

A NEW INTERPRETATION OF HAMMARLUND'S K-LINE

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In earlier letters to the PNL (2,3), I have assumed that L-84, the K-line of Hammarlund, is characterized by a T(1-5) interchange. Later, however, karyotypic studies of this line (cf. Fig. 1 B) have made me suspicious of this interpretation. Moreover, Folkeson, working with BSG staining (1), has suggested that chromosome 3 rather than 5 may be involved in the interchange.

For elucidating this question further, I grew L-91, a gray dwarf N-type derived from the cross L-84 x L-2. The structure of L-91 was identical to that of L-84. Thus the F1 hybrid was perfectly fertile. Measurements of the interchange chromosomes were made on ten mitotic root tip plates from each of these lines. An analysis of variance shows that the results, given below, could be pooled.

Chromo- some	Length of arms in		Quotient L:S
	L (long)	S (short)	
3 ⁶	1.4 [±] 0.04	1.0 [±] 0.04	1.5 [±] 0.03
6 ³	3.5 [±] 0.08	2.7 [±] 0.05	1.3 [±] 0.03

Next, I studied the karyotype of the F1 hybrid between L-741, N-type (Fig. 1A), and L-91. The hybrid turned out to be a T(3-6) interchange heterozygote (Fig. 1C) and consequently L-84 and L-91 were of similar structural type. Measurements on microphotos of twenty root tip metaphases from this semisterile F1 hybrid gave the following results:

Chromo- some	Length of arms in		Quotient L:S
	L (long)	S (short)	
3	3.1 [±] 0.10	1.0 [±] 0.02	3.2 [±] 0.10
6	2.6 [±] 0.07	1.5 [±] 0.05	1.7 [±] 0.05
3 ⁶	1.5 [±] 0.03	0.8 [±] 0.03	1.8 [±] 0.06
6 ³	3.3 [±] 0.10	2.5 [±] 0.06	1.3 [±] 0.04

The total length of chromosomes 3 + 6 was 8.2-0.01 and that of 3⁶ + 6³ 8.1-0.01 .

In an F2 progeny of this cross in addition to 147 diploid plants-five trisomies were obtained. Table 1 gives the results from the F2 analysis of the 2n plants. The Fs:fS segregation has been omitted since the scoring on this point unfortunately was unreliable. In Table 2 the cytogenetical characters of the trisomies are recorded. Selfed seed harvested on these plants was used to score for Fs.

As a comment to Table 1, It should be mentioned that among the six linkage relations between the four genes only Gp-Cp gave a significant recombination value viz. 14.7-3.19.

In earlier investigations, the karyotypes of the trisomies have all been of the same structure viz. N-type + 3⁶ (3,4). It is interesting to note that the trisomic interchange heterozygote represented by plant No.5 of Table 2 had improved pollen fertility in comparison with the semi-sterile diploid F1 hybrid that had 47% of sterile pollen grains. The diagram of Fig. 1D illustrates the probable pachytene pairing of the translocation heterozygote and the approximate location of some marker genes. According to Pellew (4) there was about 20% crossing-over between the T-point and the gene Fs but a recalculation of her data gives a nonsignificant chi-square value. In future research, all relations between the T-point and the genes Cri and Ce ought to be investigated.

1. Folkeson, D. 1985. PNL 17:15-16.
2. Lamm, R. 1974. PNL 6:29.
3. Lamm, R. 1976. PNL 8:36-37.
4. Pellew, C. 1940. J. of Genet. 39:363-390.

Table 1. Data concerning the diploid F2 progeny from the Fj of L-741, N-type, Ust fs gp cp d x L-91, T(3-6), u Fs Gp Cp D.

Linkage relation	Number of plants				Chi-square linkage	Recomb. fraction
	Fertile		Semi-sterile			
	+	-	+	-		
T - <u>D</u>	47	23	56	21	0.51	free
T - <u>Ust</u>	53	17	53	24	1.00	free
T - <u>Gp</u>	32	38	76	1	54.58**	1.1±1.19
T - <u>Cp</u>	35	35	70	7	32.11**	7.6±3.13

** Significant at 1% level.

Table 2. Cytogenetical data of the five trisomics in the F₂ progeny of L-741, N-type x L-91, T(3-6).

