A new gene for flower color (*crw, cream wings*) in *Pisum sativum* L. located on LG I

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A line with tolerance to *Aphanomyces euteiches* was obtained in 1998 from Dr. Earl Gritton (University of Wisconsin-Madison, USA) as WI 9301. Before its inclusion in the Polish *Pisum* Gene Bank in Wiatrovo (as accession Wt 11166) it was thoroughly characterized, and a new character, cream-colored wings on the flowers in the *a* genotypic background (no anthocyanin synthesis) was observed. The sail and keel remained white.

The line Wt 11166 was crossed to Wt 3527 with normal white color of sail, wing and keel. The F_1 plants had white flowers. Among 128 F_2 plants 96 were white flowering and 32 showed cream wings.

The line Wt 11166 was crossed to testerlines with gene markers for different linkage groups. An inheritance of the new character was confirmed. Data in the Table 1 show clear monohybrid segregation with recessive nature of *cream wings* even though some populations are not particularly large. The reason is the *A* genotype of some testerline parents resulting in ¼ of total F_2 population with the *a*-allele on which *cream wings* can be observed (see tables 1, 2 and 3). Gene symbol *crw* is suggested.

Table 1. Monohybrid segregation for the investigated gene *cream wings* and gene markers in the linkage group I in F_2 populations of the linkage test cross Wt 11166 x : 11238 (K.2296), 11540 (K.2423), 11288 (K.2425), 15860 (K.2559) 11777 (K.2558), 11909 (K.2720), 10357 (K.2796), 11143 (K.2799) 10488 (K.2797), Id 860 (K.2800)

Cross	Gene	Dom	rec	Total	chi square
K.2296	*crw*	33	10	40	0.07
K.2423	*crw*	43	11	54	0.62
K.2425	*crw*	42	7	49	3.00
K.2559	*crw*	27	9	36	0.00
K.2558	*crw*	56	22	78	0.43
K.2720	*crw*	113	56	169	5.97
K.2796	*crw*	20	7	27	0.01
K.2799	*crw*	83	35	118	1.37
K.2797	*crw*	18	4	22	0.54
K.2800	*crw*	56	19	75	0.00
	Am1	111	41	152	0.32
	Aero	136	53	189	0.93
	I	152	34	186	4.48
	A	152	37	189	2.96

Table 2. Distribution of phenotypes in F_2 populations (Wt 11166 x testerlines) and the linkage test for the gene *crw*

Testerline	Pair of genes	DD	Dr	rD	rr	Total	Joint chi square	Cr-O(±SE) (per cent)		Phase
Wt 11238	A- Crw	1	1	33	10	43	2.0	66.4	±13.3	C
	K-Crw	31	10	1	1	41	1.0	65.1	±9.6	R
	Wb-Crw	29	9	4	1	43	0.0	46.9	±11.8	R
	Tl-Crw	28	9	5	1	43	0.0	43.3	±12.2	R
	Cp-Crw	25	9	8	1	43	0.8	35.4	±13.2	R
	Te-Crw	24	9	9	1	43	0.8	33.3	±13.4	R
	Gp-Crw	25	9	8	1	43	0.8	35.4	±13.2	R
	S-Crw	30	9	3	1	43	0.0	51.5	±11.2	R
Wt 11540	*Crw-Gp*	29	14	11	1	54	5.2	27.8	±12.4	R
	Crw-Wb	35	8	9	2	54	0.0	49.6	±10.2	R
	Crw-A	2	40	1	11	53	1.0	58.4	±11.2	C
	Crw-Aat2	20	7	3	2	32	1.4	58.9	±11.9	R
	Crw-Lap1	21	6	4	1	32	0.0	48.1	±13.5	R
	Crw-Pgm1	18	9	5	1	32	1.4	37.2	±15.0	R
	Crw-Pgm2	17	10	3	2	32	0.0	48.2	±13.0	C
	Crw-Aldo	19	8	3	2	32	0.0	56.4	±12.3	R
	Crw-Skdh	18	9	4	1	32	1.0	40.3	±14.6	R
	Crw-Acp1	7	5	2	2	16	0.0	45.3	±17.6	C
	Crw-Pgdp	18	8	5	1	31	1.4	38.8	±15.0	R
Wt 11288	*Crw-A*	1	42	1	7	49	2.0	73.6	±13.1	C
	Crw-St	35	7	6	1	49	0.0	47.4	±11.0	R
Wt 15860	*Crw-Creep*	24	3	8	1	36	0.0	50.0	±12.5	R
	Crw-A	1	26	1	9	35	2.0	64.7	±14.6	C
Wt 11777	*Crw-Arg*	44	12	17	5	78	0.0	48.9	±8.4	C
	Crw-Art	45	11	18	4	78	0.0	48.6	±8.6	R
	Crw-Wlo	44	12	19	3	78	0.4	42.3	±9.2	R
	Crw-Pl	41	14	18	4	77	0.4	56.0	±9.1	C
Wt 11909	*Crw-Def*	87	25	40	13	165	0.2	51.7	±5.7	R
	Crw-Chi5	80	17	44	9	150	0.0	49.4	±6.2	R

