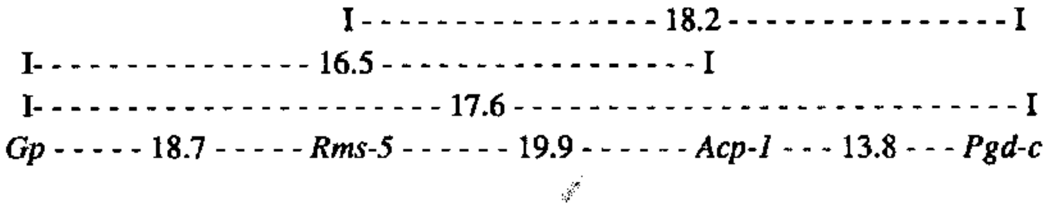
A new *ramosus* gene on chromosome 5

Apisitwanich, S. Department of Genetics, Kasetsart University
Bangkok, Thailand
Swiecicki, W.K. Inst, of Plant Genetics, Polish Academy of Sciences
Poznan, Poland
Wolko, B. Plant Experiment Station, Wiatrowo
Wagrowiec 62100, Poland

The *ramosus* mutant *rms* was obtained by Blixt (2) after X-irradiation of the cv. Parvus. The locus is on chromosome 3 (2). The mutant allele has several pleiotropic effects: there are many basal branches, the stems are hard, seemingly more lignified, and the peduncles are shortened (2).

In 1982, a mutant with a similar phenotype to *rms* was found in the M$_2$ population of cv. Porta treated with 170 r Nf. Segregation of our mutant in the M$_2$ family, in the F$_2$ of a cross between the mutant and its initial line, and in other crosses (Table 1), indicated monogenic recessive inheritance. The mutant line was included in the Pisum Genetics Stocks at Wiatrowo in 1985 under the catalogue number Wt15244. The locus identity cross between Wt15244 and the type line for *rms* (Wt15237) gave normal F$_1$ plants, i.e. both mutants are controlled by different loci. In accordance with Arumingtyas et al (1) we propose symbol *rms-5* for the new gene with Wt15244 as type line.

To test for linkage, line Wt15244 was crossed with marker lines Wt10345, Wt11143, Wt11288 and Wt11540 from the Wiatrowo collection. These lines have morphological markers for chromosomes 2-6. In addition, we analysed segregation for the isozyme loci *Idh* (chr. 1), *Pgm-p* (chr. 2), *Pgd-c* and *Acp-1* (chr. 5), and *Aat-m*, *Pgm-c* and *Pgd-p* (chr. 7). Significant deviations from random assortment were found only in the F$_2$ population of cross Wt15244 x Wt11540 (Table 1) where the *ramosus* locus showed significant linkage with *gp, Acp-1* and *Pgd-c* which are located on the lower half of chromosome 5 according to the recent map of Weeden et al (3). The data indicate that *rms-5* is located on chromosome 5, most probably between *Gp* and *Pgd-c* as shown below.



For more precise mapping, more markers should be considered for this segment, namely, *lk*, *cri* and *creep*. We will also try to obtain results from a larger population of cross Wt15244 x Wt11540. The present data (Table 1) show a small but significant ($P < 0.05$) excess of *gp* and *Pgd-c*^{S} segregates.

Table 1. Phenotypic distribution in an F_2 population from cross Wt15244 (*rms-5 Gp Pgd-c*^{f} *Acp-1*^{f}) x Wt11540 (*Rms-5 gp Pgd-c*^{s} *Acp-1*^{s})

Monohybrid segregation

Locus	Phenotype*			χ^2 (3:l)
	D	R	Total	
Rms-5	78	19	97	1.5
Gp	62	32	94	4.1
Pgd-c	64	33	97	4.2
Acp-1	62	26	88	1.0

Dihybrid segregation

Loci	Phenotype*					χ^2	Recomb. fract.	SE	Phase
	DD	DR	RD	RR	Total				
Rms-5/Gp	44	32	18	0	94	11.5	18.7	9.9	R
Rms-5/Pgd-c	45	33	19	0	97	12.2	18.2	9.8	R
Rms-5/Acp-1	43	26	19	0	88	10.2	19.8	10.2	R
Gp/Pgd-c	53	9	8	24	94	33.9	17.6	4.4	C
Gp/Acp-1	53	7	7	19	86	32.4	16.5	4.4	C
Pgd-c/Acp-1	56	6	6	20	88	39.8	13.8	4.0	C

* D = homozygous dominant or fast + heterozygous plants; R = homozygous recessive or slow plants.

1. Arumingtyas, E.L., Floyd, R.S., Gregory, M.J. and Murfet, I.C. 1992. Pisum Genetics 24:17-31.
2. Blixt, S. 1976. Agri Hort. Genet. 34:83-87.
3. Weeden, N.F., Ambrose, M. and Swiecicki, W.K. 1991. Pisum Genetics 23 Cover.