Proteome and secretome analysis of *Xanthomonas campestris* pv. *campestris* in the interaction with the host plant

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The genus *Xanthomonas* is formed by several species which cause severe losses in agriculture around the world. In Brazil, one of the most relevant species is *X. campestris* pv. *campestris*, which is responsible for black rot in cruciferous plants. This pathogen causes yield losses in several cultures, including cabbage, cauliflower and broccoli. Although the sequence of this bacterium has been revealed, there is little information about the global gene and protein expression of this pathogen in the interaction with the host plant. The objective of the present work was to analyze the proteins of *X. campestris* pv. *campestris* expressed during the interaction with the host plant *Brassica oleracea*, as well as detect the activity of extracellular enzymes involved in pathogenicity. The bacterium was infiltrated in leaves of the susceptible plant and later recovered for analysis. The supernatant was also recovered for the analysis of the secretome and for the detection of the activity of xylanases, alfa-arabinofuranosidases, poligalacturonases and cellulases. The recovered cells and supernatant were used for protein extraction and the proteins obtained were separated by bidimensional gel electrophoresis. The protein profile of the bacterium cultured in the complex medium NYG and the supernatant recovered after infiltration of leaves with distilled water were used as control conditions. In the proteome analysis, five differentially expressed proteins were analyzed by mass spectrometry and two of them were identified as a ribosome recycling factor" – RRF and an enoyl-CoA hydratase. The secretome analysis revealed a group of acidic differentially expressed proteins, which were absent in the control map obtained. These proteins will be further analyzed by mass spectrometry in order to identify their functions. The analysis of the extracellular enzymes revealed a higher activity in leaves infiltrated with the bacterium when compared to the control condition. We hope to contribute to a better understanding of the pathogenicity mechanisms of *X. campestris* pv. *campestris*.

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