COMMENTS ON THE CHROMOSOME MAPS OF PISUM SATIVUM

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Recent investigations have revealed that earlier conclusions concerning the identities of the interchange chromosomes of a translocation tester set of *Pisum* were erroneous (4,11). A new case is L-111, 'Merton-l', earlier interpreted as a T(3-7) interchange (6) but in the present paper denoted as T(4-5)a. The karyotype of L-lll (cf. Fig. 1) deviates from the normal type by an exchange of the short arms of chromosomes 4 and 5 with proximal locations of the T-points. Giemsa C-banded mitotic metaphase plates of L-lll confirm this interpretation.

From the configurations observed at meiotic M I of the F1 hybrids L-84 x L-111, L-112 x L-84, and L-111 x L-112 (12,2), it may be concluded that the interchange of Winge's L-112 is of the type T(3-4). In L-108, one of the SAT-chromosomes is involved (4), the other partner being easily recognized as chromosome 2 (10). In the F1 hybrids L-108 x L-111 and L-108 x L-112, two rings of four are developed at M I of meiosis (12). Hence the interchange of L-108 corresponds to the structure T(2-7). On the basis of these new results the structures of the translocations in eight lines of the tester set are given in Table 1 below.

Table 1. Interpretations of interchanges in the lines of a translocation tester set in Pisum.

L-110	Roi des gourmands	N-type.	L-83	Extra Rapid N IV	T(3-5)b.
L-114	Nilsson's N I	T(l-2)a.	L-84	Hammarlund's K-line	T(3-6)a.
L-180	Nilsson's N III	T(l-5)a.	L-112	Winge	T(3-4)a.
L-108	Nilsson's N II	T(2-7)a.	L-lll	Merton 1	T(4-5)a.

Analysis of the configurations at meiotic M I of the 28 possible F1 hybrids among these eight lines has confirmed the structures given in Table 1 (12,2). More drastic interchanges can be discerned reliably only in a few interchange lines of *Pisum*. One of these lines, L-4, produced by Ezhova and Gostimski (1) is obviously of the type T(1S-3S). Thus a ring of six at M I of meiosis of the F1 hybrid between L-4 and L-21 is in agreement with the new interpretation of L-112 (Table 1). The structures of L-21 and L-112 are identical (6). This is a further proof of the localization of the genes Gp and R in chromosome 3 (cf. Fig. 1).

The tentative chromosome maps of Fig. 1 demonstrate the approximate locations of the T-points (arrowed) and the loci of neighboring marker genes connected by strong linkage with these T-points. It may appear peculiar that the genes B and St of chromosome 5 are joined by linkage (5) but this is explained by the rare formation of chiasmata in the interstitial segment between the centromere and the T-point of L-83 in the 5L arm (cf. Fig. 1). In contrast the chiasma frequency is high in the long interstitial segment proximal to the T-point of L-112 in chromosome 3. This explains the weak but significant linkage between this T-point and the gene Gp_ (12,5). In Fig. 2D the interstitial chiasma of the F1 hybrid of L-112 x L-488 has been formed in this segment.

A valuable complement to the translocation tester set was obtained by Klein's L-488, characterized by two interchanges, of which one isolated as my L-88 (8) apparently is a T(4L-7S) interchange (14) whereas the other, earlier denoted as T(2-3) (8), should probably rather be T(l-5)b with proximal points of interchange. Configurations resulting from crosses between L-488 and members of the original tester set are illustrated by the meiotic photos of Fig. 2, and are also listed in Table 2.

Table 2. Maximum configurations in PMCs at M I of meiosis in F1 hybrids between L-488, T(l-5)b + T(4-7)a and lines of a translocation tester set in Pisum sativum.

	No. of configurations				% Sterile gametes		
		Rings of					
Parental lines	Bivalents	four	six	eight	male	female	References
L-110, Normal x L-488	3	2	0	0	70	69	Fig. 2A
L-488 x L-114, T(l-2)a	2	1	1	0	78	80	(7)
L-488 x L-180, T(l-5)a	3	2	0	0	73	76	Fig. 2B
L-488 x L-108, T(2-7)a	2	1	1	0	72	81	Fig. 2C
L-488 x L-83, T(3-5)b	2	1	1	0	81	80	(7)
L-112, T(3-4)a x L-488	2	1	1	0	72	78	Fig. 2D
L-488 x L-84, T(3-6)a	1	3	0	0	79	-	(7)
L-488 x L-91, T(3-6)a	1	3	0	0	75	77	Fig. 2E
L-lll T(4-5)a x L-488	3	0	0	1	74	–	Fig. 2F

The coordination between chromosomes and marker genes suggested by my results is illustrated by the tentative chromosome maps of Fig. 1. The cytogenetical investigations of L-83, L-84, L-91, and L-112 lead to the conclusion that the Fs_, Gp_, and R genes generally assigned to chromosome 5 are actually located in chromosome 3 whereas the B and St genes earlier assigned to chromosome 3 in view of the results in L-83, L-lll, and L-180 rather reside in chromosome 5. Hence a revised linkage map of chromosome 5 (3) should probably be applied to chromosome 3. There is strong linkage between Le and V and the T-point of Lamprecht's L-58, 'Graues Posthornchen' (13). In the translocations of L-58 and L-114 the same chromosomes, 1 and 2, are involved (9). Unfortunately, my earlier interpretation of the interchange of L-58 was wrong (4) and new considerations suggest that the genes involve viz. Le and V are located in the 1S arm.

