

Identification of *Chlamydia pneumoniae* antigens via immuno-proteomics using high resolution FTICR mass spectrometry

Iuliana Susnea¹, Sebastian Bunk², Corinna Hermann² and Michael Przybylski¹

¹Laboratory of Analytical Chemistry and Biopolymer Structure Analysis,
Department of Chemistry, University of Konstanz
E-mail: iuliana.susnea@uni-konstanz.de

²Laboratory of Biochemical Pharmacology, Department of Biology, University of
Konstanz

Chlamydia pneumoniae is an important respiratory pathogen that causes approximately 5 % of all cases of bronchitis and it is believed to be responsible for about 10 % of the cases of community-acquired pneumonia. *C. pneumoniae* is an obligate intracellular bacteria with an unique life cycle alternating between an infectious but non-replicating elementary body (EB) and a non-infectious but metabolically active reticulate body (RB). More than 50 % of the adult European population has antibodies against *C. pneumoniae*. There is evidence that *C. pneumoniae* can persist in the host after primary infection, which may be associated with atherosclerosis leading to cardiovascular diseases. Although this association has been investigated by seroepidemiological studies for more than 15 years, the role of *C. pneumoniae* infection still remains controversial and is presently unresolved. One major problem of current studies is the lack of reproducibility of serological tests. The aim of the present study is to identify the *C. pneumoniae* antigen structures that are relevant for serodiagnosis.

The combination of 2D-gel-electrophoresis with immuno-blotting and high resolution FT-ICR mass spectrometry has been found to be an excellent tool for the identification of antigens. Detailed studies were carried out on the optimization of the *C. pneumoniae* culture and the 2D-gel sample preparation. For immuno-blotting sera from 18 seropositive and 9 seronegative donors were used. Approximately 50 antigenic spots were found, the most characteristic of which were subjected to further analysis. Antigenic spots were excised from the gels, digested with trypsin and analysed by FT-ICR-MS. The appearance of two antigenic protein spots, one in almost all seropositive donors, and the other indicative of a persistent infection, have been of particular interest. These proteins may represent potential biomarkers for serodiagnosis.

ACKNOWLEDGEMENT

This work has been supported by the Deutsche Forschungsgemeinschaft, Bonn, Germany (Forschergruppe "DNA- and Oligosaccharide Chips – Analyse sekundärer Genprodukte").