

ANALYSIS OF THE *ARABIDOPSIS THALIANA* - *XANTHOMONAS CAMPESTRIS* PV. *CAMPESTRIS* PATHOSYSTEM USING PROTEOMICS TOOLS

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The proteome is the complement of proteins expressed at a particular point in time. It reveals the expression of the genome including how proteins are modified during a biological interaction. Only recently has a proteomics approach begun to be used to study plant-pathogen interactions due to their complexity. *Xanthomonas campestris* pv. *campestris* (Xcc) causes black rot of cabbage, and can infect a large number of species in the Brassicaceae family, including *Arabidopsis thaliana*. Worldwide black rot is considered the most important disease of brassicas. To begin to understand the interaction between Xcc and a resistant *A. thaliana* ecotype, we have used a proteomics approach to identify plant proteins that display altered expression in the presence of the Xcc pathogen. Two dimensional gel electrophoresis of *Arabidopsis* leaf proteins six days after Xcc or mock-inoculation with buffer was performed. After silver staining, gel images were compared using the BioNumerics software to determine the differential protein expression pattern. The results obtained were also confirmed using software ImageMaster™ 2D Platinum 6.0. A total of 98 proteic spots were selected based on their differential expression between the two treatments. These proteic spots are being analyzed by mass spectrometry for identification.

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