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Proteome reorganization of the bacterium upon invasion of a host cell as a mechanism of adaptation: A *Mycoplasma gallisepticum* model

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What strategies do bacteria employ for adaptation to its host and are these strategies different for varied hosts? At the moment, there are a lot of studies concerned interaction of bacteria with their hosts but still has not been fully understood, which global changes bacteria undergo during invasion and persistence in the host cell and how these changes depend on the type of host. In this study, we used a *Mycoplasma gallisepticum* model because members of the genus *Mycoplasma* are characterized by a reduced genome, the size of which varies from 0.58-2.20 Mb, low content of GC bases, lack a cell wall and many metabolic pathways. All these qualities make *M. gallisepticum* convenient model for the study of system biology. It was shown using a combination of two-dimensional differential gel electrophoresis, MALDI-MS, LC-MS and MRM methods that *M. gallisepticum* S6 was capable to switch to another proteome state during the invasion of various eukaryotic host cells (human, chicken and mouse) and maintain that state for several passages. Eukaryotic cells induced similar proteome reorganization of *M. gallisepticum* during infection, despite different origins of the host cell lines. The most notable changes involved oxidative stress response, glycolysis, translation factors and hemagglutinins of VlhA family. We observed the up-regulation of the two regulatory proteins: SpxA and YebC/PmpR. We constructed SpxA- and YebC/PmpR-overexpressing strains of *M. gallisepticum* and identified the protein response similar to the one observed in intracellular conditions. We proposed their role as regulators of the adaptation to intracellular environment.

Biography

Matyushkina Daria is a graduate Student in the Laboratory of Proteomic Analysis of the Federal Research and Clinical Centre of Physical-Chemical Medicine (Moscow, Russia) and published 12 papers in reputed journals.

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