

Abstract – Regulation and targets of the Ysa T3SS of *Yersinia ruckeri*

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Y. ruckeri is an important fish pathogen, causing important losses, notably in rainbow trout (*Oncorhynchus mykiss*) in Austria. Sequencing has shown that this bacterium harbours a type III secretion system, which is an important virulence factor for many Gram-negative bacterial pathogens. However, almost nothing is known about this virulence factor in *Y. ruckeri*.

The project aims to identify the proteins secreted through the T3SS: The first step will be to determine the best conditions for the bacteria to express the T3SS using Real-Time Quantitative PCR (RT-qPCR). Afterwards, targeted mutation will be applied to silence this virulence factor. The secretome of the mutant will be compared to that of the wild type under conditions optimal for the expression of the T3SS with the hypothesis that proteins that disappear from the secretome of *Y. ruckeri* following silencing of the T3SS are proteins that require the T3SS to be secreted. Therefore, identifying these proteins will allow us to identify effectors of the T3SS in *Y. ruckeri*. Secretomes will be compared by either SDS-PAGE or 2D gel-electrophoresis and differentially expressed proteins will be excised and identified based on homology by chromatography.

This project will allow to better understand the virulence of this important fish pathogen and will constitute the first step to characterising the role of the Ysa T3SS of *Y. ruckeri* in the disease process.