VapBC toxin-antitoxin modules of *Sinorhizobium meliloti:* Actors of the nitrogen-fixing symbiosis

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Background: The symbiotic interaction between *Sinorhizobium meliloti* and the model legume *Medicago truncatula* leads to the formation of new root organs, the nodules, where differentiated bacteria reduce the atmospheric nitrogen into ammonium.

Objectives: To better understand the intracellular lifestyle adaptation of bacteria during symbiosis, we examine the role of *S. meliloti* VapBC Toxin-Antitoxin (TA) systems. These TA systems are composed of a stable toxin (VapC) and a labile antitoxin (VapB) inactivating the toxin. In response to a signal, antitoxin degradation by bacterial proteases releases the toxin, acting as a post-transcriptional regulator due to its RNase site-specific activity.

Methods: Importance of VapBC modules was studied by phenotyping the interaction between *Medicago* and bacterial mutants deficient in the VapC toxin on their ability to nodulate, differenciate, fix nitrogen and persist in nodules. Lastly, identification of the consensus site of cleavage of representative VapC toxins was performed by an RNA-seq method and is currently under functional validation.

Results: Infection of *M. truncatula* with *vapC* mutants show that some of them have an altered symbiotic phenotype: defect in nitrogen fixation or delayed nodule senescence. This study demonstrates the importance of TA systems at major steps of symbiosis, making them essential actors in the plant-microbe interaction fitness. RNA-seq approach will contribute to identify the RNA targeted by specific VapCs, and to connect a defined symbiotic function to a specific VapBC module.

Technics : The RNA-seq will be mainly discussed in order to show how this technology could be an useful tool for many topics. In fact, this technic is mostly used to compare gene expression profile between biotic or abiotic conditions. However, the sequencing of RNA can offer many answers to biological questions by defining, for example, the modulation of the alternative splicing of RNAs by proteins of interest, the stability of RNAs or the identification of the consensus site of recognition of RNAs by RNases. Key steps in the pipeline of RNA-seq will be discussed, from the preparation of the libraries to the statistical analyses, and the finding of the appropriate company to sequence the samples. This offers a good opportunity to collect information about why, how and where the use of this technic can complete a defined research project.