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Leptosphaeria maculans, a hemibiotrophic fungus responsible for 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. While TE-rich regions are enriched in putative effector-encoding genes strongly over-expressed during early infection ('early' effectors), gene-rich regions contain putative effector-encoding genes specifically expressed during late infection ('late' effectors). Here, we analysed nucleosome positioning, chromatin structure and gene expression at the genome scale combining MAINE-seq, ChIP-seq and RNA-seq data during axenic growth and performed functional analysis of two players of heterochromatin assembly (Kmt1 and Kmt6). We analysed *in vitro* ChIP-seq data targeting two heterochromatin modifications, H3K9me3 and H3K27me3, and a euchromatin modification, H3K4me2, and found that gene-rich regions are associated with H3K4me2 and H3K27me3 while TE-rich regions are associated with H3K9me3. Analysis of *in vitro* MAINE-seq data showed distinct nucleosome organization for genes located in TE-rich or gene-rich regions, and according to gene expression level. While RNAi silencing of *KMT1*, which encodes a protein involved in H3K9me3 deposition, induced an over-expression of genes located in TE-rich regions, particularly 'early' effector genes, silencing of *KMT6*, involved in H3K27me3 deposition, leads to a deregulation of genes not only associated with H3K27me3 in the wild type strain, suggesting a relocation of different histone modifications.