

# Diversity of bacterial soft rot-causing *Pectobacterium* species affecting cabbage in Serbia

Aleksandra Jelusić<sup>1</sup>, Petar Mitrović<sup>2</sup>, Sanja Marković<sup>1</sup>, Renata Iličić<sup>3</sup>, Predrag Milovanović<sup>4</sup>, Slaviša Stanković<sup>5</sup> and Tatjana Popović Milovanović<sup>6,\*</sup>

<sup>1</sup> University of Belgrade, Institute for Multidisciplinary Research, Kneza Višeslava 1, 11030 Belgrade, Serbia;

<sup>2</sup> Institute for Field and Vegetable Crops, National Institute of the Republic of Serbia, Maksima Gorkog 30, 21000 Novi Sad, Serbia;

<sup>3</sup> Faculty of Agriculture, University of Novi Sad, Trg Dositeja Obradovića 8, 21000 Novi Sad, Serbia;

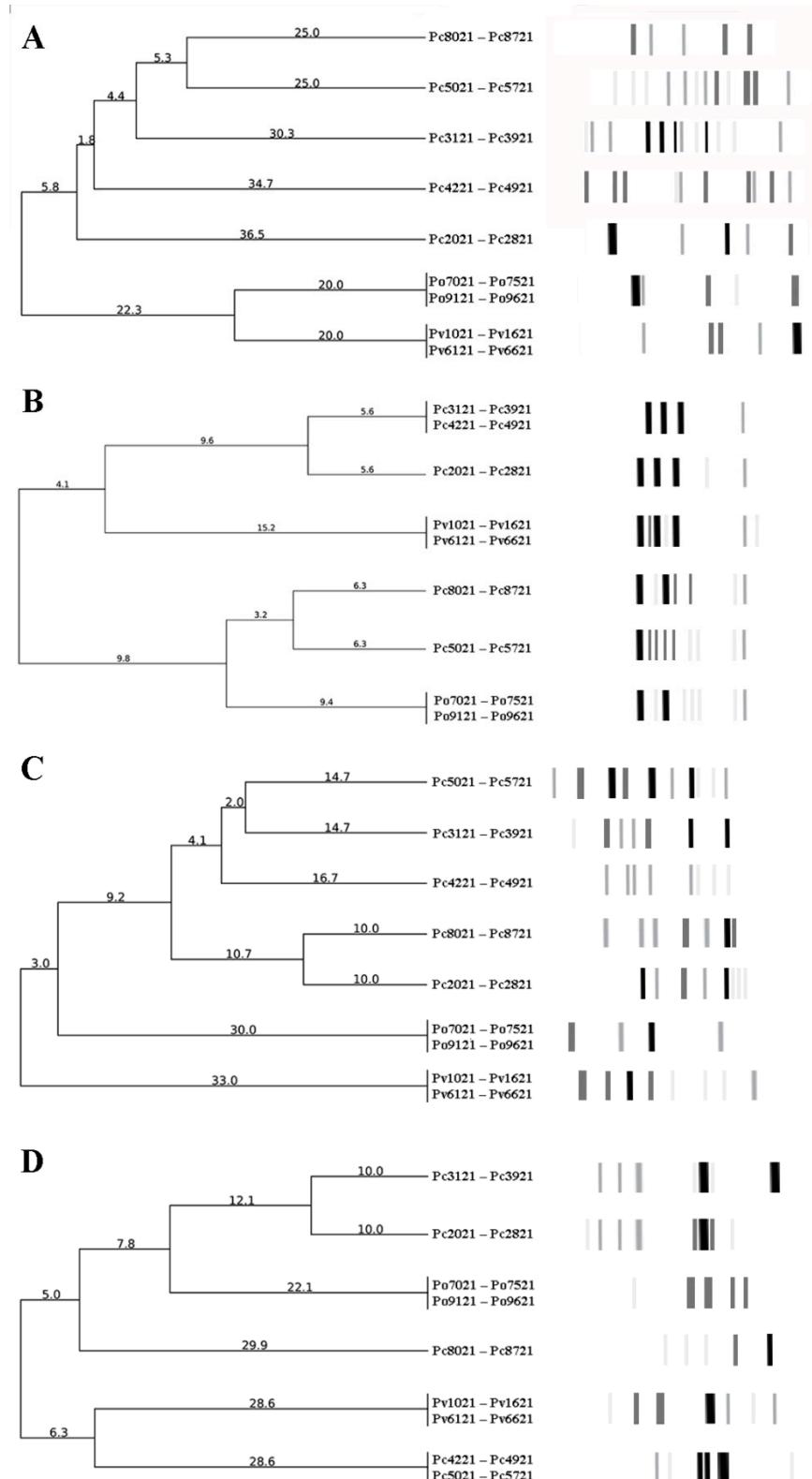
<sup>4</sup> Agrosava doo, Palmira Toljatija 5, 11070 Belgrade, Serbia;

<sup>5</sup> University of Belgrade, Faculty of Biology, Studentski Trg 16, 11000 Belgrade, Serbia;

<sup>6</sup> Institute for Plant Protection and Environment, Teodora Dražera 9, 11040 Belgrade, Serbia.

\* Correspondence: tanjaizbis@gmail.com (T.P.M.); jelusic.aleksandra@gmail.com (A.J.)

## SUPPLEMENTARY MATERIAL



**Figure S1.** Unweighted pair group method with arithmetic mean (UPGMA) phylogenetic trees of the 67 tested cabbage *Pectobacterium* spp. isolates and virtual gel images depicting rep-PCR fingerprinting patterns for each of the obtained isolate groups based on (A) BOX-PCR, (B) ERIC-PCR, (C) GTG<sub>5</sub>-PCR, and (D) REP-PCR.