A new Fix⁻ mutation in pea shows linkage with group 3 marker *M*

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The recessive mutant Sprint-2Fix⁻ was isolated after chemical (EMS) mutagenesis from our laboratory line Sprint-20 (*a, d, M*, *Fs*). This mutation leads to the formation of white ineffective nodules without nitrogenase activity and to severe chlorosis of the shoot when the plant is grown on a nitrogen-free medium. Differentiation of bacteroids is morphologically unnoticeable; the symbiosomes have abnormal structure as they contain several bacteroids in one envelope (1).

An allelism test between the Fix⁻ mutant E135f (*sym13;* 3) and our Sprint-2Fix⁻ mutant showed that the two mutants are not allelic. Since allelism tests have not yet been made against six further Fix⁻ mutants (2, 4, 5), a gene symbol has not been assigned to the Sprint-2Fix⁻ mutant gene at this stage.

The mutant line Sprint-2Fix⁻ was crossed with testerline NGB1238. The F_2 segregation data in Table 1 provide significant evidence (P = 0.0005) of linkage between the mutant gene in line Sprint-2Fix⁻ and the linkage group 3 marker *M*. None of the previously mapped symbiotic genes is located in this region of the pea linkage map (4, 6).

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Table 1. F_2 segregation data from cross NGB1238 *(m,* Fix⁺) x Sprint-2Fix⁻ (*M*, Fix⁻).

Number of plants with phenotype					Chi-squared		Recomb.
M Fix⁺	*M* Fix⁻	*m* Fix⁺	*m* Fix⁻	*M–m*	Fix⁺–Fix⁻	Joint	fract. ± SE
74	31	45	2	2.84	0.88	12.20*	21.4±7.7%

* P = 0.0005

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