

Template for Taxonomic Proposal to the ICTV Executive Committee Creating Species in an existing genus

Code † **2007.064P.04** To designate the following as species in the genus:

Cheravirus

belonging to the family° : **unassigned**

Stocky prune virus

† Assigned by ICTV officers

° leave blank if inappropriate or in the case of an unassigned genus

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Old Taxonomic Order

Family unassigned

Genus *Cheravirus*

Type Species

Cherry rasp leaf virus

Species in the Genus

Apple latent spherical virus

Tentative Species in the Genus

Arracacha virus B

Artichoke vein banding virus

New Taxonomic Order

Order *Picornavirales* (order under consideration by ICTV, see 2006 proposal)

Family currently unassigned [but see proposal for family *Secoviridae* (2007.057-9P.02)]

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ICTV-EC comments and response of the SG

Species demarcation criteria in the genus

Type of biological vector
Host range
Absence of serological cross-reaction
Absence of cross-protection
Sequence similarity: Less than 75% amino-acid sequence identity in the CPs within a species
Less than 75% amino-acid sequence identity in the proteinase-polymerase region

Argumentation to justify the designation of new species in the genus

Stocky prune virus (StPV) was first isolated in diseased French prunes (Candresse et al, 1998). Although originally referred to as a tentative nepovirus (Candresse et al, 1998), recent molecular characterization of the virus suggests that it belongs to the genus *Cheravirus* (Candresse et al, 2006). The genus *Cheravirus* is currently unassigned but is being proposed to become part of the suggested family *Secoviridae* (see proposal on the creation of the family *Secoviridae*). StPV has icosahedral particles 28-30 nm in diameter and a bipartite positive-strand RNA genome. RNA1 and RNA2 are approximately 7,400 and 3,700 nts in length, respectively. The virus particles consist of three coat proteins (CPs) of approximately 23, 23.5 and 24.5 kDa. Each RNA encodes a polyprotein from which mature viral proteins are released. The size of the RNAs and the number of CPs is similar to those of members of the genus *Cheravirus* (Le Gall et al, 2005). Cherry rasp leaf virus (CRLV), the type member of the genus *Cheravirus*, is transmitted by nematodes and is seed-transmitted (Hansen et al, 1974). No information is available regarding the transmission and possible vectors of other tentative or definite species of the genus. The vector for StPV has not been identified. However, its spread in the field and its limited geographic distribution suggest a nematode vector (Candresse et al, 2006). Phylogenetic studies using the amino acid sequence between conserved motifs of the proteinase (CG motif) and polymerase (GDD motif) confirmed that it groups with other members of the genus *Cheravirus* and not with members of the genera of bipartite plant picorna-like viruses (*Comovirus*, *Fabavirus*, *Nepovirus*, or *Sadwavirus*). An exception is strawberry latent ringspot virus (SLRSV) a tentative sadwavirus that groups with the cheravirus branch (Le Gall et al, 2007; see also Annex). The taxonomic position of SLRSV will need to be reevaluated at a later time as more information becomes available on sadwaviruses and cheraviruses (see discussion in proposal for the creation of the family *Secoviridae*).

StPV is a distinct species within the genus *Cheravirus* based on the following observations. In serological assays, StPV does not cross-react with CRLV (Desvignes, 1990). The StPV CPs have only a low level of sequence identity with the CPs of apple latent spherical virus (ALSV, 24%) and CRLV (27%) (Candresse et al, 2006). In phylogenetic analysis using the Pro-Pol region (Candresse et al, 2006, see also Annex), StPV although branching with the two other sequenced cheraviruses, was only distantly related to ALSV and CRLV. These characteristics meet the criteria established for species demarcation in the genus *Cheravirus* (Le Gall et al, 2005).

In conclusion, although StPV is only distantly related to definite species of the genus *Cheravirus*, its properties (presence of 3 CPs, size of the two RNAs, phylogenetic grouping using the Pro-Pol region) are consistent with its suggested classification as a new species in the genus *Cheravirus*.

