Symbiotic locus *Sym38* is localized in linkage group V.

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Three independent mutations have been isolated in symbiotic gene *sym38*: RisFixF [1, Duc, Sagan, pers. comm.], SGENod$^-$-4 and SGENod$^-$-8 [2,3]. It was shown that those mutations block infection thread growth inside root hair [3].

For localization of locus *Sym38* on genetic map the mutant line SGENod$^-$-4 was crossed with multiply marked line NGB1238. F_1 and F_2 plants had full fertility. Two independent populations F_2 (SGENod$^-$-4 x NGB1238) were analyzed. In the first F_2 population segregation by morphological markers *d*, *le*, *s*, *wb*, *k*, *b*, *tl*, *Fs* and U^{st} were analyzed and segregation by locus *Sym38* was analyzed in F_3 plants to identify F_2 plants homozygous and heterozygous by WT and mutant alleles of *Sym38*. As a result, linkage between symbiotic locus *Sym38* and *Tl* of linkage group V was observed (Table 1). In the second F_2 population segregation by marker loci *R*, *Tl* and *Gp* of linkage group V and *Sym38* was analyzed and again linkage between *Sym38* and *Tl* (Table 1) was shown. However, barely significant linkage between *Sym38* and *Gp* and no linkage between *Sym38* and *R* were observed (Table 1). Previously in this linkage group symbiotic loci *Sym16* [4] and *Sym27* [5] were localized. Further mapping experiments are necessary to position the symbiotic locus *Sym38* in certain segment of linkage group V accurately.

Table 1. Joint segregation data in the F_2 populations of crosses 1) NGB1238 (*tl*) x SGENod$^-$-4 (*sym38*), 2) NGB1238 (*tl, r, gp*) x SGENod$^-$-4 (*sym38*).

Cross	Locus pairs	Phase	Number of progeny with designated phenotype[1]									Total	Joint χ^2	Prob	RCV	SE
			A/B	A/h	A/b	h/B	h/h	h/b	a/B	a/h	a/b					
1	*Tl–Sym38*	C	17	11	3	5	31	6	0	17	18	108	46.5	<0.0001	23.3	3.4
	Tl–Sym38	C	20		6				2	5	15	83	29.2	<0.0001	18.8	4.7
	R–Sym38	R	41		20				20		2	83	4.7	<0.05	28.9	9.9
2	*Gp–Sym38*	R	41		19				19		1	80	5.6	<0.025	22.4	10.5

[1] **A/a first gene; B/b second gene; h, heterozygous. When both genes are dominant, the capital letter stands for the dominant allele. When the second gene is codominant, the capital A stands for the dominant allele of the first gene and capital B for an allele of the second gene in coupling with A. When both genes are codominant, the capital letter stands for an allele of the first parent. The calculations have been made using Rozov's program, CROS.**

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