



**HAL**  
open science

**Investigating the involvement of the  
heterochromatic-associated histone modification,  
H3K27me3, in the control of effector gene expression in  
Leptosphaeria maculans**

Colin Clairet, Jessica L. Soyer, Françoise Blaise, Julie Gervais, Isabelle Fudal

► **To cite this version:**

Colin Clairet, Jessica L. Soyer, Françoise Blaise, Julie Gervais, Isabelle Fudal. Investigating the involvement of the heterochromatic-associated histone modification, H3K27me3, in the control of effector gene expression in *Leptosphaeria maculans*. Effectome meeting 2016, Nov 2016, Lauret, France. hal-02795172

**HAL Id: hal-02795172**

**<https://hal.inrae.fr/hal-02795172>**

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.

## Investigating the involvement of the heterochromatic-associated histone modification, H3K27me3, in the control of effector gene expression in *Leptosphaeria maculans*

Colin Clairet, Jessica L. Soyer, Françoise Blaise, Julie Gervais and Isabelle Fudal

UMR BIOGER, INRA, AgroParisTech, Université Paris-Saclay, 78850 Thiverval-Grignon, France  
*Leptosphaeria maculans*, a hemibiotrophic fungus responsible of stem canker, colonises oilseed rape in two stages: an early stage of cotyledon or leaf colonisation, and a late colonisation stage during which the fungus colonises systemically without visible symptom the plant before stem canker appears. *L. maculans* presents a bipartite genome structure alternating gene-rich and transposable element (TE)-rich regions. TE-rich regions, which encompass one third of the genome, are enriched in putative effector-encoding genes that present the same expression pattern (no or a low expression level during *in vitro* growth and a strong over-expression during early infection in cotyledons and leaves; ‘early’ effectors; Rouxel et al., 2011). In contrast, gene-rich regions were recently reported to contain putative effector-encoding genes specifically expressed during the late stages of stem infection (‘late’ effectors; Gervais et al., in press). We have previously investigated the involvement of the chromatin structure of repeat-rich regions on the expression of ‘early’ effector genes: RNAi silencing of two genes encoding key players in heterochromatin assembly through histone modification H3K9me3, HP1 and KMT1, induced an over-expression of genes located in AT-isochores, particularly ‘early’ effector genes but no modification of ‘late’ effector genes expression. Here, we investigated the involvement of another key player in heterochromatin assembly, KMT6, involved in the heterochromatic-associated histone modification H3K27me3. For this purpose, we silenced expression of *KMT6* by RNAi and obtained five transformants in which *KMT6* expression was decreased to less than 20 % residual expression. Preliminary characterization of the transformants including growth, conidiation, pathogenicity and expression of a few ‘early’ and ‘late’ effector genes will be presented.

- Gervais J., Plissonneau C., Linglin J., Meyer M., Labadie K., Cruaud C., Fudal I., Rouxel T. and Balesdent M.H. (2016). Different waves of effector genes with contrasted genomic location are expressed by *Leptosphaeria maculans* during cotyledon and stem colonisation of oilseed rape. *Molecular Plant Pathology* (in press)

- Rouxel T., Grandaubert J., Hane J.K., Hoede C., van de Wouw A.P., Couloux A., et al. (2011). Effectors diversification within compartments of the *Leptosphaeria maculans* genome affected by RIP mutations. *Nature communications* 2: 202.