Emergence of a new plum pox virus variant in Romanian Prunus domestica orchards

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Abstract

Plum pox virus (PPV), the causal agent of sharka disease, is the most damaging viral pathogen affecting stone fruits. Among the ten recognized PPV strains (D, M, EA, C, Rec, T, W, An, CR, and CV), PPV-D, PPV-M and PPV-Rec are the most prevalent in Europe, with PPV-M being the most aggressive and epidemic. Despite Romania status is a PPV-endemic country, PPV-M had not been reported in the past two decades, even after extensive surveys. To assess whether PPV-M had been introduced through imported planting material, a post-control survey was conducted in newly established plum orchards using trees imported from Hungary, Germany, Italy, the Netherlands, Austria, and the Czech Republic. PPV monitoring was based on symptom observation, serological testing and molecular strain typing using RT-PCR with strain-specific primers targeting CP and 6K1-CIP genomic regions. PPV-D and/or PPV-Rec were detected in 10 of 11 surveyed orchards. Moreover, PPV-M was identified in one year post-planting symptomatic trees from a new orchard in Vaslui County, Romania, which used planting material from Hungary. Two symptomatic *Prunus domestica* cv. Grossa di Felisio trees were selected for high-throughput sequencing (HTS) using RNA-Seq with ribodepletion on an Illumina platform, leading to the first complete genome sequencing of two Romanian PPV-M isolates. This is the first confirmed molecular identification and characterization of PPV-M in Romania, raising concerns about the potential spread of this aggressive strain. If proper containment measures are not implemented, PPV situation in Romania could significantly worsen, impacting stone fruit production.

Keywords: Sharka, PPV-M, HTS, detection, disease management

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