Table 2 *(continued)*. Distribution of phenotypes in F_2 populations (Wt 11166 x testerlines) and the linkage test for the gene *crw*

Testerline	Pair of genes	DD	Dr	rD	rr	Total	Joint chi square	Cr-O(±SE) (per cent)		Phase
	Crw-Wa	81	21	45	9	156	0.2	46.3	±6.2	R
	Crw-Pgdp	80	32	41	14	167	0.1	47.7	±5.9	R
	Crw-Skdh	90	20	40	12	162	0.7	54.2	±5.6	R
Wt 10357	*Crw-Tac*	16	4	6	1	27	0.0	44.3	±15.3	R
	Crw-Pet	17	3	5	2	27	1.5	61.2	±12.5	R
Wt 11143	*Crw-N*	54	29	25	8	116	1.7	42.7	±7.5	R
	Crw-Fa	71	12	26	8	117	1.2	58.3	±6.3	R
	Crw-V	68	15	23	10	116	2.3	59.3	±6.2	R
Wt 10488	*Crw-Fa*	17	0	3	1	21	2.3	72.0	±11.9	R
	Crw-Led	15	3	3	1	22	0.0	57.1	±14.7	R
	Crw-N	13	3	3	1	20	0.0	55.1	±15.8	R

Table 3. Distribution of phenotypes in F_2 population (Wt 11166. *crw* x Id 860. *am1 aero I*; K.2800) and the linkage test for the gene *crw*

		Phenotype							
Gene pair	Phase	DD	Dr	rD	rr	Total	Joint chi square	Cr-O ±SE (per cent)	
Am1-Crw	R	1	0	28	9	38	1	34.3	14.1
Am1-Aero	C	100	11	12	29	152	55.4	16.0	3.3
Am1-I	R	82	27	40	0	149	11.5	18.6	7.8
Crw-Aero	R	22	34	15	4	75	10.2	26.8	10.6
Crw-I	C	54	1	13	6	74	12.5	15.2	4.6
Aero-I	R	100	34	52	0	186	17.4	16.2	7.1

Linkage test showed that in most of F_2 populations Wt 11166 (*crw*) X testerline deviations from a correct dihybrid segregation *crw* – gene marker were not found (Table 2). An exception was K. 2800 (Wt 11166 X Id 860) segregating for *crw* and *A am1 aero I* (Table 1). Id 860 is the IPG PAS selection with above mentioned markers of LG I. Dihybrid segregation was disturbed for all gene pairs (joint *chi* square from 10.2 to 55.4) except for *Am1* – *Crw*. Data for this gene pair are "artificial" as *am1* is hypostatic to *a* and *crw* to *A*. Data in the Table 3 suggests the following locus order: C*rw* – *I*– *Aero* – A*m1*. This is in agreement with the current *Pisum* map (1) and provides LG I with a new morphological marker below *i*. A confirming linkage test should include the *af* marker.

1. Weeden, N.F., Ellis, T.H.N., Timmerman-Vaughan, G.M., Święcicki, W.K., Rozov, S.M. and Berdnikov, V.A. 1998. Pisum Genetics 30: 1-4.