Linkages for a new *fasciata* gene

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The fasciata phenotype is very useful in pea genetics and breeding; yet there remains a certain ambiguity regarding its genetic basis. In the international pea gene bank the line WL 6 was considered as the type line for two recessive genes, *fa* (linkage group [LG] IV) and *fas* (LG III), and the line WL 1143 is a tester line for LG IV with two markers *fa* and *n*, (*v* is not on LG IV) (2). Genetic analyses on *fasciata* resources in the collection at Wiatrowo resulted in the following conclusions (3):

1. The line WL 6 appeared to be the type line for *fa*, exclusively, implying that no type line for *fas* exists.
2. The gene *fa* in the tester line WL 1143 appeared to have very poor penetrance.
3. Stem fasciation in most of lines is controlled by the gene *fa* on linkage group IV.
4. The *dichotomous branching* mutation [type line Wt 10 785 (Gottshalk 37B)] is caused by an allele at *Fa* with the following dominance (Fa-fa^{bif}-fa).
5. The line Wt 12 185 has a fasciated phenotype that does not display allelism with *fa*. The objective of this study was to determine if Wt 12 185 could contain the gene *fas*.

As a type line for *fas* is not available for an identity test, a mapping approach was used. Presumably, if fasciation in Wt 12 185 was produced by *fas*, the phenotype should demonstrate linkage with markers on LG III. Several tester lines with markers were involved for the linkage tests.: Wt 11 288 (*st, b, M* – LG III), Wt 10 357 (uni^{tac}, *pet* - LG III), Wt 15 237 (*rms1* – LG III), Wt 12 371 (*was, led* – LG IV) and Wt 11 238 (*i, d, A, s, k, wb, tl, gp, U)*.

The linkage analysis revealed that the locus controlling fasciation in Wt 12 185 segregated independently of each of the loci on LG III, as well as *was, led, i, a, d, s, k, wb, r* and *tl* (Table 1). However, significantly disturbed

Table 1. Distribution of phenotypes in F_2 populations (Wt 12185 x testerlines) and the linkage test for the gene *fa**

Testerline	Pair of genes	Phenotype				Total	Joint chi square	Cr-O value+SE (percent	Phase
		DD	Dr	rD	rr				
Wt 11 288	*fa* - st*	44	14	16	2	76	1.71	37.0±9.7	R
	fa – b*	38	9	11	2	60	0.00	46.3±10.1	R
	fa – M*	33	10	10	2	55	0.58	55.8±10.8	C
Wt 10 357	*uni - fa**	88	29	36	11	164	0.00	48.9±5.9	R
	*pet - fa**	95	33	29	7	164	0.76	44.9±6.2	R
Wt 15 237	*fa* – rms1*	45	18	16	1	80	3.81	25.7±10.3	R
Wt 12 371	*fa* - was*	92	22	24	15	153	5.82	63.0±5.1	R
	Fa – led*	84	29	37	2	152	7.53	25.7±7.5	R
Wt 11 238	*fa* – i*	96	32	25	4	157	2.10	39.7±6.6	R
	fa – A*	105	28	22	7	162	0.25	47.5±5.7	C
	fa - d*	81	23	16	6	126	0.31	53.9±6.4	R
	fa - s*	93	31	20	7	151	0.00	50.7±6.0	R
	fa – k*	93	40	21	8	162	0.20	48.3±6.0	R

fa* – wb	99	32	21	6	158	0.00	48.3±6.1	R
fa* – r	96	32	20	9	157	0.21	54.2±5.7	R
fa* - tl	102	31	22	7	162	0.00	50.6±5.8	R

dihybrid segregations were found for the gene pairs *fa** - *gp* and *fa** – *U* (tables 2 and 3) with *Cr-O* values 17.6 and 21.4, respectively. Considering the above results one could conclude that the locus responsible for the fascinated phenotype at Wt 12 185 is localized between *Gp* and *U* on chromosome V. I suggest the gene symbol *fa2* for this new mutation and revise *fa* to *fa1* for the gene on LG IV). The symbol *fas* should remain reserved for the gene on LG III, although suitable germplasm needs to be located in order to confirm its localization .

Table 2. Monohybrid segregation for the investigated gene *fasciata2* and gene markers in the linkage group V in F_2 population of the linkage test cross K. 2749 (Wt 12 185 x Wt 11 238

	Allele			
Locus	**Dom**	**Rec**	**Total**	**χ^2 (3:1)**
Fa2	133	29	162	4.35
Gp	119	48	167	1.24
A	132	36	168	1.14
U	88	41	129	3.16

Table 3. Distribution of phenotypes in F_2 population (Wt 12 185 x Wt 11 238) and the linkage test for the gene *fasciata2*

	Phenotype							
Pair of genes	**DD**	**Dr**	**rD**	**rr**	**Total**	**Joint χ^2**	***Cr-O* value + SE (per cent)**	**Phase**
fa2 - gp	88	45	29	1	162	13.4	17.6 ± 7.6	R
fa2 - U	81	22	6	18	127	23.3	21.4 ± 4.2	C
gp - U	59	37	28	4	128	7.0	30.0 ± 7.9	R

In segregating populations *fasciata* genes can show certain lack of recessives caused by a reduced penetrance (e.g. very strong in WL 1143). But some sources of *fa1* (e.g. WL 6) give undisturbed 3:1 segregation what suggest the influence of a genotypic background. In most of populations of the linkage test presented above (excluding the cross in Table 2) the monohybrid segregation of *fa2* did not deviate significantly from the expected 3:1 ratio.

Wt 12 185 x Wt 11 288: 59 *Fa2:18 fa2*, $\chi^2 = 0.11$;
Wt 12 185 x Wt 10 357: 124:40, $\chi^2 = 0.03$;
Wt 12 185 x Wt 15 237: 63:18, $\chi^2 = 0.33$;
Wt 12 185 x Wt 12 371: 114:39, $\chi^2 = 0.02$

1. Blixt, S. 1976. Agri Hort. Genet. 34: 83-87.
2. Lamprecht, H. 1974. Monographie der Gattung *Pisum*. Steiermärkische Landesdruckerei, Graz. p. 655.
3. Święcicki, W.K. 2001. *Pisum* Genet. 33: 19-20.