



HAL
open science

Investigating the involvement of the chromatin state in the control of effector gene expression in *Leptosphaeria maculans*

Colin Clairet, Nicolas Lapalu, Adeline Simon, Françoise Blaise, Julie Gervais, Jessica L. Soyer, Isabelle Fudal

► To cite this version:

Colin Clairet, Nicolas Lapalu, Adeline Simon, Françoise Blaise, Julie Gervais, et al.. Investigating the involvement of the chromatin state in the control of effector gene expression in *Leptosphaeria maculans*. 40th New Phytologist Symposium, Sep 2017, Vienne, Austria. 2017. hal-02786095

HAL Id: hal-02786095

<https://hal.inrae.fr/hal-02786095>

Submitted on 4 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 chromatin state in the control of effector gene expression in *Leptosphaeria maculans*

Colin Clairet, Nicolas Lapalu, Adeline Simon, Françoise Blaise, Julie Gervais, Jessica L. Soyer 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). 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). 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 performed analysis of nucleosome positioning, chromatin structure and gene expression at the genome scale combining MAINE-seq, ChIP-seq and RNA-seq data during *in vitro* growth of *L. maculans*. We analysed *in vitro* ChIP-seq data targeting heterochromatin modifications, H3K9me3 and H3K27me3, and a euchromatin mark, H3K4me2 and found that gene-rich regions are associated with H3K4me2 and H3K27me3 while TE-rich regions are associated with H3K9me3. Effector genes are also associated with distinct heterochromatin marks according to their genomic location and expression kinetics: while ‘early’ effector genes located in TE-rich regions are associated with H3K9me3, ‘late’ effector genes located in gene-rich region are associated with H3K27me3. Genome-wide nucleosome positioning was analysed using MAINE-seq data, showing distinct nucleosome organization for genes located in TE-rich or gene-rich regions, and according to gene expression level. Finally, we recently investigated the role of another key player in heterochromatin assembly, KMT6, involved in the heterochromatic-associated histone modification H3K27me3, on the control of effector gene expression. RNAi silencing of *KMT6* leads to a deregulation of genes not only associated with H3K27me3 in the wild type strain, suggesting a relocation of different histone modifications.