A new chlorophyll gene *(xach, xantha chlorescens)* in *Pisum sativum* L. located on LG II

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Induced mutations substantially increase the range of genetic variation in *Pisum* (eg. new genes *orp, art, nec, lum* etc.).N

Plant Experiment Station at Wiatrowo (1, 2). Some of these, such as the one discussed in this paper, were obtained after treatment of both physical and chemical mutagens.

Dry seeds of cv. Paloma (Wt 3527) were treated with 200 rNf +0.014% NEU, and a chlorophyll mutant from the terminalis group was selected in the M_2 generation. During germination and initial growth (up to 4-5 leaves) mutant plants are gold-yellow-green (Figure 1A) and could be used as an ornamental pea. After this initial growth the plant becomes green and is fertile (Figure 1B). The phenotype is clearly different from other described chlorophyll mutations of this group. The mutant has been included in the Polish pea collection under the name *xantha-chlorescens* (accession number Wt 10889).

Figure 1. Mutantplants of cultivar Paloma snowing chlorosis during early vegetative growth (A) and recovery of normal gr

This line was crossed to following testerlines with gene markers: Wt 11540 - A, *wb, Pgm-p* (LG II); gp, tl, *Acpl* (LG V); *Aat-m, Skdh, Estl, Est-2* (LG VII); Wt 11288 - *A* (LG II); st, b, (LGIII) and Wt 15860 - *A* (LG II); *creep, ce* (LG V). Segregation of the mutation in the F_2 in 1999 showed no deviations from an expected monohybrid segregation (Table 1). The gene symbol, *xach,* is suggested for the *xantha-chlorescens* mutation in the type line Wt 10889.

Table 1. Monohybrid segregation for the investigated gene xach (xanta-chlorescens) and gene markers in the linkagegroup II in F2 populations of the linkage test crosses.

Cross no.	Parents	Gene	Dom	Rec	Total	*chi²*
K. 2022	Wt 11540 x Wt 10889	*Xach*	70	25	95	0.09
		A	74	17	91	1.94
K. 2024	Wt 11288 x Wt 10889	*Xach*	72	22	94	0.13
		A	72	10	82	7.17
K. 2026	Wt 10889 x Wt 15860	*Xach*	69	25	94	0.13
		A	62	11	73	3.84
K. 2718	Wt 10886 x Wt 16054	*Xach*	97	29	126	0.26
		Rms3	79	20	99	1.22
K. 2795	Wt 10886 x Wt 15869	*Xach*	108	38	146	0.08
		A	88	41	129	3.16
		Pal	118	20	138	8.13
K. 2894	Wt 10886 x Wt 11300	*Xach*	89	30	119	0.00
		A	89	30	119	0.00
		Crd	95	24	119	1.48
K. 3012	Wt 3838 x Wt 10888	*Xach*	174	55	229	0.12
		A	161	60	221	0.54
			161	55	216	0.02

Analyses of the dihybrid segregation in the three mapping populations showed independent assortment between *xach* and all genes listed in Table 2. In contrast, substantial deviations were observed for *Xach-A* with the joint *chi* square from 21.4 to 50.8 and *Cr-O* values 8.27 in K.2022, 12.3 in K.2024 and 15.5 in K.2026. This suggests localization of *xach* on LG II (3).

Table 2. Distribution of phenotypes in F2 populations (Wt10889xach type line x testerlines) and the linkage testfor the new ger

Testerline (Cross no.)	Pair of genes	DD	Dr	rD	rr	Total	Joint *chi* square	Cr-o (±S.E) (per cent)		Phase
Wt 11 540 (K. 2022)	*Xach-Gp*	53	16	14	4	87	0.01	49.2	8.11	R
	Xach-Tl	52	18	17	2	89	1.98	35.1	9.16	R
	Xach-Wb	54	15	15	3	87	0.22	45.4	8.44	R
	Xach-Ac	57	9	16	5	84	0.08	46.7	8.48	R
	Xach-Aat-m	32	7	9	2	50	0.00	50.2	10.6	R
	Xach-Skdh	28	10	9	2	49	0.30	43.3	11.5	R
	Xach-Acpl	27	11	10	1	49	1.82	69.1	12.8	C
	Xach-Pgm-c	32	7	10	1	50	0.50	39.1	11.8	R
	Xach- Pgm-p	25	11	9	1	46	1.72	68.7	13.2	C
	Xach-Est-1	30	9	9	2	50	0.12	45.8	11.1	R
	Xach- Est-2	28	11	9	2	50	0.45	58.0	11.5	C
Wt 11 288 (K.2024)	*Xach-St*	56	16	10	5	87	0.84	57.7	7.32	R
	Xach-B	51	17	2	2	72	1.22	64.7	7.29	R
Wt 15 860 (K.2026)	*Xach-Creep*	51	17	11	6	85	0.73	56.8	7.50	R
	Xach-Ce	38	15	1	2	56	1.98	70.9	7.45	R

K.2024 and K.2026 single plants were selected from F_2 segregating populations and lines were multiplied with linked genes *xach-A* in repulsion phase (Wt 10888 and Wt 10886, respectively). These lines were crossed to additional LG II marker lines: Wt 16054 (rms3), Wt 15869 *(pal),* Wt 11300 (crd) and Wt 3838

(lf) (Table 1.). Analysis of the dihybrid segregation in the F_2 confirmed that *xach* is linked with *A*, although *Cr-O* values in repulsion were larger (from 19.6 to 29.3) than in coupling (Table 3). No linkages of *xach* with markers *rms3, pal* and *crd* were observed. However, in the population K.3012 substantial deviations from the expected dihybrid segregation were stated for three gene pairs: *Xach-A*, *Xach-Lf* and A-Lf. Cr-O values suggest the following gene order: *Xach-14-Lf-19-A*.

Table 3. Distribution of phenotypes in F_2 populations (xach lines x testerlines) and the linkage test for the new gene.

Cross no.	Pair of genes	DD	Dr	rD	rr	Total	Joint *chi* square	*Cr-O* (±S.E) (per cent)		Phase
K. 2022	*Xach-A*	68	2	5	14	89	50.8	8.27	3.07	C
K.2024	*Xach-A*	68	3	4	7	82	31.4	12.3	3.92	C
K.2026	*Xach-A*	59	5	3	6	73	21.4	15.5	4.68	C
K2718	*Xach-Rms-3*	73	20	6	1	99	1.27	43.0	8.10	R
K.2795	*Xach-A*	68	40	20	1	129	9.26	19.6	8.40	R
	Xach-Pal	89	19	29	1	138	3.26	26.0	7.84	R
	A-Pd	74	13	35	6	128	00.0	50.3	6.65	C
K.2894	*Xach-A*	61	28	28	2	119	8.31	25.6	8.47	R
	Xach- Crd	69	20	26	4	119	1.11	41.1	7.52	R
	A-Crd	83	6	12	18	119	40.0	16.4	3.78	C
K.3012	*Xach-A*	113	55	48	5	221	10.3	29.3	6.07	R
	Xach-Lf	111	54	50	1	216	19.5	14.0	6.64	R
	A-Lf	138	16	22	38	214	65.2	18.9	3.03	C

References

1. Swiecicki W.K. 1984. *Pisum* Newslet. 16: 84-86.
2. Swiecicki W.K. 1998. Crop Gene Resources. Nation. Conf. Pulawy: 53-54.
3. Weeden N.F., T.H.N. Ellis, G.M. Timmerman-Vaughan , W.K. Swiecicki, S.M. Rozov and V.A. Berdnikov. 1998. *Pisum* Genetics 30: 1-4.