Mycoplasma--host cell interaction mechanisms at the transcriptomic level

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Due to the small size of the genome, the bacteria bacteria of the genus Mycoplasma can serve as a model for a minimal cell. The classic way to study mycoplasma as a minimal cell is to use various perturbation models. One of the most interesting models for studying mycoplasma is the model of intracellular parasitism, its study will make it possible to draw conclusions about the possibilities and principles of the minimal cell structure. The aim of our work was to study the adaptation and regulation mechanisms of Mycoplasma gallisepticum at the transcriptomic level during intracellular infection. Infection was initiated by co-culturing HD3 cells with M. gallisepticum S6 culture, and then getting rid of extracellular mycoplasmas by treatment with gentamicin. Then, intracellular mycoplasmas were released by lysis of eukaryotes and cultured for several passages, after which RNA was isolated and libraries were prepared for sequencing, which was performed on a HiSeq 2500 device (Illumina). There were no large-scale changes in gene expression relative to the control culture cultivated on a rich medium. Only the gene of the family of lipoproteins and hemagglutinins (VlhA) showed a 4-fold increase in expression. Previously, proteins of the VlhA family were described as important for mycoplasmas in pathogenesis and escape from the immune response. Changes in the expression of other genes indicate that invasion is stressful for the pathogen - the expression of other variable genes (10) is suppressed. Previously, we studied the change in the proteomic profile of M. gallisepticum in the same model and found significant changes in the proteome of mycoplasma. The observed differences in the adaptation of mycoplasma to the intracellular environment at the level of mRNA and proteins indicate an alternative way of regulating the response to stress in the minimal cell. This work was supported by the RSF grant No. 19-15-00427

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