

A two genes – for – one gene interaction between Leptosphaeria maculans and Brassica napus.e

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

▶ To cite this version:

Yohann Petit, Alexandre A. Degrave, Michel Meyer, Francoise Blaise, Benedicte Ollivier, et al.. A two genes – for – one gene interaction between Leptosphaeria maculans and Brassica napus.e. Workshop on experimental approaches for the investigation of effector function, Feb 2015, Tel-Aviv, Israel. hal-01456011

HAL Id: hal-01456011

https://hal.science/hal-01456011

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 hemibiotophic 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 RIm10 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 encore for small secreted proteins (SSP), are coregulated 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. Communoprecipitation experiments are also in progress to confirm this interaction.