SUMMARY

Francisella tularensis belongs to the most virulent bacteria. The infectious dose even in humans is very low, at most 10 CFU. Because of real threat of terrorist misuse, the scientific interest has been focused on the bacterium recently.

Despite of great improvements made in the understanding of its virulence mechanism in recent years, a substantial part of this key process remains to be revealed yet. The main goal of the presented thesis was to identify proteins that may play a significant role in the pathogenesis of tularemia. Based on that goal, we performed proteomics analyses of responses to several environmental factors that may be meet by the bacterium during the infectious cycle. Analysis of oxidative stress response revealed among other the induction of synthesis of HSP species and AhpC/TSA family protein. Increased production of the same enzyme was also observed during iron-starvation and during the stationary phase of growth as well. Furthermore, analysis of oxidative stress response excluded the regulatory role of IglC protein in the adaptation. Moreover, the detailed analysis performed later on, has clearly ruled out the involvement of IglC protein in a response to the oxidative stress induced by 5 mM hydrogen peroxide. Results obtained from proteome of bacterium grown in medium without any source of iron indicate that genes encoded in *igl* operon belong to a large group of bacterial virulence factors characterized by responsiveness to iron concentration. The findings were further strengthened by the previous study on mRNA level. Shotgun quantitative proteomics study in combination with exploratory data analysis revealed close regulation of expression *iglABC* and *pdpABC* genes under four different growth condition. There is a hope that the similarly regulated genes may be involved in similar biological process. Members of *igl* and *pdp* operons play a crucial role in pathogenesis of tularemia. Thus a hypothesis has arisen that proteins arranged with *k*-means clustering of iTRAQ data in the same cluster as Igl and Pdp proteins may also participate on the virulence.

Bacteria associated with, as high pathogenic potential as *Francisella tularensis*, must dispose very effective molecular tools for its virulence. Within the scope of the presented thesis, we applied the proteomics methods for mapping of molecules potentially associated with virulence in *Francisella tularensis*. The obtained and successfully published results conclusively proved efficiency of selected approach.