

Fix⁻ mutants RisFixA and RisFixV carry mutations in newly identified pea genes *sym41* and *sym42*, respectively

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A large set of pea symbiotic mutants induced in cv. Finale with the use of different mutagens was obtained by K. Engvild (3). Different mutants from this set have been intensively studied phenotypically (6,7,8,11). The genetic analysis of this collection has been performed in two laboratories: at Station de Genetique et d'Amelioration des Plantes, INRA, Dijon, France and at Laboratory of Genetics of Plant-Microbe Interactions, All-Russia Research Institute for Agricultural Microbiology (Duc, Sagan, pers. comm.).

In the present study we concentrated on two Fix⁻ mutants: RisFixA and RisFixV. RisFixA forms a few small white nodules (8) whereas RisFixV forms two types of nodules: small greenish and nitrogen-fixing pink ones (7,8). In mutant RisFixA, formation of infection threads and infection droplets, bacteroid differentiation and nodule persistence are affected (6). Mutant RisFixV is impaired in nodule persistence, and it is also characterized by an abnormal thickening of infection threads during the process of "maturation and senescence" (6,7).

We have conducted tests for allelism of RisFixA and RisFixV with all Fix⁻ mutant tester lines: E135f (*sym13*) (4), R50 (*sym16*) (5), P59 (*sym23*), P60 (*sym24*), P61 (*sym25*) (2, Duc, Sagan, pers. comm.), P63 (*sym26*), RisFixM (*sym26*), RisFixT (*sym26*), P12 (*sym27*), RisFixQ (*sym27*) (2, 3, Duc, Sagan, pers. comm.), Sprint-2Fix⁻ (*sym31*) (1), RisFixL (*sym32*) (3, Duc, Sagan, pers. comm.), SGEFix⁻2 (*sym33*), SGEFix⁻1 (*sym40*) (10) and mutant FN1 (9). Results of our tests for allelism showed that both mutants RisFixA and RisFixV are non-allelic to each other and to all mentioned-above mutant tester lines and therefore they carry mutations in pea symbiotic genes unidentified earlier. Accordingly, the gene symbols *sym41* and *sym42* have been assigned to the mutant genes of lines RisFixA and RisFixV.

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