PROTEIN SPECIES-SPECIFIC REGULATION OF PHOSPHOPROTEINS IN *HELICOBACTER PYLORI* INFECTED AGS CELLS DETECTED BY METABOLIC LABELLING

P.R. Jungblut[(1)], C. Holland[(1)], M. Schmid[(1)], U. Zimny-Arndt[(1)], R. Stein[(2)], and T.Meyer[(1)]

[(1)]Max Planck Institute for Infection Biology, [(2)]I&B Informatics and Biology, Berlin Germany

Half of the world's population is infected by *Helicobacter pylori*. The infection may cause chronic inflammation of the gastric mucosa leading to peptic ulceration and/or gastric cancer. With the aim to find *H. pylori* induced variation in the phosphoproteome of infected human AGS cells we compared SILAC labelled cells after infection with unlabelled cells without infection by 2-DE/MALDITOFTOF-MS after enrichment of phosphoproteins from the soluble proteins of AGS cells by IMAC. Many proteins of the 2-DE protein pattern occurred in series of protein spots, which represented different protein species of one protein per series. Quantification by SILAC revealed for several of these proteins a protein species-specific regulation after infection with *H. pylori*. In the case of SNRNP-70 we identified by MS 26 protein species, from which 10 were up-regulated, 5 were down-regulated and 11 were not regulated after infection with *H. pylori*. From the quantification data three other proteins were worked out in detail: SFRS2, SFRS3, and U2AF2. These proteins belong to the SR proteins, which are known to include an enormous number of phosphorylation sites and other posttranslational modifications. All of them showed again a characteristically protein species-specific regulation after infection. Here we have shown that protein speciation represents a regulatory level for host-pathogen interaction. The next challenge will be to elucidate the complete primary structure and the function of each protein species.

These results confirm the protein species concept, which claims the need to separate proteins into their different protein species to reach the functional level of proteomics. Only then functionally relevant molecules may be detected, which will be useful as biomarkers.