Resource Summary Report

Generated by RRID on Apr 29, 2025

Descriptions of Plant Viruses

RRID:SCR_006656
Type: Tool

Proper Citation

Descriptions of Plant Viruses (RRID:SCR_006656)

Resource Information

URL: http://www.dpvweb.net/

Proper Citation: Descriptions of Plant Viruses (RRID:SCR_006656)

Description: DPVweb provides a central source of information about viruses, viroids and satellites of plants, fungi and protozoa. Comprehensive taxonomic information, including brief descriptions of each family and genus, and classified lists of virus sequences are provided. The database also holds detailed, curated, information for all sequences of viruses, viroids and satellites of plants, fungi and protozoa that are complete or that contain at least one complete gene. For comparative purposes, it also contains a single representative sequence of all other fully sequenced virus species with an RNA or single-stranded DNA genome. The start and end positions of each feature (gene, non-translated region and the like) have been recorded and checked for accuracy. As far as possible, nomenclature for genes and proteins are standardized within genera and families. Sequences of features (either as DNA or amino acid sequences) can be directly downloaded from the website in FASTA format. The sequence information can also be accessed via client software for PC computers (freely downloadable from the website) that enable users to make an easy selection of sequences and features of a chosen virus for further analyses. The public sequence databases contain vast amounts of data on virus genomes but accessing and comparing the data, except for relatively small sets of related viruses can be very time consuming. The procedure is made difficult because some of the sequences on these databases are incorrectly named, poorly annotated or redundant. The NCBI Reference Sequence project (1) provides a comprehensive, integrated, non-redundant set of sequences, including genomic DNA, transcript (RNA) and protein products, for major research organisms. This now includes curated information for a single sequence of each fully sequenced virus species. While this is a welcome development, it can only deal with complete sequences. An important feature of DPV is the opportunity to access genes (and other features) of multiple sequences quickly and accurately. Thus, for example, it is easy to obtain the nucleotide or amino acid sequences of all the available accessions of the coat protein gene of a given virus species or

for a group of viruses. To increase its usefulness further, DPVweb also contains a single representative sequence of all other fully sequenced virus species with an RNA or single-stranded DNA (ssDNA) genome. Sponsors: This site is supported by the Association of Applied Biologists and the Zhejiang Academy of Agricultural Sciences, Hangzhou, People"s Republic of China.

Synonyms: DPV

Resource Type: data or information resource, topical portal, database, portal

Keywords: family, fungi, gene, amino acid, comparative, development, dna, genome, genomic, genus, nomenclature, non-translated, nucleotide, organism, plant, product, protein, protozoa, region, rna, satellite, sequence, single, specie, taxonomic, transcript, viral databases, viroid, virus, bio.tools

Funding:

Resource Name: Descriptions of Plant Viruses

Resource ID: SCR_006656

Alternate IDs: nif-0000-21127, biotools:dpvweb

Alternate URLs: https://bio.tools/dpvweb

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250429T055107+0000

Ratings and Alerts

No rating or validation information has been found for Descriptions of Plant Viruses.

No alerts have been found for Descriptions of Plant Viruses.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

, et al. (2024) Commodity risk assessment of Petunia spp. and Calibrachoa spp. unrooted cuttings from Kenya. EFSA journal. European Food Safety Authority, 22(4), e8742.

Peters D, et al. (2024) The plant virus transmissions database. The Journal of general virology, 105(3).

Ala-Poikela M, et al. (2019) A Novel Interaction Network Used by Potyviruses in Virus-Host Interactions at the Protein Level. Viruses, 11(12).

Jo Y, et al. (2018) Peach RNA viromes in six different peach cultivars. Scientific reports, 8(1), 1844.

Tian YP, et al. (2014) Analysis of potato virus Y coat protein epitopes recognized by three commercial monoclonal antibodies. PloS one, 9(12), e115766.

Rubio L, et al. (2013) Genetic variability and evolutionary dynamics of viruses of the family Closteroviridae. Frontiers in microbiology, 4, 151.

Meder F, et al. (2013) The role of surface functionalization of colloidal alumina particles on their controlled interactions with viruses. Biomaterials, 34(17), 4203.

Powdel BR, et al. (2009) A study in entire chromosomes of violations of the intra-strand parity of complementary nucleotides (Chargaff's second parity rule). DNA research : an international journal for rapid publication of reports on genes and genomes, 16(6), 325.

Kelloniemi J, et al. (2008) Three heterologous proteins simultaneously expressed from a chimeric potyvirus: infectivity, stability and the correlation of genome and virion lengths. Virus research, 135(2), 282.