

Phosphoproteome profiles of the phytopathogenic fungi *Alternaria brassicicola* and *Botrytis cinerea* during exponential growth in axenic cultures

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Auteur	Davanture, Marl�ne [1], Dumur, J�r�me [2], Bataille-Simoneau, Nelly [3], Campion, Claire [4], Valot, Beno�t [5], Zivy, Michel [6], Simoneau, Philippe [7], Fillinger, Sabine [8]
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R�sum� en anglais	<p>This study describes the gel-free phosphoproteomic analysis of the phytopathogenic fungi <i>Alternaria brassicicola</i> and <i>Botrytis cinerea</i> grown in vitro under nonlimiting conditions. Using a combination of strong cation exchange and IMAC prior to LC-MS, we identified over 1350 phosphopeptides per fungus representing over 800 phosphoproteins. The preferred phosphorylation sites were found on serine (>80%) and threonine (>15%), whereas phosphorylated tyrosine residues were found at less than 1% in <i>A. brassicicola</i> and at a slightly higher ratio in <i>B. cinerea</i> (1.5%). Biological processes represented principally among the phosphoproteins were those involved in response and transduction of stimuli as well as in regulation of cellular and metabolic processes. Most known elements of signal transduction were found in the datasets of both fungi. This study also revealed unexpected phosphorylation sites in histidine kinases, a category overrepresented in filamentous ascomycetes compared to yeast. The data have been deposited to the ProteomeXchange database with identifier</p>
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