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Review on the Research work of Ms Malgorzata GOLANOWSKA

presented in order to obtain a doctoral thesis from the Intercollegiate Faculty of Biotechnology UG & MUG, Gdansk, Poland /Institut National des Sciences Appliquées de Lyon, France

Thesis title: « Characterisation of *Dickeya solani* strains and identification of bacterial and plant signals involved in virulence»

The doctoral thesis of Ms Malgorzata GOLANOWSKA focuses on the study of the phenotypic and genomic diversity of the emergent enterobacterial phytopathogen *Dickeya solani*, that has recently become a severe threat to potato culture in Europe and the South Mediterranean countries. The manuscript is organized in five chapters that are, respectively, the Introduction, Materials, Methods, Results and Discussion.

In the introduction, after a presentation of the different bacterial species responsible for soft rot and blackleg diseases, M. GOLANOWSKA nicely presents the life and disease cycle of soft rot bacteria. She then makes an extensive review of the battery of virulence factors so far identified in these bacteria, followed by a brief overview of the regulatory networks that control virulence factors production in *Dickeyas*. The next introduction's section deals with a short description of methods used in identification and differentiation of soft rot enterobacteria. The final section presents the economical importance of diseases caused by these bacteria and more specifically the importance of deepening the understanding of the adaptation of the new emergent *D. solani* species to potato. This introduction section explains

clearly the context leading to the objectives of this work and brings all needed information for the understanding of the experimental part of the thesis.

The Materials and Methods sections are very complete and carefully presented, providing easy to follow and precise protocols.

The Results chapter is divided in three sections. The first section presents a thorough comparison of virulence traits for 1) *D. dadantii*, *D. dianthicola* and *D. solani*, the three *Dickeya* species known to cause disease on potato, and 2) fifteen strains of *D. solani* strains coming from different climatic zones (Poland, Finland, Israel). These comparisons were made at three different temperatures to analyse the possible adaptations to different climatic environments. M. GOLANOWSKA showed *D. solani* strains exhibit higher plant cell wall degrading activities than *D. dianthicola*, the other species found in diseased potato in Europe. Interestingly, *D. solani* strains from different origins show a quite high variation in their production of cell wall degrading enzymes, the Polish strains being the most efficient. Furthermore, while the different Polish strain phenotypes are very homogenous, much more variability was found between Finnish and Israeli strains. The demonstration of this variability between *D. solani* strains is novel and clearly highlights the pertinence of the wide study undertaken in this thesis. Another interesting conclusion of this work is that 28°C is the optimal temperature for all *Dickeya* strains irrespective of their geographic origin indicating no sign of warm climate adaptation for Israeli strains.

The second section of the Results addresses the regulation of *D. solani* virulence traits by examining the influence of potato extracts on the expression of a few selected *D. solani* genes known to be involved in virulence in the model species *D. dadantii*. M. GOLANOWSKA showed the activation by plant extracts of two genes, *pelL* encoding a secondary pectate lyase and *lfaA* controlled by a regulator of the LacI family. Interestingly, the *pelL* gene presents such activation only in *D. solani* and not in *D. dadantii*. These results open the way to the identification of the plant signals responsible for this activation.

The last section of the Results is dedicated to the analysis of the genomic diversity within the *D. solani* species by comparing 10 genomic sequences of strains originating from different geographic area. Determination of the *D. solani* core genome revealed that most virulence genes and their identified regulators are totally conserved, confirming the very high homogeneity of this species at the genomic level. She also showed that the highly virulent Polish isolate was more distant phylogenetically than the other strains. However, this first genome analysis didn't give any clues about genetic traits that could explain variation in

virulence or in the phenotypic traits related to virulence analysed in the first section of the Results chapter.

Finally, the last chapter presents a synthetic summary of the main results and integrates them into what was previously reported in the literature and what is known about disease aetiology, more specifically in the view of climate change. I would have appreciated here to find proposed some directions for future research, in particular how to reconcile the observed phenotypic variations with the high homogeneity of genomic sequences.

To conclude this report, the results presented in this manuscript are novel and interesting; they shed a new light on the phenotypic diversity of *D. solani*, a long debated question in the research field. During this work, M. GOLANOWSKA gained the theoretical and technical skills in bacterial physiology and plant pathology but also in bacterial genetics and genome analysis. The analysis of the genome of one of the strains analysed in this thesis was published in the Genome Announcements Journal with M. GOLANOWSKA as the first author. The results on phenotypic diversity could certainly be valorised in a second publication. I therefore state that this thesis can clearly be publicly defended before a jury.

Paris, September 7 2015

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