

**ABSTRACT BOOK**



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## PT168 Metagenomic analysis of microbial communities associated with diseased potato tubers

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**Background:** Pectolytic *Dickeya* and *Pectobacterium* species that cause blackleg, aerial stem rot and soft rot are commercially important pathogens in potato production. Blackleg symptom caused by these bacteria has been recorded in potato production field in Bačka region (Vojvodina, Serbia) in 2018.

**Objectives:** Metagenomic approach was used to reveal microbial communities colonizing the diseased potato tubers with the aim of better understanding of pathogens distribution.

**Methods:** Single colonies of potential pathogenic bacteria were isolated on nutrient agar and checked for pectolytic activity on potato slices. Ten selected bacterial isolates were identified to the species level after PCR amplification with *gapA* and *mdh* primers. The 16S rRNA sequences from diseased potato tubers samples were obtained using Next generation sequencing (NGS) Illumina platform. The obtained sequencing data was processed bioinformatically.

**Results:** Mixed infection of the diseased potato plants with *Dickeya dianthocola* and *Pectobacterium carotovorum* pv. *brasiliensis* was revealed after pathogen identification with *gapA* and *mdh* genes. All isolates caused soft rot symptoms on potato slices. Metagenomic analysis revealed that present bacteria belong to phylum Bacteroidetes (*Bacteroides*, *Empedobacter*, *Dysgonomonas*, *Myroides*, and ud-Porphyromonadaceae), Firmicutes (*Vagococcus*, *Lactococcus*, *Clostridium* XIVa, *Enterococcus*, and ud-Acidaminococcaceae) and Proteobacteria (*Acinetobacter*, ud-Pseudomonadaceae, ud-Enterobacteriaceae, *Wohlfahrtiimonas*, ud-Neisseriaceae, *Enterobacter*, *Providencia*, *Arcobacter*, and *Kerstersia*) as the most common representatives. Genus *Pectobacterium* was present in 0.5%.