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Résumé en anglais	Background Glutathione transferases (GSTs) represent an extended family of multifunctional proteins involved in detoxification processes and tolerance to oxidative stress. We thus anticipated that some GSTs could play an essential role in the protection of fungal necrotrophs against plant-derived toxic metabolites and reactive oxygen species that accumulate at the host-pathogen interface during infection. Results Mining the genome of the necrotrophic Brassica pathogen Alternaria brassicicola for glutathione transferase revealed 23 sequences, 17 of which could be clustered into the main classes previously defined for fungal GSTs and six were 'orphans'. Five isothiocyanate-inducible GSTs from five different classes were more thoroughly investigated. Analysis of their catalytic properties revealed that two GSTs, belonging to the GSTFuA and GTT1 classes, exhibited GSH transferase activity with isothiocyanates (ITC) and peroxidase activity with cumene hydroperoxide, respectively. Mutant deficient for these two GSTs were however neither more susceptible to ITC nor less aggressive than the wild-type parental strain. By contrast mutants deficient for two other GSTs, belonging to the Ure2pB and GSTO classes, were distinguished by their hyper-susceptibility to ITC and low aggressiveness against Brassica oleracea. In particular AbGSTO1 could participate in cell tolerance to ITC due to its glutathione-dependent thioltransferase activity. The fifth ITC-inducible GST belonged to the MAPEG class and although it was not possible to produce the soluble active form of this protein in a bacterial expression system, the corresponding deficient mutant failed to develop normal symptoms on host plant tissues. Conclusions Among the five ITC-inducible GSTs analyzed in this study, three were found essential for full aggressiveness of A. brassicicola on host plant. This, to our knowledge is the first evidence that GSTs might be essential virulence factors for fungal necrotrophs.
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