

**ABSTRACT BOOK**



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## PT274 Genetic heterogeneity among *Xanthomonas campestris* pv. *campestris* isolates originated from oilseed rape determined with different rep-PCR techniques

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**Background:** Oilseed rape (*Brassica napus*) is an oil-producing crop, significant for vegetable oil and biodiesel production. The phytopathogenic bacterium *Xanthomonas campestris* pv. *campestris* (*Xcc*) causing bacterial leaf blight was recorded for a first time in 2010 on self-growing winter oilseed rape in Serbia. Ever since, it continued appearing on cultivated crops too.

**Objectives:** The aim of this research was to reveal genetic heterogeneity among 25 *Xcc* isolates, originated from different cultivars of winter oilseed rape obtained in nine-year period (2010-2018) from different localities in Vojvodina region (Serbia) using repetitive sequence-based PCR (rep-PCR) fingerprinting.

**Methods:** Genomic DNA was extracted using CTAB method. Specific primer pair XCF/XCR, amplifying a DNA fragment of *hrpF* gene from *X. campestris* was used for rapid preliminary identification of all tested isolates. Rep-PCR using BOX, ERIC and REP-PCR primers was used to detect presence of genetic heterogeneity among *Xcc* isolates.

**Results:** All 25 tested isolates were preliminary identified as *Xcc* based on a positive PCR reaction after amplification of 525 bp region using XCF/XCR primers. BOX and ERIC-PCR generated seventeen different DNA fingerprinting profiles, unlike REP-PCR where only nine different profiles were detected. These results show presence of genetic polymorphism among *Xcc* isolates from winter oilseed rape, which could indicate either their affiliation to some of the identified *Xcc* races, or formation of a new *Xcc* ecotype.