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**ELECTRONIC  
ABSTRACT BOOK**

**797 / PATHOGENIC BACTERIAL POPULATION CAUSING SOFT  
ROT ON CABBAGE: CASE STUDY IN FUTOG (SERBIA)****09****Keywords:** *cabbage, soft rot, Pectobacterium***Aleksandra Jelušić** / University Of Belgrade, Institute For Multidisciplinary Research, *Serbia***Aleksandra Jelušić** / University of Belgrade, Institute for Multidisciplinary Research, Belgrade, *Serbia***Petar Mitrović** / Institute of Field and Vegetable Crops, Novi Sad, *Serbia***Sanja Marković** / University of Belgrade, Institute for Multidisciplinary Research, Belgrade, *Serbia***Renata Iličić** / University of Novi Sad, Faculty of Agriculture, Novi Sad, *Serbia***Slaviša Stanković** / University of Belgrade, Faculty of Biology, Belgrade, *Serbia***Tatjana Popović** / Institute for Plant Protection and Environment, Belgrade, *Serbia***BACKGROUND**

Futog (Vojvodina, Serbia) is known for the five-century long tradition of cabbage cultivation, which is grown in two forms during the season, summer and autumn. Pectobacteriaceae causing soft rot disease are among the most destructive pathogens, influencing the yield and quality of this crop. These pectolytic bacteria cause maceration of attacked tissues, often followed by specific odor caused by the colonization of saprophytic bacteria that inhabit damaged tissues.

**OBJECTIVES**

Within this work, we aimed to identify soft rot-causing bacteria observed on two summer cabbage hybrids (Cheers F1 and Hippo F1) grown in Futog in 2021.

**METHODS**

Crystal Violet Pectate (CVP) medium was used for bacterial isolation from six collected cabbage samples showing soft rot. The pathogenicity of isolates was checked on cabbage heads by making holes at the top and filling them with bacterial suspensions. Multilocus sequence typing (MLST) of cabbage isolates was performed by sequencing of *proA* and *dnaX* genes. Additionally, the Neighbour-joining phylogenetic analysis was performed with concatenated sequences.

**RESULTS**

Isolations resulted in the prevalence of pit-forming colonies on CVP. Water-soaked lesions followed by a specific odor appeared on cabbage heads 24 h after inoculation with all tested isolates, and complete head destruction occurred after seven days. MLST performed with genes *proA* and *dnaX*, identified isolates as *Pectobacterium carotovorum* on hybrids Cheers F1 and Hippo F1 and *Pectobacterium versatile* only present on Hippo F1, indicating combined infection on this hybrid. On the phylogenetic tree, *P. versatile* isolates were separated from *P. carotovorum* isolates, clustered into four groups.