10.9 ANALYSIS OF *BOTRYTIS CINEREA* SECRETOME. F.J. Fernández-Acero, T. Colby, A. Harzen, U. Wieneke, C. Garrido, M. Carbú, I. Vallejo, J. Schmidt and J.M. Cantoral. *Laboratory of Microbiology, Marine and Environmental Sciences Faculty, University of Cádiz, Pol. Río San Pedro s/n, Puerto Real, 11510, Cádiz, Spain. Email: jesusmanuel.cantoral@uca.es*

The ascomycete *Botrytis cinerea* is a phytopathogenic fungus infecting a number of crops including tomatos, grapes and strawberries, and causing significant yield losses in these crops in Andalusia (Spain) each year. In the last few years, *B. cinerea* has been adopted as an important model system in molecular phytopathology. Several approaches have been applied to this fungus to unravel its mechanisms of infection. These studies have revealed the complexity and wide variety of infection strategies used by *B. cinerea* that are mediated by a complex set of genes/proteins called pathogenicity factors. Many of these factors have been described in phytopathogenic fungi as proteins excreted to the media (secretome). The study of this differential subproteome can contribute to a comprehensive view of the role of these factors and may reveal new foci for the fight against the pathogen. In this work a proteomic approach based on 2-DE has been developed to establish the proteins secreted to culture media supplemented with various plant elicitors. Proteins were obtained from the culture media by an improved method based on DOC-TCA precipitation and phenol extraction. From the 2-DE analyses, a relevant set of proteins has been identified including known virulence factors such as pectin methyl esterases and proteases. Identification of other enzymes implicated in the infection mechanism indicate that this proteome-mining is a promising strategy for discovering new pathogenicity factors.