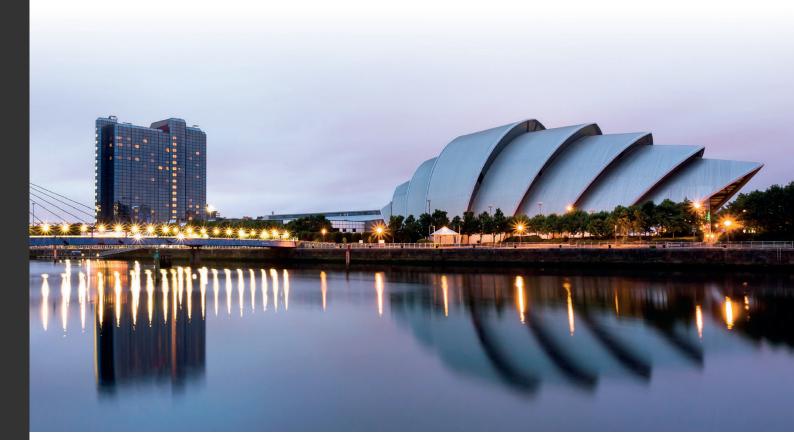
ABSTRACT BOOK



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PT186 Comparative metagenomics of microbial communities inhabiting the phyllosphere of the diseased and healthy oilseed rape

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Background: A wide variety of different saprophytic and pathogenic bactera, both living epiphytic or endophytic, colonize physically and nutritionally different microhabitats on plants phyllosphere. *Xanthomonas campestris* pv. *campestris* (Xcc) is phytopathogenic bacteria causing bacterial blight symptom on oilseed rape (*Brassica napus*) and black rot on other cultivated *Brassica oleaceae* vegetables.

Objectives: Metagenomic approach was used to reveal differences in microbial communities colonizing the phyllosphere of four different winter oilseed rape varieties with expressed bacterial blight symptoms and one healthy variety, all collected from five different localities in Vojvodina (Serbia) in 2018.

Methods: Next generation sequencing (NGS) Illumina MiSeq platform was used to obtain 16S rRNA sequences from five tested samples, and to gain insight into their alpha and beta diversity. Comparative taxonomic analysis of the obtained sequencing metadata was processed bioinformaticaly.

Results: Different percetages of bacterial species belonging to three bacterial phyla-Proteobacteria, Firmicutes, and Actinobacteria were dominant in phyllosphere of all five oilseed rape varietes. Bacteria from the phylum Proteobacteria (66-91%) were dominant in diseased varieties, unlike healthy variety where only 38% belonged to this phylum. Genus *Xanthomonas* (40-74%) was the most abundant in diseased plants phyllosphere. Only 0.2% of *Xanthomonas* representatives were present in healthy plants, where order Enterobacteriales (*Pantoea, Buchnera*, and ud-Enterobacteriaceae) were the most abundant. The genus *Exiguobacterium* was the most abundant in healthy variety (47%). Bacteria from phylum Acintinobacteria were least represented, with less then 1% in diseased and up to 12% (ud-Micrococcaceae, *Kocuria, Arthrobacter*, and ud-Microbacteriaceae) in healthy oilseed rape variety.