Plant number	Karyotype	Phenotype	% Sterile pollen
1	L-741 + 3 ⁶	<u>u fs gp D</u>	11
2	L-741 + 3 ⁶	<u>Ust fs gp D</u>	15
3	L-91 + 6	<u>u Fs Gp D</u>	16
4	L-91 + 6	<u>u Fs Gp D</u>	16
5	F ₁ L-741 x L-91 + 3 ⁶	<u>Ust Fs Gp D</u>	34

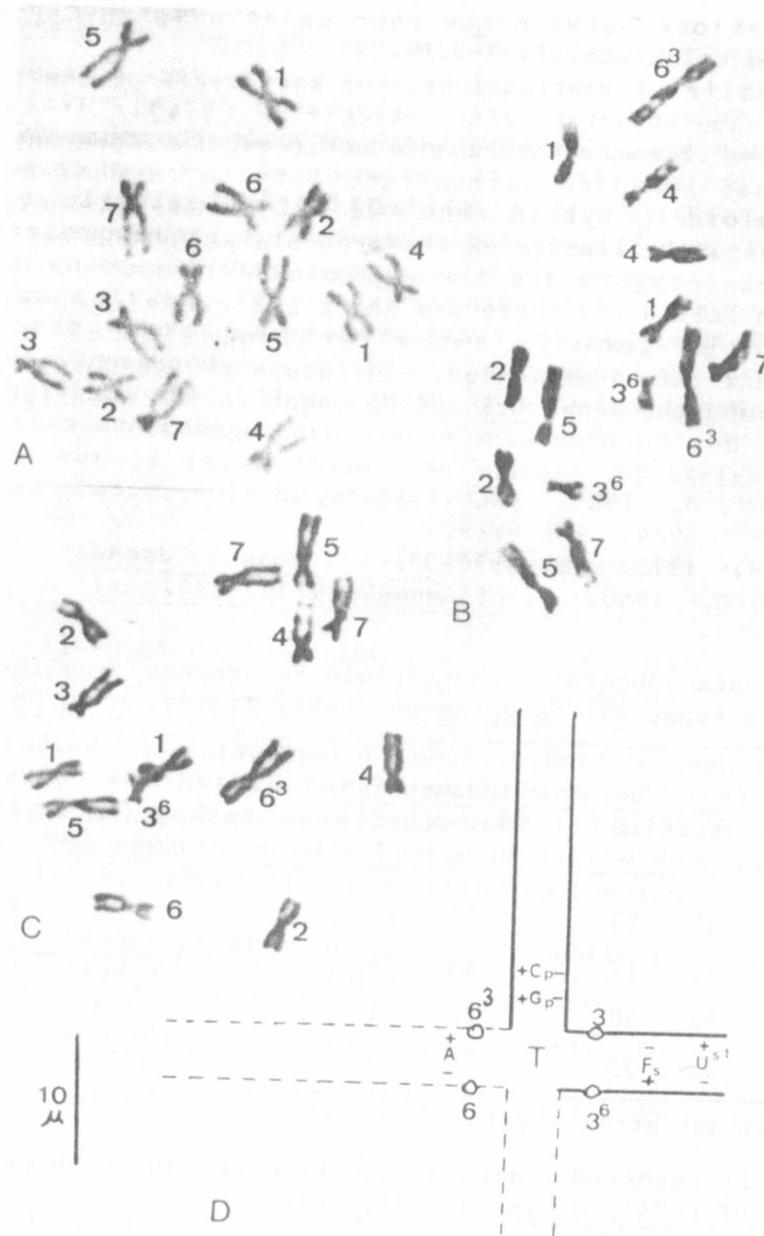


Fig. 1. A-C. mitosis in root tips of (A) [L-741, N-type], (B) [L-84 Hammarlund's K-line, T(3-6)], and (C) F1 of L-741 x L91, T(3-6). D Indicates the probable pairing at pachytene of the F1 hybrid with tentative locations of five marker genes.