TITRE DU SUJET DE RECHERCHE : Role of the main nucleoid Associated Protein LRP in coordination of virulence functions in the bacterium Dickeya dadantii

TOPIC : III-1. Génomé fonctionnel et protéinome ; Functional genome and proteinomist

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Abstract/Présentation du sujet :

In bacteria, the regulation of gene expression is under the control of DNA supercoiling and variable composition of transcription factors changing with growth conditions. The abundant Nucleoid Associated Proteins (NAPs) coordinate the chromatin architecture and transcription, whereas numerous transcription factors with more local effects act upon the regulatory constraints imposed by a few highly abundant global regulators including the NAPs. In addition, bacterial DNA topology directly responds to environmental changes and together with NAPs modulates the distribution of transcription machinery in the genome.

The pectinolytic Dickeya spp. are necrotrophic Gram-negative bacteria causing severe disease in a wide range of economically important plant species. It is listed in the top of the most important bacterial plant pathogens. During the last years, damages caused by Dickeya increased in potato culture in Europe where it is now considered as an emergent pathogen.

Successful infection by D. dadantii, alike human pathogens, requires temporal coordination of gene expression presumably orchestrated by the NAPs. However, the general control mechanisms used by these global regulators remain poorly understood. This project aims to decipher the genetic and DNA structural information utilized by the major NAP Leucine responsive Regulator (LRP), to modulate the genomic response of D. dadantii to adverse conditions encountered during pathogenesis. Initial investigations have revealed that LRP is involved in the regulation of various marker genes required during the different phases of infection. The main objective of this project will consist in the definition of the regulon of LRP in the different conditions encountered by D. dadantii during the infection (exponential and early stationary growth phases, oxidative and osmotic stresses, acidic shock). This will be carried out using dRNAseq approach. The obtained results will be compared to those obtained under the conditions of DNA relaxation in order to appreciate the impact of DNA topology on the regulation of D. dadantii genome expression by LRP. ChIP-Seq experiments
will be further used to analyse the impact of DNA topology on LRP binding to the *D. dadantii* genome. This transdisciplinary approach will combine the classical methods of microbiology, biochemistry, molecular genetics and physiopathology with transcriptomics and bioinformatics in order to integrate the genomic functional expression with chromosomal structural dynamics.

This project will be performed in collaboration with Patrick Sobetzko (Philipps-University Marburg, Germany) and Marc Hütt (Jacobs University Bremen, Germany) for the modeling of the impact of LRP on the *D. dadantii* genome expression dynamics and on the structural-functional domains.

References:


