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**Quantitative proteomic profiling of host – pathogen interaction: The interaction of *Francisella tularensis* LVS with macrophage using J774.2 cell line**A. Hartlova<sup>1</sup>, M. Link<sup>2</sup>, J. Lenco<sup>2</sup>, J. Stulik<sup>2</sup>

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*Francisella tularensis* is a facultative intracellular pathogen that can invade and replicate inside macrophages. The bacterium evades antimicrobial mechanisms of macrophages by escaping from phagosome into cytosol. There is growing evidence that various intracellular bacteria exploit specialized plasma membrane microdomains, commonly called membrane rafts, as an infectious strategy to mediate an alternative endocytic pathway avoiding fusion with lysosomes. Inhibition of phagosome-lysosome fusion has been proposed as a mechanism for survival inside host cells. Here, we present evidence that plasma membrane organization in membrane rafts is critical to *Francisella tularensis* uptake. Cholesterol depletion by methyl- $\beta$ -cyclodextrin and filipin significantly inhibited *Francisella tularensis* LVS uptake. Contemporary, we analyzed membrane raft proteins of macrophages that were recruited at the bacterial entry using proteomic quantitative approach. The response of the macrophage proteome to *Francisella tularensis* LVS internalization reflects the host immunity reaction as well as bacterial induced mechanisms that may be beneficial for pathogenic microbe.