

Identification of DNA markers linked to an induced mutated gene conferring resistance to powdery mildew in pea (*Pisum sativum* L.)

Graça Pereira · Cátia Marques · Rui Ribeiro ·
Sandra Formiga · Mafalda Dâmaso · M. Tavares Sousa ·
Mário Farinhó · José M. Leitão

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Abstract We have recently induced two powdery mildew (*Erysiphe pisi* Syd) resistant mutants in *Pisum sativum* L. via ethylnitrosourea (ENU) mutagenesis. Both mutations (*er1mut1* and *er1mut2*) affected the same locus *er1* that determines most of the identified natural sources of powdery mildew resistance (PMR) in this crop. The mutated gene *er1mut2* was mapped to a linkage group of 16 DNA markers combining three main strategies: near isogenic lines (NILs) analysis, bulked segregant analysis and genetic mapping of randomly identified polymorphic markers, together with three DNA-markers techniques: ISSR, RAPDs and AFLPs. Markers located closer to the PMR locus, OPO06_{1100y} (0.5 cM), OPT06₄₈₀ (3.3 cM) and AGG/CAA₁₂₅ (5.5 cM), were cloned and converted into SCAR markers. Markers AH1R₈₅₀ and AHR_{920y} were found to be allelic and converted into the co-dominant marker ScAH1 (16.3 cM). Two previously known DNA markers, ScOPE16₁₆₀₀ and A5_{420y}, were mapped at 9.6 and 23.0 cM from the PMR locus, respectively. The novel markers identified in this study are currently

being transferred to a new F2 mapping population derived from a cross between the induced PMR mutant line F(*er1mut2*) and a more genetically distant susceptible line of *Pisum sativum* var. *arvense*.

Keywords *Pisum sativum* · Pea · Powdery mildew · Resistance gene · Mutagenesis · DNA markers

G. Pereira · C. Marques · R. Ribeiro · S. Formiga ·
M. Dâmaso · M. Farinhó · J. M. Leitão (✉)
BioFIG, FCT, Universidade do Algarve, Campus de
Gambelas, 8005-139 Faro, Portugal
e-mail: jleitao@ualg.pt

G. Pereira · M. Tavares Sousa
INRB, L-INIA/ex-ENMP, Apartado 6, 7350-951 Elvas,
Portugal