Mapping of gene *Inci*, accompanied by new translocation, on linkage group III

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The line WIR2521 (*Pisum sativum* ssp. *syriacum*) has deeply incised leaflets produced by a dominant allele at the locus *Inci*. Linkage between *Inci* and *b* (pink wing petals) of linkage group III have been reported (2, 3). I.C. Murfet and T.H.N. Ellis have placed *M, st, b, Np, le* on the same linkage group (1). To more precisely map *Inci*, the line WL1238 was crossed with line WIR2521. Line WL1238 possesses a normal karyotype and produces fertile pollen. The karyotype of WIR2521 has not been determined, but its pollen is completely fertile. The F_1 plants exhibited semi-sterile pollen (Fig.1A). Cytogenetic analysis was done to investigate the cause of the sterile pollen. There are 7 bivalents in meiotic metaphase I of pollen mother cells of the line WL1238. In metaphase I of F_1 hybrids of the cross WL1238XWIR2521 one can see 5 bivalents and 1 quadrivalent instead of 7 bivalents (Fig.1 B, C). These results suggest that a transloction in the line WIR2521 may be responsible for semisterility of F_1 hybrids.

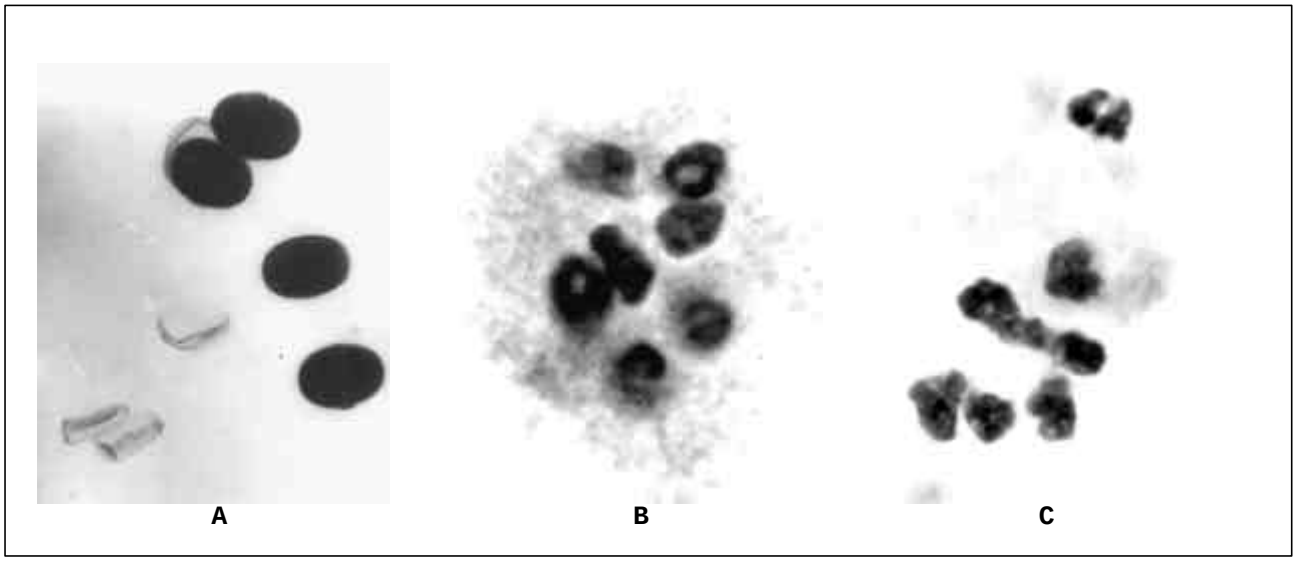

Fig.1. Acetocarmine staining of mature pollen (A) and metaphase I of pollen mother cells (B, C). A – sterile and fertile pollen of F_1 hybrid WL1238xWIR2521; B – seven bivalents at metaphase I in PMC of line WL1238; C – five bivalents and one quadrivalent at metaphase I in PMC of F_1 hybrid WL1238xWIR2521.