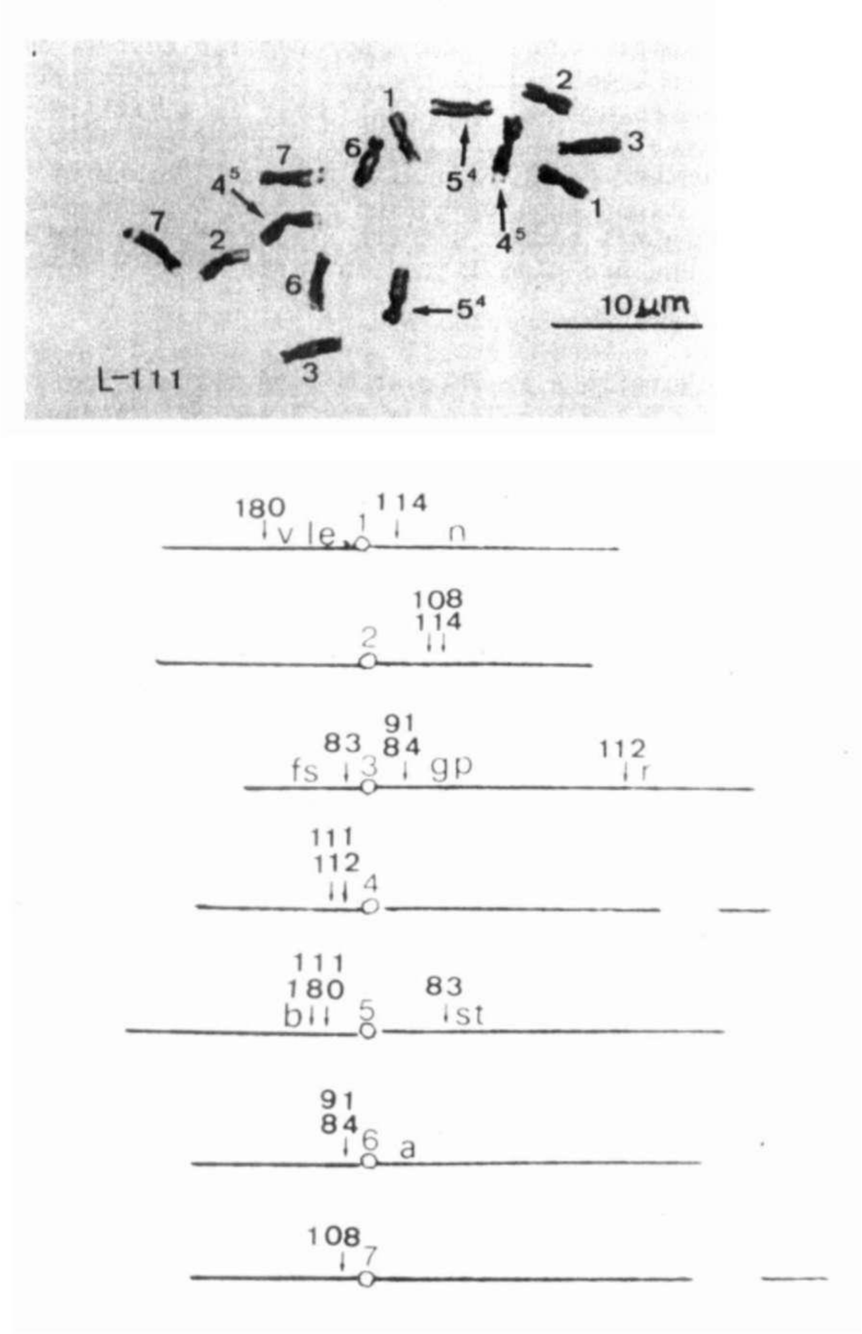

Fig. 1. At the top of this Fig.: Metaphase oi mitosis in a root tip of L-lll, Merton 1, T(4-5)a. Below: Tentative chromosome maps with arrows indicating the approximate positions of T-points in relation to centromeres and neighboring marker genes.

If it could be shown by further studies that my hypothesis concerning the T(l-5)b interchange of L-488 were true and also that significant linkage relations between this T-point and genes of the chromosomes involved, e.g. Le, *B*, and St, could be established this would mean an important support for the new chromosome maps of Fig. 1. Apart from this, the creation of new reliable chromosome maps will require collection and cytogenetical investigations of new suitable translocation lines.

