

PEA POWDERY MILDEW *er1* RESISTANCE IS ASSOCIATED TO LOSS-OF-FUNCTION MUTATIONS AT A *MLO* HOMOLOGOUS LOCUS

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The powdery mildew disease affects several crops and is also one of the major threats for pea (*Pisum sativum* L.) cultivation all over the world. The powdery mildew resistance gene *er1*, first described over sixty years ago, is widely used in pea breeding and still maintains its efficiency in the field. Genetic and phytopathological features of *er1* resistance are similar to those of barley, Arabidopsis and tomato *mlo* powdery mildew resistance, which is caused by the loss of function of specific isoforms of the MLO protein family. Here, we describe the obtainment of a novel *er1* resistant line by experimental mutagenesis with the alkylating agent diethyl sulfate. This line was found to carry a single nucleotide polymorphism in the *PsMLO1* gene sequence, predicted to result in premature termination of translation and a non-functional protein. A cleaved amplified polymorphic sequence (CAPS) marker was developed on the mutation site and shown to be fully co-segregating with resistance in F₂ individuals. Sequencing of *PsMLO1* from commercial *er1* resistant cultivars also revealed an important mutation, expected to be associated to a non-functional allele. Taken together, results point to the identity between *er1* and *mlo* resistances and are expected to be of great breeding importance for the development of cultivars via marker-assisted selection. Furthermore, our study strongly suggests that reverse genetics approaches targeting *MLO* homologs are likely to lead to broad-spectrum powdery mildew resistance across crop species.