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The approach to infection research by mass spectrometry

Naoya Hatano[1) 2)]

Mass spectrometry is an analytical technique becoming increasing important in bioscience research. It enables not only to identify biomolecules such as peptides and metabolites, but also to perform a high-sensitive and semi-quantitative analysis of biomolecules. Especially in infectious disease study, the most famous tool is known as “Biotyper”, which is a microbial identification system based on MALDI-TOF mass spectrometry allowing unbiased identification of microorganisms. Nowadays, this system is used in many hospitals to provide the best medical treatment. Thus, mass spectrometry is useful system to discriminate among organisms. Therefore, we thought that the proteomic study of cells infected with bacteria was useful for the elucidation of the mechanism of bacterial infection.

Here, we introduce a previous research about the infection of *Helicobacter pylori* (*H. pylori*) using proteomics by mass spectrometry. *H. pylori* is a spiral-shaped, Gram-negative, and microaerophilic bacterium which colonizes the human gastric epithelium and is associated with gastritis, gastric and duodenal ulcers, and gastric cancer. So far, two important virulence factors, CagA and VacA, have been identified. CagA is delivered into gastric epithelial cells by the *cag* type IV secretion system where it is tyrosine-phosphorylated and wired to host signal transduction pathways. To find other virulence factors, we infected AGS (human gastric adenocarcinoma) cells with *H. pylori* strain 26695, whose genome has been completely sequenced. After infection, host cell cytosol and membrane fractions were separated from bacteria. We found the *H. pylori* membrane proteins in host membrane fraction by proteomics techniques using mass spectrometry. These *H. pylori* proteins might have important roles in the attachment of *H. pylori* to epithelial cells.

1）Department of Medical Technology, Faculty of Health Sciences

2）Graduate School of Interdisciplinary Science and Engineering in Health Systems, Okayama University