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## Functional analysis of Mlo genes in powdery mildew resistance in melon

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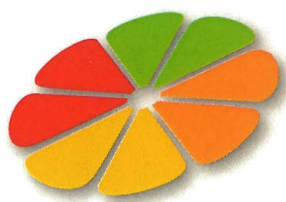
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**Functional analysis of *Mlo* genes in powdery mildew resistance in melon**

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Powdery mildew is one of the most damageable diseases in *Cucurbitaceae* crops. Two fungal species, *Podosphaera xanthii* and *Golovinomyces cichoracearum* are the main causal agents. Powdery mildews are ascomycete, obligate biotroph fungi. They thus require host plant genes for their infection cycle. These genes involved in host plant susceptibility are promising targets for powdery mildew resistance. Among them, members of the *Mlo* family are used by powdery mildews in a conserved mechanism across plant species.

In this work, we aim to investigate the function of *Mlo* genes in the interaction between melon and cucurbit powdery mildews, with the aim of creating new, broad spectrum resistance sources to these pathogens.

We identified 15 *Mlo* genes that are well conserved across the three *Cucurbitaceae* species, melon, cucumber and watermelon. Phylogenetic analysis identified 5 members as candidates for powdery mildew susceptibility. Among these genes, *CmMLO2* was shown to be highly overexpressed upon powdery mildew infection. To validate the function of the genes, we used a TILLING approach. We identified a *Cmmlo2* non sense mutant in a melon mutagenized population. This mutant exhibited a complete resistance to *G. cichoracearum* and a partial resistance to several strains of *P. xanthii*. In parallel, we carried out an allele mining approach to search for natural diversity of *CmMLO* genes in a melon collection.

In this work, we demonstrated the involvement of *Mlo* genes from melon in susceptibility to two powdery mildew species and created novel alleles of resistance, not found in the natural diversity.

**Key words:** *Cucumis melo*, *Golovinomyces cichoracearum*, *MLO*, *Podosphaera xanthii*, resistance, TILLING