kit, 2x150bp paired-end, Illumina) was conducted at the DSMZ Plant Virus Department (Leibniz-Institut, Braunschweig). Bioinformatic analysis of raw data (quality trimming, removal of duplicate reads, pairing of reads, subtraction of host genome-specific reads, de novo assembly of reads into contigs) was performed at our institute with Geneious Prime 2020.04 (Biomatters, Auckland, New Zealand). 6 contigs were assembled to SPV-1 genome sequence. The German SPV-1 isolate 07/17 with six predicted open reading frames and the Canadian accession share over 98% nucleotide identity. The retrieved sequence will be verified and completed at the 5' and 3' ends by reverse transcription PCR (RT-PCR) and rapid amplification of cDNA ends (RACE)-PCR in order to determine the complete virus genome. The results obtained so far as well as phylogenetic analyses of open reading frame sequences (ORFs) of the German SPV-1 isolate 07/17 and representative species in the family Luteoviridae are presented.

166 - Genetische Variabilität der Nucleoprotein- und Transportprotein-kodierenden Regionen des aspen mosaic-associated virus

Genetic diversity of aspen mosaic-associated virus based on nucleo- and movement proteins

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A new *Emaravirus*, aspen mosaic-associated virus (AsMaV), has been identified in association with mosaic symptoms in *Populus tremula* (von Bargen et al., 2020). The genome of AsMaV consists of five negative sense single stranded RNA (-ssRNA) molecules. The RNA1 (7.1 kb) encodes for the viral RNA-dependent RNA polymerase (RdRP, 268.2 kDa), RNA2 (2.3 kb), RNA3 (1.6 kb), RNA4 (1.6kb) and RNA5 (1.3kb) encode for the glycoprotein precursor (GPP, 73.5 kDa), viral nucleocapsid protein (N, 35.6 kDa), a putative movement protein (MP, 41.0 kDa) and a protein of unknown function (P28, 28.1 kDa), respectively. Since viral nucleocapsid protein and movement protein have been used for studying genetic diversity of many -ssRNA viruses including emaraviruses (Roßbach et al. 2015, Walia et al. 2014), these regions with flanking non-coding regions were used to study genetic diversity of AsMaV in Finland and Sweden. To do this, full-length AsMaV-RNA3 and RNA4 have been amplified via RT-PCR with specific primer pairs. Subsequently, the amplicons were investigated by RFLP and selected variants subjected for sequencing. The results showed similar distribution pattern of AsMaV variants in both countries. AsMaV variants were discriminated better based on the RNA3 rather than RNA4.

Literatur

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Diagnose- und Nachweisverfahren

167 - Viroide in Apfel in Deutschland

Viroids in apple trees in Germany

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