Lines WL1238 (*m, b, tr, inci, np, le*) and WIR2521 (*M, B, Tr, Inci, Np, Le*) were used to make the testcrosses WL1238x(WL1238xWIR2521) and (WL1238xWIR2521)xWL1238. Line WL1238 was used as a female parent to avoid nuclear-cytoplasmic conflict. Such complications are observed when line WIR2521 is used as female parent (unpublished data). All markers were in coupling phase and segregated in accordance with a 1:1 ratio (Table 1). Segregation ratios obtained for *Inci*, also confirmed its monogenic nature. Dominant symbol *Tr* was used for designation of semisterile plants carrying the translocation. Accordingly, fertile plants without translocation were marked by recessive symbol *tr*.

Table 1. Chi-square values for monohybrid segregation at loci of testcrosses WL1238 x (WL1238 x WIR2521) and (WL1238 x WIR2521) x WL1238.

	Loci					
c^2	*M*	*b*	*Inci*	*Np*	*Le*	*Tr*
WL1238x(WL1238xWIR2521)	0.1	1.4	0.1	0.1	1.4	0.3
(WL1238xWIR2521)xWL1238	0.1	1.9	2.6	2.6	2.6	1.9

$P_{0,01} = 6.6$

One hundred-fifty hybrid plants of two testcrosses were examined. One plant of the cross (WL1238 x WIR2521) x WL1238 and four plants of the cross WL1238 x (WL1238 x WIR2521) showed recombination between the loci *b, Tr* and *Inci* (Table 2). The data generate the following locus order:

B – Tr – Inci

Thus the break point of the translocation (*Tr*) was mapped between *B* and *Inci*.

Table 2. Phenotypes of four plants exhibiting crossing-over between *B, Tr, Inci* in the testcross WL1238 x (WL1238 x WIR2521)

Plant	Phenotypes											
No.	i	le	Inci	d	wb	tl	b	M	k	gp	*Tr*	Np
15	D	D	R	D	D	D	D	R	D	D	R	R
17	D	D	R	D	D	D	D	R	D	D	R	R
22	D	D	R	D	D	D	D	R	D	D	R	R
85	R	R	R	R	D	R	D	D	R	R	D	R

The plants number 15, 17 and 22 have *m, B, inci/m, b, inci* genotype. They are the result of double crossing-over between the loci *M* and *Inci*. These plants were taken into account for more precise determination of the distance between the genes *M* and *Inci* (Table 3).

Both crosses gave nearly the same results. The linkage map shown in Fig. 2 is based only on results of the testcross WL1238 x (WL1238 x WIR2521).

The results can be presented as the follow segment for linkage group III:

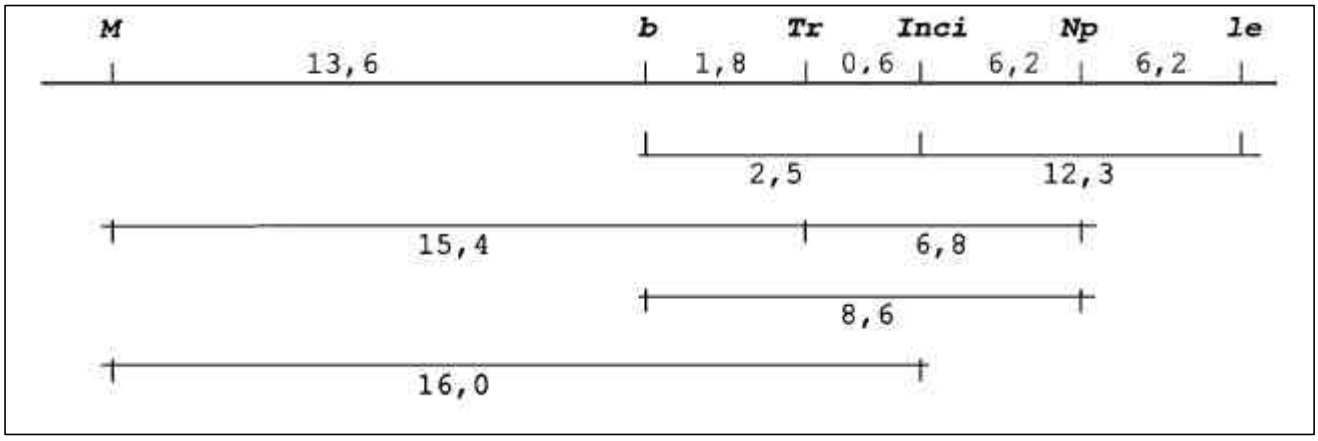

Fig 2. Linkage map based on the data presented in Table 3.

