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Sub-spontaneous *Prunus cerasifera* trees in North Macedonia harbor a particularly high *Plum pox virus* diversity

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Understanding plant virus spread and evolution at the agro-ecological interface is crucial to design appropriate disease management strategies and prevent variant emergence. Perennial plants are prone to harbor a high viral genetic diversity due to repeated and long-lasting infections and may thus provide a conducive environment to the emergence of new virus genotypes.

Sharka, a serious disease of stone fruits (*Prunus*) worldwide, is caused by the plum pox virus (PPV, genus *Potyvirus*). Ten strains have been described so far, among which only three are widely distributed across Europe. In this study, we assessed the role of the wild compartment as a potential reservoir of PPV genetic diversity. We carried out a country-wide survey in North Macedonia, targeting cultivated, sub-spontaneous trees (*P. cerasifera*) and wild bushes (*P. spinosa*). For PPV diagnosis and strain assignment, we used polyvalent and strain-specific RT-PCR tests followed by partial sequencing. In *P. cerasifera*, we identified 5 previously described strains (i.e., PPV-M, -D, -Rec, and the geographically restricted -T and -An strains). A PPV isolate distant from all known strains was also detected and fully sequenced using Nanopore and Sanger technologies. Based on genetic distance, this isolate belongs to a new PPV strain, that we called PPV-P. Its aphid transmissibility to cultivated *Prunus* species was assessed experimentally. In contrast to *P. cerasifera*, cultivated species harbored only 1 (peach), 2 (apricot) or 4 (plum) strains. These results suggest that *P. cerasifera* in the Balkans may be implicated in the emergence of the PPV strains spreading in Europe.