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Deciphering molecular functions and cellular processes targeted by structural families of effectors from *Leptosphaeria maculans* using experimental and computational approaches

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The main strategy to control the fungus *Leptosphaeria maculans*, the causal agent of stem canker in *Brassica napus* (oilseed rape), is genetic control by plant varieties carrying resistance (R) proteins. However, the massive deployment of a single source of resistance in the fields exerts strong selection pressures towards pathogen populations, leading to the rapid breakdown of the resistance. Recently, advances in effector repertoire prediction, in effector protein heterologous production and structural prediction algorithms have resulted in the identification of several effector families in *L. maculans*, these families being also present in other plant pathogenic fungi, mainly from the Dothiomycetes and Sordariomycetes. Furthermore, some of the structural analogues identified both in *L. maculans* and other plant pathogenic fungi share conserved functions during plant infection, suggesting an interesting evolutionary model. In addition, using transcriptomic data collected along the *L. maculans* life-cycle highlighted expression waves of distinct structural families, suggesting a striking coordination of them during the infection process. Here, we will review the recent advances in structural prediction / structure determination among *L. maculans* secretome and their implication to gain insight into the putative functions of candidate effectors. We will also propose possible strategies to improve resistance management or increase R proteins recognition spectrum using structural effector families.

Keywords: *Leptosphaeria maculans*, *Brassica napus*, structural prediction, effector, RNA-seq transcriptome, avirulence proteins, plant pathogen