

Functional analysis of Mlo genes in powdery mildew resistance in melon

Sonia Elbelt, Nathalie Giovinazzo, Verane Sarnette, Marc Bardin, Christelle Troadec, Abdelhafid Bendahmane, Catherine Dogimont

► **To cite this version:**

Sonia Elbelt, Nathalie Giovinazzo, Verane Sarnette, Marc Bardin, Christelle Troadec, et al.. Functional analysis of Mlo genes in powdery mildew resistance in melon. 5. ISHS International Symposium, Curcubits 2015, Jun 2015, Murcia, Spain. hal-02744309

HAL Id: hal-02744309

<https://hal.inrae.fr/hal-02744309>

Submitted on 3 Jun 2020

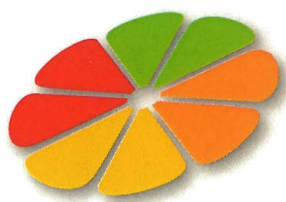
HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Cucurbits 2015

V ISHS International Symposium



Programme and Book of Abstracts

Organization:



S2.3

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

S. Elbelt¹, N. Giovinazzo¹, V. Sarnette¹, M. Bardin², C. Troadec³, A. Bendahmane³, C. Dogimont¹

¹ INRA, UR1052 Génétique et Amélioration des Fruits et Légumes, Domaine St Maurice - Allée des Chênes CS 60094, 84143 Montfavet Cedex, France

² INRA, UR407 Pathologie végétale, Domaine St Maurice - Allée des Chênes CS 60094, 84143 Montfavet Cedex, France

³ INRA, UMR1165 Unité de Recherche en Génomique Végétale, 2, rue Gaston Crémieux, CP5708, 91057 Evry Cedex, France

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