

Map position of the locus *Ins2*

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The gene *Ins2* participates in the formation of a compound leaf, acting as a synergist of the gene *Af* and an antagonist of the gene *Uni (I)*. The mutation *ins2*, usually produces incisions on leaflet tips, with their central veins continuing as tendrils. However the mutation exhibits varying expression and dominance, depending on the genetic background [here this mutation is printed in lower case although it often displays dominance (1)]. The varying degree of dominance of *ins2* complicates its mapping in most crosses, but heterozygotes can usually be recognized at the stage of flowering. In F₂ of a cross of our line AFD (1), homozygous for *ins2*, and the multi-marker line WL851, the mutation *ins2* behaved as dominant and showed linkage with some markers of linkage group II. Segregation of phenotypes is shown in Table 1.

Table 1. Segregation for the genes of the Linkage Group II in F₂ progeny of the cross AFD (*Wb, K, ins2, His7¹, His(2-6)¹¹²³*) x WL851 (*wb, k, Ins2, His7², His(2-6)¹²²¹*).

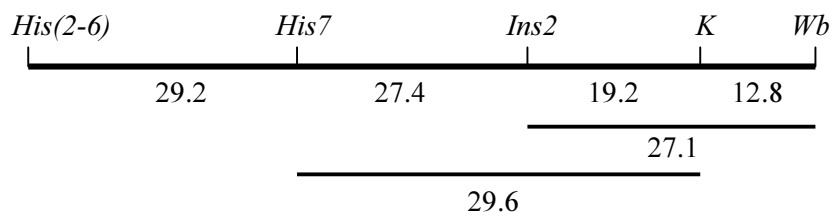
Gene pair	Number of progeny with phenotype ¹									Joint Chi-sq.	Recomb. frac.	Stan. Error
	A/B	A/h	A/b	h/B	h/h	h/b	a/B	a/h	a/b			
<i>ins2-His(2-6)</i>	21	36	19	--	--	--	2	15	7	3.9	41.8	6.0
<i>ins2-His7</i>	19	49	8	--	--	--	1	14	9	11.9*	27.4	5.1
<i>ins2-wb</i>	71	--	7	--	--	--	5	--	10	13.2**	27.1	5.3
<i>ins2-k</i>	65	--	9	--	--	--	8	--	16	28.3***	19.2	4.5
<i>His(2-6)-His7</i>	7	17	2	9	36	6	1	10	12	21.2**	29.3	4.0
<i>wb-His(2-6)</i>	22	42	19	--	--	--	1	9	7	4.4	36.9	5.8
<i>k-His(2-6)</i>	20	36	16	--	--	--	3	12	9	3.4	38.7	6.0
<i>wb-His7</i>	20	51	12	--	--	--	0	12	5	6.1	31.0	5.4
<i>k-His7</i>	20	44	8	--	--	--	0	17	7	10.7*	29.6	5.4
<i>wb-k</i>	72	--	10	--	--	--	1	--	15	46.9***	12.8	3.7

¹Designations: - A,a - first gene; B, b - second gene; h - heterozygous; capital letters refer to alleles from the first parent. *ins2, wb, k* are in coupling phase.

*, **, *** - probabilities less than 0.01, 0.001 and 0.0001 respectively.

All calculations were done by the maximum likelihood method with the use of the program 'Cros'

These data allow us to construct the following map, in which distances are expressed in crossing-over percentage.



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1. Berdnikov, V.A., Gorel, F.L., Bogdanova, V.S. and Kosterin, O.E. 2000. *Pisum Genetics* 32: 9-12.