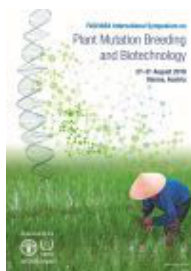


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MUTATION BREEDING FOR POWDERY MILDEW RESISTANCE IN PEA (*PISUM SATIVUM* L.)

The broad-spectrum (mlo) resistance to powdery mildew in barley (*Hordeum vulgare* L.) was demonstrated to be conferred by recessive mutations at the Mlo locus. In the Laboratory of Genomics and Genetic Improvement (LGGI), we induced for the first time, via experimental chemical mutagenesis, two powdery mildew resistant mutants in pea (*Pisum sativum* L.). Via complementation crosses the two recessive mutations were found to affect the same locus, identified as the naturally mutated in the resistant line Mexique locus er1, genetically mapped to the pea linkage group VI. After isolation and sequencing of the barley gene Mlo, other research groups identified the expressed sequence of a homologous gene in pea, which was found to coincide with er1, which, accordingly, was renamed as PsMLO1. The identification by our laboratory of the genomic sequence of this locus allowed the identification of the specific point mutations induced in our mutants, which create stop codons and truncate the cell transmembrane protein coded by this gene. In both cases, the mutations eliminated a restriction enzyme recognition site allowing the easy identification of the mutated loci by CAPS analysis. More recently, we have validated a hyper-variable SSR marker within the PsMLO1 gene as highly useful for marker-assisted selection in multiple pea powdery mildew resistance breeding programmes. Two advanced lines derived from crosses involving one of our PM resistant mutants will be next year submitted for release as new cultivars. The identification of Mlo homologous genes in other crops and the future prospects of mutation breeding for powdery mildew resistance are discussed.

Country or International Organization

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