

LETTER TO THE EDITOR

A new potyvirus identified in Czech Republic

T. SARKISOVA, K. PETRZIK*

Department of Plant Virology, Institute of Plant Molecular Biology, Biology Centre of the Academy of Sciences of Czech Republic, v.v.i., Branišovská 31, 370 05 České Budějovice, Czech Republic

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In summer 2008 specimens of plant *Lupinus polyphyllus* (large-leaved lupine) with mosaic symptoms and inter-veinal yellowing were collected in the south of Czech Republic. A native of Northern America, this plant has been grown as an ornamental plant in gardens or as a food for wildlife also in Europe.

Filamentous virus particles of 690 nm in length were visible under electron microscope in negative-contrast stained plant sap preparation. The newly isolated virus was maintained by a mechanical passage in *Chenopodium quinoa* causing mild mosaic symptoms on the non-inoculated leaves. RT-PCR using degenerate potyvirus-specific primers (1) and a walking primer approach resulted in several products. Approximately 2.7 kb of the amplified segments were sequenced. The sequenced region spanned C-terminal part of the viral protease (NIa) coding region, complete RNA polymerase (NIb) coding region, complete coat protein (CP) coding region, and 3' untranslated region (3'UTR). The NIa/NIb cleavage site was recognized between amino acids DDVNSQ↓SG and the NIb/CP cleavage site between amino acids NEVYHQ↓SG that was unique among recently sequenced potyviruses. The polymerase coding region was 1554 nt long. All 9 motifs characteristic of RNA-dependent RNA polymerases (Ia to VIII) were present in the NIb protein (2). The CP coding region was 819 nt long terminated with UAA and coded for a protein of 273 amino acids. On the N-terminal part of CP,

there was found an amino acid motif DAG, which implicated a transmission of the virus by an aphid vector (3). The 3'UTR was 211 nt long excluding the poly(A) tail.

Narcissus yellow stripe virus, Pepper veinal mottle virus, and Chilli veinal mottle virus were identified as closely related viruses with 64.4%, 64.3%, and 63.1% amino acid identity, respectively, for the CP coding region. However, phylogenetic analysis of the RNA-polymerase amino acid sequences classified the new lupine virus in the cluster of Plum pox virus. According to the species demarcation criteria, the lupine virus was well below the 76% amino acid identity threshold for the CP coding region (4) and consequently, it represented a true new species of the genus *Potyvirus*. It was tentatively named Large-leaved lupine mosaic virus (LLMV) and its nucleotide sequence was deposited in GenBank under Acc. No. EU847625.

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*Corresponding author. E-mail: petrzik@umbr.cas.cz; fax: +42038-5310363.

Abbreviations: CP = coat protein; NIa = viral protease; NIb = RNA polymerase; UTR = untranslated region