



Different waves of effector genes with contrasted genomic location are expressed by *Leptosphaeria maculans* during cotyledon and stem colonization

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POSTER SESSION ABSTRACTS
Session CS2 Pathogenesis and symbiosis
CS2M21

Monday 4th April
14:00 - 16:00

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Different waves of effector genes with contrasted genomic location are expressed by *Leptosphaeria maculans* during cotyledon and stem colonization

Leptosphaeria maculans, causal agent of blackleg disease, colonizes oilseed rape (*Brassica napus*) in two stages: a short and early colonization stage corresponding to cotyledon and leaf colonization leading to leaf spots development, and a late colonization stage during which the fungus colonizes systemically and symptomlessly the plant during several months before stem canker appears. To date, determinants of late colonization stage are poorly understood. Here, we hypothesized that *L. maculans* deployed effectors different from the one deployed in the early colonization and enabling the symptomless colonization. To get insight into these determinants, we performed a RNA-seq pilot project comparing fungal gene expression during the early colonization and the late colonization stages. Despite the low fraction of fungal material in infected tissues, enough fungal transcripts were detected to conduct a RNA-seq analysis focused on the discovery of new effector genes. 175 late effector candidates under-expressed in the early colonization stage and over-expressed in the infected stem were identified with this approach. These effector genes putatively involved in the systemic colonization are located in gene-rich regions, whereas the early effector genes involved in cotyledon colonization are located in gene-poor regions of the genome. Our analysis reveals a link between the expression pattern of effectors and their genomic location.
