Map position of the *Rms6* locus

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A recessive mutant with increased basal branching, S2-271, was obtained at Versailles by EMS treatment of cv Solara. We found S2-271 was not allelic with *ramosus* mutants *rms1* through *rms5*, which all show increased basal and aerial branching (1-3), but was allelic with mutant K586, which has a similar but weaker basal branching phenotype (2). The new *ramosus* locus was symbolised *rms6*, with S2-271 as type line for allele *rms6-1* and K586 as type line for allele *rms6-2* (5). In contrast to the situation in wild-type and *rms1* through *rms5* plants, buds in the cotyledonary axils of *rms6* plants tend to be released from dormancy and may grow into secondary stems.

To test for linkage with conventional markers, S2-271 was crossed with multiple marker line HL111. *Rms6* showed linkage in repulsion phase with group V markers *r* and *tl*. A pure line, HL293, homozygous for *bt*, *r*, *tl*, *gp*, and *rms6* was selected from cross S2-271 × HL111 and crossed with wild-type lines Borek and Torsdag. The coupling phase F_2 data (Table 1) indicate *Rms6* is in group V with a map sequence of: *Bt*…33…*R*…3…*Tl*…22…*Rms6*…35…*Gp*

Table 1. Combined F_2 dihybrid segregation data for *rms6* and pea linkage group V markers *bt, r, tl* and *gp* from crosses Torsdag (*Bt R Tl Rms6 Gp*) × HL293 (*bt r tl rms6 gp*) and Borek (*Bt R Tl Rms6 Gp*) × HL293; n = 128, 64 plants per cross. All individual segregations are in accordance with a 3:1 ratio (P > 0.1). D = dominant, R = recessive, first named locus shown first. *P < 0.01, **P < 0.00001.

Loci		Phenotype				Joint seg.	Recomb.	
		DD	DR	RD	RR	Chi-sq.	fract.	SE
Rms6	*Bt*	65	23	28	12	0.21	47.3	6.4
Rms6	*R*	74	14	18	22	20.79**	26.6	4.7
Rms6	*Tl*	78	11	16	23	30.21**	22.1	4.3
Rms6	*Gp*	74	14	25	15	7.31*	34.6	5.4
R	*Bt*	74	18	19	17	9.96*	32.8	4.7
R	*Tl*	91	1	3	33	108.83**	2.7	1.5
R	*Gp*	73	19	26	10	0.75	44.6	6.2
Bt	*Tl*	75	18	19	16	9.06*	33.4	4.9
Bt	*Gp*	70	23	29	6	0.84	56.5	7.1
Tl	*Gp*	74	20	25	9	0.38	46.0	6.3

Analysis of the F_2 of cross S2-271 × Torsdag using molecular markers confirmed that the *Rms6* locus is in group V about 3 cM below marker R3_2000 (see 4) on the *Gp* side. A molecular map and detailed report on the *rms6* mutants will be given elsewhere (5). We note the *Rms5* locus is also in group V, but on the opposite side of *Gp* (1).

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