

Mechanisms of infection and response of the fungal wheat pathogen *Zymoseptoria tritici* during compatible, incompatible and non-host interactions

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Zymoseptoria tritici causes Septoria tritici blotch on wheat. *Z. tritici* is an attractive model to investigate infection phase-specific gene expression and to conduct effector functional characterization. In our study, we conducted differential gene expression, gene ontology, KEGG enrichment and candidate effector prediction to determine differential responses of *Z. tritici* during infection. We evaluated different comparisons during a compatible interaction of *Z. tritici* with the susceptible cultivar Taichung29, two incompatible interactions with the resistant cultivars Veranopolis and Israel493, and one non-host interaction with barley, at 1, 3, 6, 10, 17 and 23 days after inoculation. We identify thirty-one putative effectors that are expressed during early disease development in a compatible interaction. To gain initial insight into their functions, we investigated their subcellular localizations using *Agrobacterium*-mediated transient expression in *Nicotiana benthamiana*. Our analyses revealed the majority of *Z. tritici* candidate effectors localized to the nucleus and cytosol. Four candidate effectors localized to the cytosol, and two candidate effectors localized to mobile cytosolic bodies, suggesting possible involvement in intracellular signaling or host gene regulation. Of the two effectors that localized to cytosolic bodies, one, Mycgr3109710, is annotated as a non-plant PR-1-like protein. PR-1 proteins from plants are involved in the activation of plant immune responses against pathogen attack. Moreover, the presence of PR-1-like in the genomes of other fungal pathogens and their role in virulence have been recently confirmed. These results advance our knowledge on the pathogen gene expression and reveal candidate effectors that might be involved in the initial plant immunity suppression.