



**HAL**  
open science

## **A two genes – for – one gene interaction between Leptosphaeria maculans and Brassica napus**

Yohann Petit, Alexandre A. Degrave, Michel Meyer, Françoise Blaise,  
Benedicte Ollivier, Thierry Rouxel, Isabelle Fudal, Marie-Helene Balesdent

► **To cite this version:**

Yohann Petit, Alexandre A. Degrave, Michel Meyer, Françoise Blaise, Benedicte Ollivier, et al.. A two genes – for – one gene interaction between *Leptosphaeria maculans* and *Brassica napus*. 2016 IS-MPMI XVII CONGRESS, Jul 2016, Portland, United States. 2016. hal-02795249

**HAL Id: hal-02795249**

**<https://hal.inrae.fr/hal-02795249>**

Submitted on 5 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.

## **A two genes – for – one gene interaction between *Leptosphaeria maculans* and *Brassica napus***

Auteurs : Yohann Petit, Alexandre Degrave, Michel Meyer, Françoise Blaise, Bénédicte Ollivier, Thierry Rouxel, Isabelle Fudal, Marie-Hélène Balesdent

*Leptosphaeria maculans* is a hemibiotrophic ascomycete which causes stem canker of oilseed rape. That phytopathogenic fungus interacts with its host (*Brassica napus*) according to the gene-for-gene concept. The most economically and environment friendly method of control of stem canker is the genetic control by using host resistance. Single gene resistance is extremely efficient, but races of the pathogen virulent towards a resistance gene can appear in a few years and necessitates continuously new breeding programs. Moreover, specific resistances are rare in oilseed rape, and a lot of efforts are made to find other resistance genes in other Brassica species. To date, 11 interactions were genetically characterized between *L. maculans* avirulence genes and corresponding resistance genes in *Brassica*, and 5 of those avirulence genes were cloned. Recently, the avirulence gene *AvrLm10* which is recognized by the resistance gene *Rlm10* of the black mustard (*Brassica nigra*) has been cloned. *AvrLm10* corresponds in fact to two avirulence genes *AvrLm10\_1* and *AvrLm10\_2* which are located in the same AT-rich genomic region. They encode for small secreted proteins (SSP), are co-regulated and over-expressed 7 days post-infection. Each of them is necessary but not sufficient to induce resistance towards *Rlm10*. Silencing of one of those genes is sufficient to abolish recognition by *Rlm10*. Silencing by RNA interference of *AvrLm10-1* induces an increase of lesion size on oilseed rape leaves while silencing of *AvrLm10-2* has no major effect on aggressiveness of the fungus. That interaction of two avirulence genes against one resistance gene is therefore different from the classical gene-for-gene concept. It suggests that *AvrLm10\_1* and *AvrLm10\_2* could directly interact and / or that they could target the same plant protein. A Y2H screen suggested a direct interaction between *AvrLm10-1* and *AvrLm10-2*. This interaction was confirmed with Bimolecular Fluorescence Complementation (BiFC) experiments. Coimmunoprecipitation experiments are also in progress to confirm this interaction.