Yersinia enterocolitica is an important gastrointestinal pathogen that causes a range of human diseases from mild diarrhea to mesenteric lymphadenitis. *Y. enterocolitica* is a heterogeneous species with varying virulence. It synthesizes a wide variety of virulence factors, such as adhesins/invasin and many secreted toxins and effector proteins. Their synthesis is tightly regulated in response to different environmental factors including temperature. To adapt to changes in environmental conditions, bacteria regulate their gene expression at both the transcriptional and post-transcriptional levels. The importance of post-transcriptional regulation has only recently become a focus of interest with the discovery of numerous small non-coding RNAs (sRNAs). *Trans*-encoded sRNAs are expressed by loci that are separate from their target genes. These sRNAs are usually 50-150 nucleotides long and they modulate mRNA translation and/or stability by imperfect base-pairing interactions. Many sRNAs require the chaperone Hfq for their function. The usual outcome of sRNA-target mRNA interaction is the silencing of gene expression. To fully understand the biological function of sRNA, it is necessary to identify the cognate interacting mRNA targets. In non-pathogenic *Escherichia coli*, two trans-encoded sRNAs, OmrA and OmrB, regulate gene expression by base pairing with target mRNAs and stimulating their degradation. This causes a reduction in the level of several cellular proteins including regulators. *Y. enterocolitica* only has OmrA and the targets of its post-transcriptional regulation are not yet known.

The main scientific goal of this project is to characterize the activity of OmrA in *Y. enterocolitica* strains of low (strain Ye9, bioserotype 2/O:9) and high (strain 8081, bioserotype 1B/O:8) virulence. Genes identified *in silico* as potential OmrA targets, including important virulence genes, will be analysed. Any changes in the gene expression profile caused by the activity of OmrA will be verified by RT-qPCR, Northern blotting and reporter gene fusion analysis. Moreover, electrophoretic mobility shift assays (EMSAs) will be performed to examine the binding of OmrA to its target mRNAs, in the absence or presence of Hfq. These molecular studies will be supplemented by the phenotypic characterization of *Y. enterocolitica* strains that differ in their OmrA content, i.e. assessment of microcolony and biofilm formation, motility, adhesion/invasion ability of and epithelial cell line, as well as evaluation of insecticidal activity.

The anticipated findings of this project will shed light on the role of OmrA in the post-transcriptional regulation of gene expression, which will help in determining the functional consequences of sRNA activity in controlling the life strategies of *Y. enterocolitica* associated with its saprophytic and pathogenic forms. The silencing of bacterial genes by sRNAs may represent a new strategy for combating pathogenic bacteria. The search for novel methods to treat bacterial infections is currently a high priority due to the spread of antibiotic-resistant strains, which makes conventional antimicrobial therapy increasingly ineffective.