List of created Species in the genus

Stocky prune virus (StPV) DQ143874/5

References

Candresse, T., Delbos, R. O., Le Gall, O., Desvignes, J.C. (1998) Characterization of Stocky prune virus, a new nepovirus detected in French prunes. *Acta Horti* 471: 175-181

Candresse, T., Svanella-Dumas, L., and Le Gall, O. (2006) Characterization and partial genome sequence of stocky prune virus, a new member of the genus Cheravirus. *Arch. Virol.* 151: 1179-1188

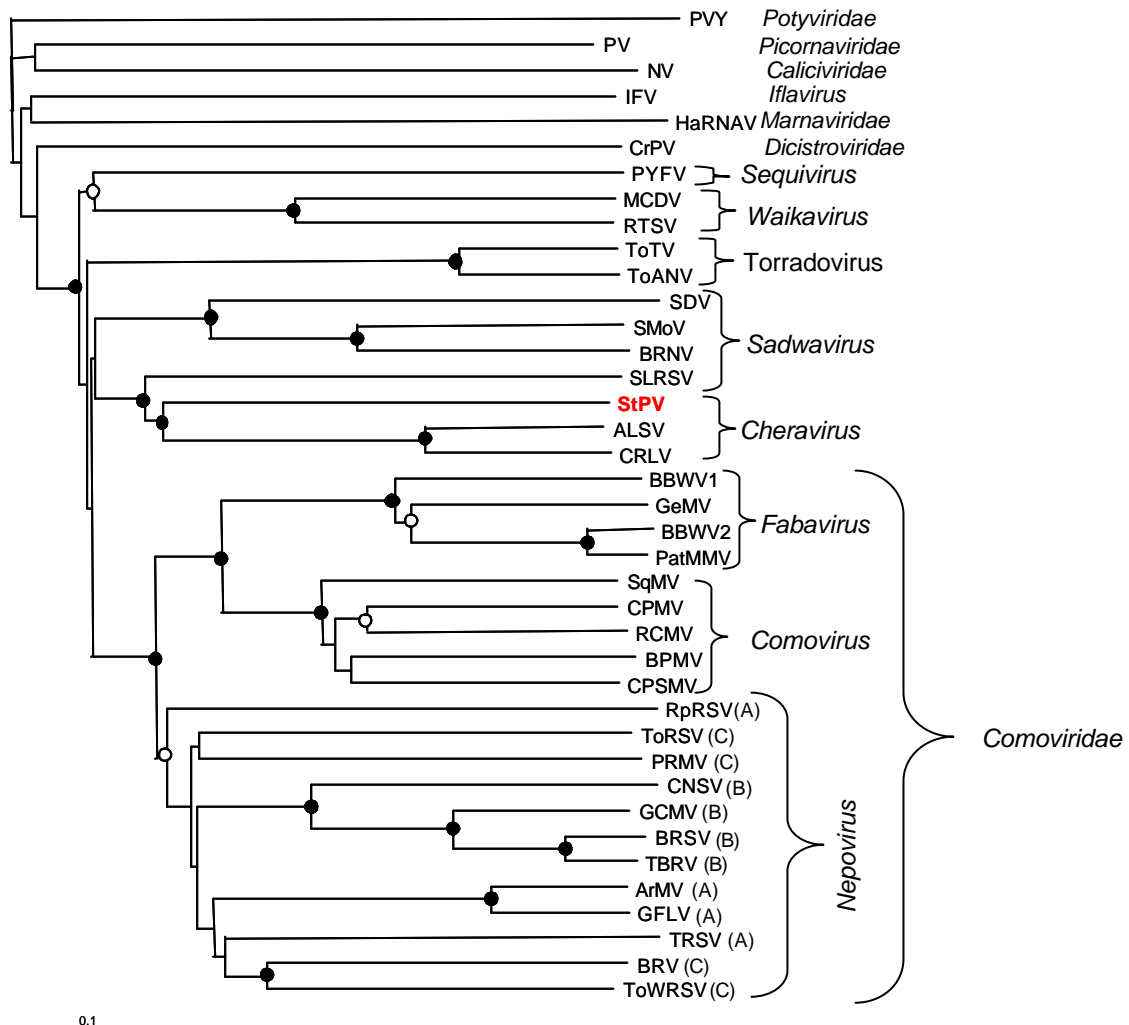
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Hansen, A. J., Nyland, G., McElroy, F. D., Stace-Smith, R. (1974) Origin, cause, host range and spread of cherry rasp leaf disease in North America. *Phytopathology* 64: 721-727.

