

Tytuł: „Characterization of the biodiversity and pan-genome of plant pathogenic bacteria from *Pectobacterium parmentieri* species”

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Abstract

Pectobacterium parmentieri (formerly virulent *Pectobacterium carotovorum* subsp. *carotovorum* or *Pectobacterium wasabiae*) is a plant-pathogenic, soft-rotting, pectinolytic bacterium that is classified to *Pectobacteriaceae* family, a member of Soft Rot *Pectobacteriaceae* (SRP). *P. parmentieri* strains are gram-negative rod-shaped necrotrophs that destroy plant tissue components through the activity of plant cellwall-degrading enzymes (PCWDE) such as pectinases, cellulases, and proteases secreted through type I or type II secretion systems.

The high economic impact of all *Pectobacterium* spp. was emphasized by listing the members of this genus among the top 10 bacterial plant pathogens. The attribution mentioned above was based not only on severe damage noted in potato production sector but also on a broad host range of the members of this genus. Specifically, bacteria from *Pectobacterium* spp. were reported to cause soft-rotting symptoms on plants from 16 dicot plant families in 11 orders and 11 monocot families in 6 orders.

Even though the appearance of *P. parmentieri* was confirmed in numerous countries from Europe, Oceania and North America, no comprehensive studies on the population structure, biodiversity, genome structure and pan-genome qualifications of *P. parmentieri* strains have been conducted. Thus, the presented PhD thesis summarizes a detailed survey focusing on the monitoring, phenome and genome characterization of *P. parmentieri* strains isolated from seed potato plantations in Poland.

In Publications presented as a PhD thesis, several objectives were covered. Firstly, *P. parmentieri* monitoring on seed potato plantations was presented, showing that it is the second most commonly detected species of soft rotting bacteria– in year 2013 and 2014 it constituted 27% of all detected SRP. Secondly, a comprehensive phenotypic, genotypic and genomic evaluation was performed, followed by establishing a pipeline for de novo genome assembly for this species. On the basis of twelve de novo assembled genomes of *P. parmentieri* strains isolated on the territory of Poland (ten strains) and Belgium (two strains) together with reference strains isolated in Finland, USA and

France, a high abundance of Mobile Genetic Elements, genome plasticity and large dispensable genome of *P. parmentieri* was shown.

The obtained results provided novel knowledge on genetic variability in the pathogenome related to divergence in the phenotypic features of the studied bacterial species. The presented data led us to the conclusion that genomic variation and genomic plasticity among *P. parmentieri* strains contribute to the wide spreading and adaptation of these bacteria, and their ability to cause disease symptoms in different climatic zones.