

### Further evidence that the mutant Fix gene in line Sprint-2Fix<sup>-</sup> is in pea linkage group III

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In a previous paper (2) we reported that the gene for our new Sprint-2Fix<sup>-</sup> mutant (1) was linked to the group III gene *M* with a recombination frequency of  $21.4 \pm 7.7\%$ . Allelism tests are still incomplete, but the mutant gene will be identified in due course by a numbered symbol in the *Sym* series. To locate the new gene more precisely, two further crosses were made involving additional group III markers. The F<sub>2</sub> data for cross NGB851 (*m, st, Fix*<sup>+</sup>) x Sprint-2Fix<sup>-</sup> (*M, St, Fix*<sup>-</sup>) indicate the new gene is located between loci *M* and *St* (Table 1). Significant linkage ( $P < 0.0001$ ) occurred with both markers. The F<sub>2</sub> data for cross SGE656 (*m, uni*<sup>iac</sup> Fix<sup>+</sup>) x Sprint-2Fix<sup>-</sup> (*M, Uni, Fix*<sup>-</sup>) indicate the new gene is located below *uni* in the direction of *st* (Table 2). The linkage with *uni* is significant at the 0.0001 level.

With help of the computer mapping program JOINMAP (3), the data from the two crosses were combined to produce the following map of the *M* to *st* region of linkage group III. The distances in this map are given in cM (the Kosambi function was used).

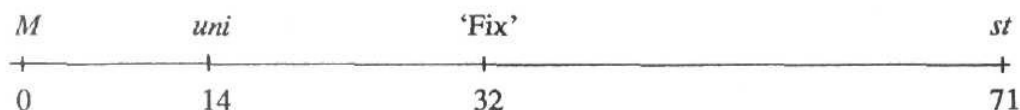


Table 1. F<sub>2</sub> segregation data from cross NGB851 (*m, st, Fix*<sup>+</sup>) x Sprint-2Fix<sup>-</sup> (*M, St, Fix*<sup>-</sup>).

Loci		Phenotype <sup>1</sup>									Joint Chi-sq	Recomb frac	SE
		A/B	A/h	A/b	h/B	h/h	h/b	a/B	a/h	a/b			
<i>M</i>	Fix	18	40	13				2	6	23	29.57**	21.1	4.5
<i>St</i>	Fix	16	8	1	9	26	4	11	12	15	26.93**	32.9	4.2
<i>M</i>	<i>St</i>	28	29	14				10	10	11	2.90	43.6	6.0

A,a - first gene; B,b - second gene; h - heterozygous. When the second gene was treated as codominant, capital A stands for the dominant allele of the first gene and capital B for an allele of the second gene, being in coupling with A. When both genes were treated as codominant, a capital letter stands for an allele of the first parent.

\*\*  $P < 0.0001$ .

Table 2. F<sub>2</sub> segregation data from cross SGE656 (*m, uni*<sup>iac</sup> Fix<sup>+</sup>) x Sprint-2Fix<sup>-</sup> (*M, Uni, Fix*<sup>-</sup>).

Loci		Phenotype <sup>1</sup>									Joint Chi-sq	Recomb frac	SE
		A/B	A/h	A/b	h/B	h/h	h/b	a/B	a/h	a/b			
<i>Uni</i>	<i>M</i>	24	2	5	5	10	4	0	2	15	47.45**	17.84	3.71
<i>Uni</i>	Fix	20	5	5	2	7	8	0	4	9	25.09**	25.38	4.76
<i>M</i>	Fix	16	6	5	2	6	5	2	4	12	17.73*	28.09	5.13

<sup>1</sup> See Table 1 footnote.

\* $P < 0.01$ , \*\* $P < 0.0001$ .

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  3. Stamm, P. 1993. *The Plant Journal* 5:739-744.