Disease Notes

Diseases Caused by Bacteria and Phytoplasmas

First Report of *Pectobacterium polaris* Causing Soft Rot and Blackleg of Potato in Russia

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Blackleg and soft rot of potato (*Solanum tuberosum*) were monitored in the Central European part of Russia within a period of 2012 to 2019. Symptoms included decay of tubers, blackening of stem vascular bundles, and partial yellowing of leaves. The disease causes serious potato yield losses in the field and storage. *Pectobacterium parmentieri*, *P. brasiliense*, *P. versatile* (syn. ‘*Candidatus Pectobacterium maceratum*’), *P. carotovorum*, *P. atrosepticum*, *Dickeya dianthicola*, and *D. solani* are considered as main causal agents of soft rot and blackleg disease in Russia (Kornev et al. 2012; Ngoc Ha et al. 2019; Shirshikov et al. 2018; Voronina et al. 2019). Potato plant samples collected in commercial fields in routine plant health assay were used for bacteria isolation on crystal violet pectate agar (CVP) (Hélias et al. 2012) as described previously (Voronina et al. 2019). Bacterial colonies producing pitting on CVP were reisolated and purified on nutrient broth yeast extract medium. DNA of bacterial isolates was extracted, and polymerase chain reaction (PCR) amplifications were performed using gapA primers (Cigna et al. 2017) followed by sequencing. DNA sequence alignment showed that the isolates F099, F100, F106, F109, and F118 were identical (deposited as part of NCBI reference sequence for F109 NZ_RRYS01000004.1, locus KHDHEBDM_RS06360) and grouped together with the type strain *Pectobacterium polaris* NIBIO1006T (CP017481), a new species described as a

potato pathogen (Dees et al. 2017). These strains were negative in diagnostic PCR assays using specific primers Y45/Y46 for the detection of *P. atrosepticum*, Br1f and L1r for *P. brasiliense* (Duarte et al. 2004), and ADE1/ADE2 for *Dickeya* sp. (Nassar et al. 1996). To further validate the identification, strain F109 of *P. polaris* was selected for genome sequencing. The genome of *P. polaris* strain F109 (NCBI reference sequence NZ_RRYS00000000.1) revealed >99% sequence similarity with the type strain *P. polaris* IPO_1606 (GenBank accession GCA_902143345.1). The strain F109 was deposited to the All-Russian Collection of Microorganisms under number VKM V-3420. Thus, the characterization of five isolates provided evidence that a previously unreported pathogen was present in the surveyed fields. The isolates were uniform in genetic and physiological properties; they were gram negative, facultative anaerobes with pectinolytic activity, negative for oxidase, urease, indole production, and gelatin liquefaction. All isolates were catalase positive, produced acid from lactose, rhamnose, saccharose, xylose, and trehalose, and were tolerant to 5% NaCl, unable to utilize malonate and citrate. All the isolates grew at 37°C. All isolates caused soft rot symptoms on 10 inoculated potato tubers. They produced typical black leg rot symptoms in young potato plants inoculated with 10⁷ CFU/ml of the pathogen by stem injection and incubated at 25°C for 48 h. The bacteria were reisolated successfully from symptomatic potato and pathogen confirmed by gapA sequencing to complete Koch’s postulates. To our knowledge, this is the first report of blackleg and soft rot caused by *P. polaris* on potato in the Russian Federation. According to the data of commercial diagnostic laboratory “Phytoengineering” (Moscow region), *P. polaris* occurred in 5% of potato seed stocks harvested in 2017 to 2019 in the Moscow region. This finding may indicate that new *Pectobacterium* strains have adapted to a diverse environment, which is consistent with widespread distribution of commercial seed potatoes.

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