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## **In silico analysis of the transcription factor repertoire in *Leptosphaeria maculans* 'brassicae' to identify putative regulators of pathogenicity**

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**POSTER SESSION ABSTRACTS**  
**Session CS4 Regulatory networks**  
**CS4T41**

**Tuesday 5th April**  
**14:00 - 16:00**

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**In silico analysis of the transcription factor repertoire in *Leptosphaeria maculans* 'brassicae' to identify putative regulators of pathogenicity**

The *Leptosphaeria maculans*-*Leptosphaeria biglobosa* species complex encompasses species showing variable abilities to infect oilseed rape (*Brassica napus*). Within this species complex, *L. maculans* 'lepidii' (Lml) and *L. biglobosa* 'thlaspii' (Lbt) are found on cruciferous weeds while *L. maculans* 'brassicae' (Lmb), *L. biglobosa* 'canadensis' (Lbc) and *L. biglobosa* 'brassicae' (Lbb) are specialized on oilseed rape though they show different abilities to cause damage and different lifestyles. Lmb is a hemibiotrophic fungus and the most devastating species towards oilseed rape while Lbb and Lbc show a necrotrophic lifestyle and have a limited impact on the host. This species complex is thus an excellent model to infer the regulatory networks involved in lifestyle specialization on the same host plant. Our study aims at identifying putative regulators involved in the infection strategy and the adaptation of *L. maculans* 'brassicae' towards oilseed rape. For this purpose, we established the repertoire of transcription factor (TF) genes of Lmb and assessed their conservation within the species complex. As Lmb exhibits a complex lifestyle compared to the *L. biglobosa* species adapted towards oilseed rape, the transcriptional behavior of the TF genes in Lmb was analyzed and compared to those of Lbc in order to highlight specifically induced regulators of Lmb compared to those of the necrotrophic species. Thirty-seven TF genes of Lmb were identified as being over-expressed in planta, including two TFs unique to Lmb and one showing a signature of accelerated evolution in Lmb. Within the 37 TF genes over-expressed in planta in Lmb, 23 were conserved in Lbc but showed a different transcriptional behavior. This in silico analysis of the Lmb TF genes now provides us with numerous candidates to analyze the regulatory networks involved in drastic changes in pathogenic programs during the complex life cycle of Lmb on oilseed rape.

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