The current generally accepted gene maps of Pisum have been illustrated on the cover of the Supplement to PNL Vol. 9, 1977. The coordination between chromosomes and marker genes of this map and the tentative maps on Fig. 1 of the present article is rather contradictory. From investigations in progress intended to be finished in the autumn of 1987 new information is expected, which will render new facts and contribute to a critical estimation of the results illustrated by Fig. 1.

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9. Lamm, R. 1982. PNL 14:32-35.
10. Lamm, R. 1983. PNL 15:33-35.
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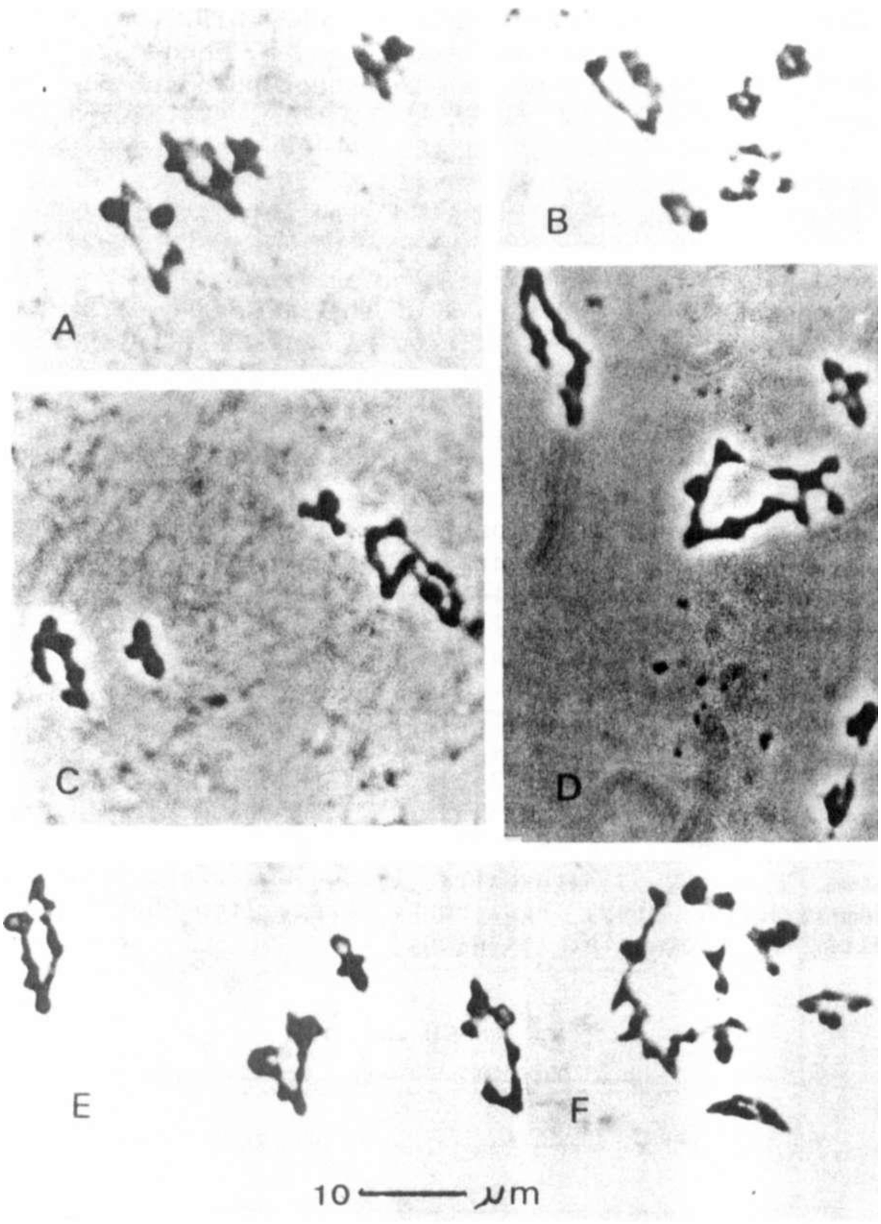
12. Lamm, R. and R. J. Miravalle. 1959. Hereditas 45:417-440
13. Lamprecht, H. 1949. Agri Hort. Genet. 7:85-95.
14. Wolff, G. 1986. PNL 18:64-66.



Maximum configurations at H I of meiosis in PMCs From F1 hybrids between Klein's L-488, T(l-5)b+ T(4-7)a, and six members of a translocation tester set (cf. Table 2), the T(l-5)b translocation so far being hypothetical. Partner in crosses with L-488: A, L-110, normal structure; B, L-180, T(l-5)a; C, L-108, T(2-7)a; D, L-112, T(3-4)a; E, L-91, T(3-6)a; F, L-lll T(4-5)a. The rings of four in C and D represent the assumed T(l-5)b translocation.

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