

'Pangenome analysis of *Dickeya solani*, pathogen responsible for economic losses in European potato production'

Agata Motyka, Laboratory of Plant Protection and Biotechnology, IFB UG & MUG

Supervisor: Professor Ewa Łojkowska; co-supervisor: Professor Alessio Mengoni; accessory supervisor: Dr eng. Wojciech Śledź

Pectinolytic bacteria from the genera *Dickeya* and *Pectobacterium* cause blackleg and soft rot in potato and other economically significant plants. Among them *Dickeya solani* gained special interest, as rejection and downgrading during certification of seed potatoes due to the presence of this species affect 20% of the stocks in The Netherlands. Control of blackleg and soft rot diseases is based solely on preventive measures. So, monitoring the presence of pectinolytic bacteria, collecting knowledge about their spread, biology and epidemiology, broad characterisation of the isolates in addition to proposing new eradication methods became of crucial importance.

In the frames of my doctoral thesis, monitoring of potato fields for the presence of pectinolytic bacteria was conducted in 2013 and 2014. It was established that *D. solani* strains occur on Polish potato fields although they are amounted by the isolates of *Pectobacterium* spp. The *D. solani* strains are homogenous on the genomic level, however they differ in the abilities to produce virulence factors (e.g. pectinases, proteases, cellulases, lipases, siderophores) and to macerate potato tissue. It is worth to mention though, that the chemical structure of *D. solani* lipopolysaccharide (LPS) is conserved and identical to the LPS of *D. dadantii* 3937 model strain. Comparative genomic approach was utilized in order to reveal the sources of phenotypic differences between 8 *D. solani* strains in the reference to *D. solani* strains IFB0099, IFB0223 and IPO2222^{TS}. Average nucleotide identity (ANI) values showed high similarity between the isolates. Also in terms of *D. solani* pangenome structure, there was a vast pool of core genes established (74.8%), while the pools of accessory and unique pangenome fractions were 11.5 and 13.7 %, respectively.

Also in the frames of this work, two new methods for eradication of phytopathogenic bacteria have been reported. Firstly, a system generating direct current atmospheric pressure glow discharge (dc-APGD) in contact with flowing bacterial suspension acting as a liquid cathode was established and tested against the representative strains of 5 plant pathogenic species, yielding CFU ml⁻¹ reduction from 3.46 log up to complete eradication. Secondly, silver nanoparticles (AgNPs) generated by the use of atmospheric pressure plasma (APP) showed antibacterial properties against *Pectobacterium* and *Dickeya* spp, combining the action of well-established antimicrobial effect of AgNPs with the ROS and RNS formed by the plasma source.

In conclusion, further research is needed to clearly explain the differences in the virulence of *D. solani* strains as they show such a high homogeneity on the genomic level. The herein reported dc-APGD system could be applied for sterilization of industrial and agricultural wastewaters, liquid wastes from microbiological laboratories, or any other putatively contaminated liquid disposals, while the APP-derived AgNPs might be used as plant growth stimulators or horticultural disinfectants, as they are more stable than the hydrogen peroxide with silver ions mixture already in use for the above-mentioned purposes.