The investigation of stress response pathways in germs is especially important because bacterial infections are still one of the leading causes of death worldwide, and there is also a significant risk of development of "super bacteria" resistant to the host immune system and antibiotics.

The aim of the proposal is to establish the role, genetic profile, and interactions between global stress response systems in cells of non-pathogenic and uropathogenic *Escherichia coli*. In the proposed study we are focusing on the role of three major stress responses (SOS, OxyR and SoxRS) that are induced by the bacterium under unfavorable conditions *eg*. UV exposure or oxidative stress induced by the host. Our basic assumption is that stress responses play a critical role in the survival and colonization process of the host during pathogenesis.

We plan to uniquely modify model non-harmful and pathogenic strains and determine the complete gene expression profiles for each system individually, and under co-activation conditions. We expect to find a new pool of regulated genes, which were not previously affected, in single constitutive mutants. We will compare the data collected from the pathogenic strain with the gene expression profiles measured in the non-harmful *E. coli*. We expect to better understand the metabolic and signaling pathways involved in the development of bacterial resistance to stress conditions, and additionally identify genes encoding for unknown virulence factors. The data will also help to better understand several other relevant phenomena, like the development of non-heritable or drug-resistant bacteria populations. We expect that the results will significantly enrich our understanding of the complicated and poorly understood ability of *E. coli* cells to survive stressful and harsh (host) conditions.