Yersinia enterocolitica is a human enteropathogen – the causative agent of yersiniosis, a zoonotic disease. Infection of the intestinal mucosa leads to inflammation and ulceration, accompanied by symptoms of fever, acute abdominal pain and diarrhea. *Y. enterocolitica* is transmitted by the fecal-oral route. The process of *Y. enterocolitica* infection is highly complex and involves the passage of bacteria from the external environment to the host organism. After the ingestion of contaminated food (undercooked meat products – especially pork, unpasteurized milk, or contaminated water) the bacteria travel through the gastrointestinal tract of the host to the terminal ileum, where they are able to invade the intestinal cells. During the initial infection as well as in the later stages of pathogenesis, *Y. enterocolitica* must adjust to several extremely different and harsh environments characterized by gastric and intracellular acidity, increased osmolarity, changing nutrients and ion availability, and competition with the host's microbiota in the intestine. In parallel with the process of infection, *Y. enterocolitica* synthesizes numerous virulence factors that appear progressively during the process of pathogenesis. These factors and the requisite metabolic pathways must be active under the correct spatiotemporal conditions and this is achieved by the modulation of gene expression.

The regulation of bacterial gene expression in response to environmental signals is dependent upon two-component signal transduction systems (TCSs). The archetype of the two-component system is EnvZ/OmpR. EnvZ is an inner membrane sensor kinase, which receives stimuli from the environment and transfers this signal to the cytoplasmic response regulator OmpR. Activated OmpR then binds to the regulatory regions of target genes to either activate or repress transcription. The EnvZ/OmpR system has been identified in a number of pathogens, where it participates in the regulation of target genes, both basic metabolism and virulence, in response to changes in osmolarity and pH.

Nothing is currently known about the OmpR-regulon (a collection of genes or operons under regulation by the OmpR protein) in the most virulent and dangerous to humans *Y. enterocolitica* bioserotype 1B/O:8. However, it has been shown that an *ompR* mutant of the 1B/O:8 bioserotype is attenuated in the murine yersiniosis model, suggesting that OmpR is involved in the virulence ability of this strain.

The aim of this project is to identify OmpR-DNA interactions occurring throughout the whole genome of the highly pathogenic *Y. enterocolitica* strain 8081 bioserotype 1B/O:8 grown at neutral and acid pH. To uncover the OmpR transcriptional regulatory network and elucidate its complex role in the virulence and adaptive abilities of *Y. enterocolitica* 1B/O:8, we will apply bacterial chromatin immunoprecipitation followed by high-throughput DNA sequencing (ChIP-seq). *In vivo* ChIP-seq will be supplemented by the electrophoretic mobility shift assay (EMSA) to analyze the ability of OmpR to bind to the promoter sequences of selected genes *in vitro*. To investigate the OmpR regulon in more depth, the direction of OmpR-dependent regulation (i.e. gene activation or repression) will be investigated. This will be done by assessing the transcript levels of a panel of genes using reverse transcription-quantitative PCR analysis (RT-qPCR).

To conclude, the identification of novel OmpR-regulated genes in this clinically important *Y. enterocolitica* strain will yield valuable insights into the role of OmpR in the modulation of the virulence, pathophysiology and adaptive abilities of this pathogen.