

Pectinolytic bacteria, classified within the family *Pectobacteriaceae* to the genera *Dickeya* and *Pectobacterium*, cause blackleg and soft rot on potato. In terms of soft rot, they also affect other crops, vegetables and ornamentals. The total economic impact of these phytopathogens may even reach $50 - 100 \times 10^6$ US dollars per year worldwide. Recently, *Dickeya solani* has gained a special interest, not only as a newly established species, but also due to high aggressiveness of these isolates. By now, control of blackleg and soft rot diseases has been solely based on preventive measures. Therefore, the aims of this thesis were set as follows: i) monitoring of the presence of *Pectobacteriaceae* on the territory of Poland, ii) investigation of phenotypic and genomic diversity in *D. solani*, iii) development of novel eradication methods for phytopathogenic bacteria.

The study of 2013-2014 analysing the presence of pectinolytic bacteria on seed potato fields in Poland revealed the occurrence of *D. solani* strains, although these isolates were outnumbered by the strains classified to the genus *Pectobacterium*. The subsequently undertaken characterisation of *D. solani* strains of different geographical origin and year of isolation showed that these bacteria are efficient in virulence factors production, including the activity of plant cell wall degrading enzymes (PCWDEs), in addition to potato and chicory tissue maceration capacity. Notably, two isolates (IFB0223 and IFB0455) exhibited lower PCWDEs activities, impeded plant tissue maceration, in addition to diminished growth rate. The chemical structure of O-antigen of the lipopolysaccharide of four *D. solani* isolates differing in virulence was established to consist of 6-deoxy-d-altrose monomers, being also identical to the one of *D. dadantii* 3937 model strain.

A genome-assembly pipeline was optimised and successfully implemented for closing of 6 *de novo* sequenced *D. solani* genomes. With this tool and the total number of 22 *D. solani* genomic sequences, the pangenome of this species has been closed, meaning that by addition of other newly-sequenced genomes the total gene pool of this species shall not enlarge. The pangenome of *D. solani* comprises a vast pool of core genes (84.7%) and minor fractions of accessory (7.2%) and unique genes (8.1 %). An enrichment of functions related to the control of transcription or associated with mobile genetic elements in the unique pangenome fraction was noted basing on the assignment of unique genes into clusters of orthologous groups (COG). Last but not least, a genome-wide phylogeny based on the core set of *D. solani* genes was stated to reflect to some point the specificity of the seed potato tubers market.

In the frames of this work, two new control methods based on direct current atmospheric pressure glow discharge (dc-APGD) have been proposed for eradication of phytopathogenic bacteria. At first, a dc-APGD reaction-discharge system working in a continuous flow mode

turned out to eliminate from all to 3.43 log phytopathogenic bacteria due to favourable plasma-chemical parameters in addition to the action of the generated radicals and UV. Such device might find application in decontamination of industrial and agricultural wastewaters or any other soluble contaminant harbouring bacterial phytopathogens. Secondly, spherical, face cubic centered, silver nanoparticles (AgNPs) of 9.33 ± 3.37 nm or 28.3 ± 11.7 nm stabilized with the use of pectins or SDS, respectively, were generated by the dc-APGD action. The accomplished minimal inhibitory and bactericidal concentrations against *Pectobacterium* and *Dickeya* spp. varied from 0.75 to 5.5 mg l⁻¹. Notably, the utilized AgNPs synthesis method requires no toxic or irritating agents, which is of crucial importance having in mind future applications within the agricultural sector.