

## DESCRIPTION FOR THE GENERAL PUBLIC (IN ENGLISH)

Bacteria of the genus *Salmonella* are proven to be the most common cause of gastrointestinal diseases in the world and are a serious epidemiological problem. Each year millions of infections caused by rod-shaped *Salmonella* are recorded worldwide. Because of the lack of hospitalized patients as well as short and often benign course of the disease, most of salmonellosis are not recorded and that is the reason why the epidemiological data on salmonellosis, from different parts of the world, are greatly underestimated. *S. Enteritidis* and *S. Typhimurium* are the two of the most frequently isolated serovars in clinical practice causing salmonellosis worldwide. Moreover, in addition to the typical course of salmonellosis, *Salmonella* infections leading to parenteral symptoms and sepsis occur more frequently and are particularly dangerous to the health and lives of children, the elderly and people with immunodeficiency.

Bacteria of the genus *Salmonella* are characterized by high virulence and the number of features that predispose them to survive in serum. Structures on the surface of bacterial cell, responsible for avoiding of immunological system, are very important factors of pathogenesis. A significant aspect in the process of bacterial virulence is generating of changes in outer membrane in order to enable the survival and the multiplication of bacteria in an extremely severe conditions. Resistance to the bactericidal activity of the serum is a key virulence factor for the development of systemic infections, including bacteremia. The resistance of *Salmonella* to the serum activity is caused by several factors such as: the variable length of lipopolysaccharide O-specific chain, possession of polysaccharide capsules or fimbriae and the presence of specific outer membrane proteins.

The scientific goal of the project is to investigate the participation of outer membrane proteins in the phenomenon of serum resistance. The project assume that the research model i.e. bacterial chromosomal mutants without the long and very long O-specific chains in lipopolisaccharides allow to determine the role of outer membrane proteins in the phenomenon of serum resistance independently from the long and very long O-specific chains in the outer membrane. Mutants will be examined to establish the changes in the composition of the outer membrane proteins. The obtained data will allow for the identification of specific outer membrane proteins, which could be a key factor in the resistance process.

The project is based on the selection of *S. Enteritidis* chromosomal mutants without the long and/or very long O-antigen. Outer membrane proteins isolated from *Salmonella* mutants without the LPS fractions will be subjected to two-dimensional gel electrophoresis and then the comparative proteome analysis. The results of outer membrane proteins identification, performed using MALDI TOF/TOF and nano-LC-MS/MS analysis, will allow the construction of chromosomal mutants devoid of identified outer membrane proteins. The last stage of the project includes the analysis of the protein mutants to the elements of innate immunity.

The planned studies will attempt to examine the independent of lipopolysaccharide impact of outer membrane proteins on generating serum resistance among bacteria of the genus *Salmonella*. It is essential to carry out systematic research to determine the function of specific outer membrane proteins in the pathogenesis of *Salmonella* infection. Proteomic studies will provide the knowledge concerning new mechanisms of resistance of *Salmonella*, and the possible discovery of new proteins or new post-translational modifications will contribute to their future use as specific markers of virulence in rapid diagnostic tests for more efficient microbial diagnosis. This is especially important because of more frequently reported cases of life-threatening infections caused by bacilli, respecting children, the elderly and people with immunodeficiency.