Le Gall, O., Iwanami, T., Karasev, A. V., Jones, A. T., Lehto, K., Sanfacon, H., Wellink, J., Wetzel, T., and Yoshikawa, N. (2005) Genus Cheravirus. In: *Virus Taxonomy: The classification and nomenclature of viruses. The eight report of the International Committee on Taxonomy of Viruses* (Fauquet, C. M., Mayo, M. A., Maniloff, J., Desselberger, U., and Ball, L. A., Eds, Academic Press, San Diego, USA) pp. 803-805

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Annex: Phylogenetic tree showing the position of StPV in the genus *Cheravirus* and with related plant picorna-like viruses



Hierarchical clustering of plant picorna-like viruses based on the Pro-Pol sequence (region between the CG motif within the proteinase and the GDD motif with the polymerase). The families and genera are delineated on the right. The letter in parenthesis after the nepovirus acronyms refer to the subgroup in which they have been classified (A, B or C). Circles indicate nodes supported by bootstrap values above 80% (closed circles) or 60% (open circles); nodes without circles are not supported to these levels. The bar represents a p-distance of 0.1. The amino-acid sequence clustering is based on the region between the Pro (CG) and the Pol (GDD) sequence motifs. The GenBank accession numbers for each virus were as follows: infectious flacherie virus (IFV, AB000906), cricket paralysis virus (CrPV, AF318039), poliovirus (PV, V01149), Norwalk virus (NV, M87661), Heterosigma akashiwo RNA virus (HaRNAV, AY337486), potato virus Y (PVY, X12456), maize chlorotic dwarf virus (MCDV, U67839), parsnip yellow fleck virus (PYFV, D14066), rice tungro spherical virus (RTSV, M95497), gentian mosaic virus (GeMV, BAD99001), broad bean wilt virus 1 (BBWV1, AB084450), broad bean wilt virus 2 (BBWV2, AF225953), patchouli mild mosaic virus, an isolate of BBWV2 (PatMMV, AB050782), squash mosaic virus (SqMV, AB054688), bean poddle mosaic virus (BPMV, U70866), red clover mosaic virus (RCMV, X64886), cowpea severe mosaic virus (CPSMV, M83830), cowpea mosaic virus (CPMV, X00206), tomato torrado virus (ToTV, DQ388879), tomato apex necrosis

virus (ToANV, EF063641), stocky prune mosaic virus (StPV, AAZ76594), black raspberry necrosis virus (BRNV, DQ344639), strawberry mottle virus (SMoV, AJ311875), strawberry latent ringspot virus (SLRSV, AY860978), satsuma dwarf virus (SDV, AB009958), apple latent spherical virus (ALSV, AB030940), cherry rasp leaf virus (CRLV, AJ621357), tomato white ringspot virus (ToWRSV which is probably an isolate of artichoke ringspot virus, ABM65096), peach rosette mosaic virus (PRMV, AAB69867), blackcurrant reversion virus (BRV, AF3682772), tomato ringspot virus (ToRSV, L19655), tomato black ring virus (TBRV, AY157993), grapevine chrome mosaic virus (GCMV, X15346), cycas necrosis stunt virus (CNSV, AB073147), beet ringspot virus (BRSV, D00322), tobacco ringspot virus (TRSV, U50869), raspberry ringspot virus (RpRSV, AY303787), arabis mosaic virus (ArMV, AY303786), grapevine fanleaf virus (GFLV, D00915).