Table 3. Joint segregation analysis for testcrosses No. 1 (WL1238 x (WL1238 x WIR2521), N = 85 and No. 2 (WL1238 x WIR2521) x WL1238, N = 65.

	Loci		Phenotype classes						Rec.	St.
Cross	A	B	A/B	A/b	a/B	a/b*	c^2	P<	fract.	Error
1	*Inci*	*B*	44	0	4	37	71.3	0.001	2.3	1.1
2			38	1	0	26	65.5	0.001	0.8	0.8
1	*Inci*	*Tr*	44	0	1	40	81.4	0.001	0.6	0.6
2			38	1	0	26	65.5	0.001	0.8	0.8
1	*Inci*	*Np*	39	5	5	36	49.9	0.001	5.9	1.8
2			36	3	3	23	48.4	0.001	4.6	1.8
1	*B*	*Tr*	45	3	0	37	75.1	0.001	1.8	1.0
2			38	0	0	27	68.7	0.001	0	0
1	*Le*	*Inci*	36	12	8	29	25.3	0.001	11.8	2.5
2			33	6	6	20	31.1	0.001	9.2	2.5
1	*Le*	*B*	39	9	9	28	31.1	0.001	10.6	2.4
2			32	7	6	20	27.9	0.001	10.0	2.6
1	*Le*	*Tr*	36	12	9	28	23.5	0.001	12.4	2.5
2			32	7	6	20	27.9	0.001	10.0	2.6
1	*Le*	*Np*	41	7	3	34	51.2	0.001	5.9	1.8
2			36	3	3	23	48.4	0.001	4.6	1.8
1	*B*	*Np*	39	9	5	32	39.7	0.001	8.2	2.1
2			35	3	4	23	44.5	0.001	5.4	2.0
1	*Tr*	*Np*	39	6	5	35	47.1	0.001	6.4	1.9
2			35	3	4	23	44.5	0.001	5.4	2.0
1	*B*	*M*	35	13	9	28	21.3	0.001	12.9	2.6
2			27	11	7	20	14.9	0.005	13.8	3.0
1	*M*	*Tr*	35	9	10	31(3)	26.4	0.001	14.7	2.7
2			27	7	11	20	14.9	0.005	13.8	3.0
1	*Inci*	*M*	34	10	10	31(3)	24.0	0.001	15.3	2.8
2			27	12	7	19	14.0	0.005	14.6	3.1
1	*M*	*Np*	30	14	14	27	10.1	0.02	-	-
2			25	9	14	17	8.3	0.05	-	-
1	*Le*	*M*	29	19	15	22	4.9	0.10	-	-
2			23	16	11	15	4.6	0.10	-	-

***The number of double crossovers is given in parentheses. Number of plants with designated phenotypes was calculated using the program 'Plant' developed by S.M. Rozov.**

To determine the second chromosome involved in the translocation linkage of *Inci* with markers *d*, *wb*, *tl*, *r*, *k*, *gp*, and *i* was studied. For all comparisons low χ^2 values were obtained, indicating that the second chromosome involved was not that associated with linkage groups I (*i*, *d*), linkage group V (*tl*, *r*, *pg*).

A new translocation of pea was described. A break point of a translocation is located between the genes *b* and *Inci*. Dominant gene *Inci* is tightly linked to the break point (nearly 1%). The translocation involves linkage group III and an unidentified chromosome. The translocation suppressed gene recombination inside of the region *M – b – Np – le.* Dominant gene *Inci* is convenient marker for genetic studying of the region *b – Np.*

1. Murfet, I.C. and Ellis, T.H.N. 1998. Pisum Genetics 30: 12-14.
2. Swiecicki, W.K. 1990. Pisum Newslett. 22: 64-65.