange point in the middle of all the combinations with the gene markers wsp, r, and bt (Table 1). This excludes the position of wsp in linkage group V (Table 1).

A persistent, negative interference which occurs in the system of wsp-T-tl/r in crosses with L-25 as well as L-112 (Tables 1, 2), i.e. rec. wsp-T) > rec. (T-tl/r) + rec. (wsp-tl/r), complicates the interpretation, but the result of crosses with L-87 (below) persuaded me to draw the present conclusion. A similar situation has been analyzed by Sybenga (19).

In a test for linkage of wsp, the following three lines of Lamm's tester set were used:

L-87 T(3-5), ref. 7,8
L-lll T(5-7L), ref. 4,7,above
L-112 T(3-7S), ref. 4,7,8.

Linkage was expected in two cases of three, but linkage was found only in one case, i.e. with L-112 (Table 2). Linkage with either L-87 or L-lll was also expected to establish whether wsp belongs to Linkage group V or the unassigned new linkage group VII. If wsp is Located in the same linkage group as the tl-r segment, crosses with L-87 or L-112 should show

Table 1. Segregation data from Lamprecht's cross no. 1062 (L-25 x L-1041) relating to the location of T, wsp, r_, bt_; see

Gene pair	XY	Xy	xY	xy	Total	Chi-square X	Chi-square Y	Chi-square Linkage	Recomb. fract.	S.E.
T-R	182	153	341	10	686	0.37	0.56	166.00	3.1	0.93
T-Wsp	234	101	283	68	686	0.37	0.05	10.64	26.7	3.53
T-Bt	228	107	289	62	686	0.37	0.05	18.67	23.2	2.99
R-Bt	425	98	92	71	686	0.56	0.05	39.53	33.9	2.31
R-Wsp	425	98	92	71	686	0.56	0.05	39.53	33.9	2.31
Bt-Wsp	391	126	125	43	685	0.08	0.04	0.01	49.1	2.84

F2 analysis of segregation data for T, <u>wsp</u>, <u>tl</u> in cross between

1. L-112 x L-150: T(3-7), Wsp, Tl x N wsp, tl, D. Folkeson unpub. 1985

2. L-112 x L-150: T(3-7), <u>Wsp</u>, Tl_ x N <u>wsp</u>, <u>tl</u>, R. Lamm, unpub.

Gene pair	XY	Xy	xY	xy	Total	Chi-square X	Chi-square Y	Chi-square Linkage	Recomb fract.	S.E.
1 T-Tl	61	50	118	4	233	0.52	0.41	54.40	3.5	1 .64
1 T-Wsp	81	30	100	22	233	0.52	0.89	2.65	28.5	6.55
1 Tl-Wsp	156	25	23	29	233	0.41	0.89	35.54	24.5	3.30
2 T-Tl	43	36	92	0	171	0.99	1.42	48.05	Absol.	-
2 T-Wsp	57	22	67	25	171	0.99	0.56	0.002	-	-
2 Tl-Wsp	109	15	26	21	171	1.42	0.56	19.99	**27.5**	**3.25**

Table 3. Compiled segregation data for interchange lines L-87 and L-111 Origin of lines cf. ref. 5, 8.

1 L-87 x L-150	T(3-5) Wsp, Tl x N, wsp, tl	Folkeson, unpub. 1987
2 L-87 x L-150	T(3-5) Wsp, Tl x N, wsp,tl	Lamm, Ref. 8
3 L-87 x L-360	T(3-5) Wsp, Tl x N, wsp, tl	Lamm, unpub.
4 L-111 x L-150	T(5-7), Wsp, Tl x N, wsp, tl	Folkeson, Ref. 5
5. L-111 x L-150	T(5-7), Wsp, Tl x N, wsp, tl	Folkeson, unpub.
6. L-111 x L-150	T(5-7), Wsp, Tl x N, wsp, tl	Lamm, unpub.
7 L-lllb x L-1072	T(5-7), wsp.tl x N, Wsp, Tl,b	Folkeson, unpub.
8 L-111 x L-119	T(5-7), B x N, b	Lamm, Ref.

No.	Gene pair	XY	Xy	xY	xy	Total	Chi-square X	Chi-square Y	Chi-square Linkage	Recomb. fract.	S.E.
1-3	Wsp-Tl	456	155	156	49	816	0.01	0.00	0.18	-	
4,7	Wsp-Tl	266	73	111	39	489	8.40	1.15	0.96	-	
4-7	T-Wsp	226	90	271	115	708	5.79	8.71	0.07	-	
7	B-Wsp	97	58	34	15	204	0.10	12.65	1.05	-	
7,8	T-B	68	67	141	14	290	1.38	1.33	61.87	8.0	2.3

the corresponding linkage for *wsp*-*tl*/r when the T-*tl*/r linkage is quite similar (cf. 8, 9; Tables 2, 3). The lack of linkage between *wsp*-*tl*/r in crosses with L-87 T(3-5) (Table 3), together with the previous statement, excludes the location of *wsp* to linkage group V. The lack of significant linkage between_ T-*wsp* in crosses within L-111 could be explained by the different location of the breakage point in the common SAT-chromosome for L-lll(L) and L-112(S) (cf. above).

The compiled data of crosses no. 7 and 8 (Table 3) for T-b renders b as the closest gene marker (previously T-st) to the interchange point of L-111. An additional linkage test for *wsp* in crosses with L-111 requires a marker gene that is linked closer to the interchange point than b.

The linkage of *6pgd-p* has previously been assigned to a segment of unknown chromosome location (20), which makes it a candidate for the missing linkage group. A linkage test for *6pgd-p* to the interchange point of L-111 has been performed, but no linkage was determined in 201 indivuais scored.

SUMMARY. The most probable location of *wsp* would be in the short arm of one of the satellite chromosomes 4 or 7 outside the interchange point of L-112/L-21.

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