

# #102

## Genome-wide histone map of the blackleg fungus *Leptosphaeria maculans*

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*Jessica L. Soyler*<sup>1,2</sup>  
Colin Clairet<sup>1,2</sup>  
Elise Gay<sup>1,2</sup>  
Françoise Blaise<sup>1,2</sup>  
Eva H. Stukenbrock<sup>1,2</sup>  
Isabelle Fudal<sup>1,2</sup>

1 UMR BIOGER, INRA,  
AgroParisTech, Paris-  
Saclay University,  
Thiverval-Grignon, France

2 Max Planck Institute for  
Evolutionary Biology,  
Plön, and Christian-  
Albrechts University of  
Kiel, Germany

*Leptosphaeria maculans*, a hemibiotrophic fungus responsible for stem canker of oilseed rape (*Brassica napus*), colonises its host in two stages: an early stage on young leaves, and a late stage during which the fungus colonises the host systemically without any visible symptom before stem canker develops. *L. maculans* presents a genomic structure alternating GC-rich, gene-rich blocks, and AT-rich, repeat-rich blocks. The latter are proposed to be heterochromatic domains, as they are gene-poor, repeat-rich and present lower recombination rates than GC-isochores. During host infection, effector genes, encoding sets of molecules facilitating invasion, are expressed in several synchronous waves. While gene-poor, AT-isochores are enriched in putative effector genes specifically expressed during plant infection. In order to get a complete view of the chromatin structure and its influence on gene expression, a genome-wide histone map was established using ChIP-sequencing targeting two heterochromatic marks, H3K9me3 and H3K27me3 and a euchromatic mark, H3K4me2, and combined with transcriptomic data in vitro. AT-isochores are enriched in H3K9me3 while GC-isochores are mainly associated with the euchromatic mark, H3K4me2. Interestingly, another heterochromatic mark, H3K27me3, was also found in GC-isochores but not in AT-isochores. Analysis of transcriptomic data confirmed that, in *L. maculans*, H3K4me2 is permissive for gene expression while H3K9me3 and H3K27me3 are associated with gene repression. In *L. maculans*, pathogenicity-related genes and genes highly induced upon host infection are associated with heterochromatin, in vitro. In order to confirm involvement of the chromatin structure in the regulation of effector genes, CRISPR-Cas9 mutants of KMT1 and KMT6, responsible for H3K9me3 and H3K27me3 deposition, have been generated and are currently characterized for their ability to infect leaves and stems of oilseed rape, and to express effector genes.

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