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BOOK OF ABSTRACTS

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SFP Société Française de Phytopathologie

The International Society for Plant Pathology & the French Phytopathological Society

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Text

The genus *Dickeya* are enterobacterial plant pathogens responsible for soft rot disease in a wide range of plant species, including economically important crops e.g. potato and rice. The infection process is divided into two main phases: the asymptomatic phase where *Dickeya spp.* produce early virulence factors to colonize the apoplastic spaces between plant cells; and the symptomatic phase, which is associated with the secretion of late virulence factors, i.e. plant cell wall degrading enzymes that macerate the plant tissue. Therefore, the spatial and temporal production of the virulence factors must be precisely controlled to ensure the efficient colonization and degradation of the host. While many transcriptional regulators are involved in controlling *Dickeya*'s virulence factors, knowledge of post-transcriptional regulation is still in infancy. Our first results on *Dickeya dadantii* RNA chaperons suggest a post-transcriptional regulation of virulence. Additionally, the obtention of *D. dadantii* transcriptional landscape allowed us to identify RNAs predicted to interact with the mRNAs of virulence factors regulators that play a role in response to oxidative stress and changing metabolic content in the apoplast. Ongoing work aims to establish a link between regulatory RNAs, virulence factors, and environmental changes encountered by bacteria during infection, which will lead to a better comprehension of the complex virulence regulatory network of *D. dadantii*.

COMPARISON OF THE ACTIVITY OF THE VFM QUORUM SENSING SYSTEM IN DIFFERENT STRAINS OF THE GENUS DICKEYA.

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Text

The Vfm Quorum Sensing (QS) system is preponderant for the virulence of different species of phytopathogenic bacteria of the genus *Dickeya*. The *vfm* gene cluster includes 26 genes involved in the biosynthesis, sensing or transduction of the Vfm signal. The transduction of the Vfm signal was shown to result into the activation of the promoter of the gene *vfmE* encoding a transcriptional regulator of the AraC family which itself activates the promoter of genes encoding the plant cell wall degrading enzymes (PCWDEs). The transcriptional regulator VfmE was shown to also activate promoters of the *vfm* gene cluster, allowing an exponential auto-induction of the Vfm QS system. Additionally, the activity of the transcriptional regulator VfmE was shown to also be controlled by Vfm-independent regulatory pathways involving the secondary messenger c-di-GMP and/or transcriptional regulators encoded outside of the *vfm* gene cluster. Here, we used a reporter gene fused to the promoter of the gene vfmE and compared the activity of the *vfmE* promoter among strains of *Dickeya*.

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