This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2016.003aP***	(to be completed by ICTV officers)

Short title: One new species in the genus *Cheravirus*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)					
	1 ☒	**2** ☒	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☐	**10** ☒

Author(s):

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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Secoviridae Study Group

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: July 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	***2016.003aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Cheravirus***
Subfamily:	
Family:	***Secoviridae***
Order:	***Picornavirales***

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Currant latent virus	currant latent virus (CuLV) isolate Hol 9/6	KT692952 (RNA1) KT692953 (RNA2)

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Species demarcation criteria for the family *Secoviridae* have been used to define the new species: aa sequence of combined CPs with less than 75% identity, aa sequence of conserved Pro-Pol region (region between the conserved "GC" motif in the protease and "GDD" motif in the polymerase) with less than 80% identity, differences in antigenic reactions, host range and/or vector specificity.

Currant latent virus

Currant latent virus (CuLV) was detected from different cultivars of red, black and white currants in the Czech Republic. These plants did not show disease symptoms. Primer-walking approach using degenerate primers derived from conserved motifs of *Apple latent spherical virus* (ALSV) and other cheraviruses and sanger sequencing revealed the presence of a virus with a typical cheravirus genome organization, but with low identities in comparison to the known cheraviruses (Petrzik et al., 2015). Double-stranded RNA isolated from representative isolate Hol 9/6 of red currant was the source material for sequencing library preparation and sequencing on HiSeq2500 system. Contigs representing RNA1 and RNA2 (mean coverage 38.6 and 21.8, respectively) were verified by amplification with specific primers. The 5´ends were amplified using 5´RACE kit and 3´ends using specific forward primers and an oligo(dT) primer. The complete RNA1 (6603 nt excluding the poly 3´polyA tail) and RNA2 (3292 nt excluding the 3´polyA tail) sequences were obtained (Petrzik et al., 2016). This virus was not mechanically transmissible to *Chenopodium quinoa*, *Nicotiana tabacum*, and *N. benthamiana*. This virus was detected in oligophagous viviparous females and in nymphs of red blister aphid

Cryptomyzus ribis (L.) and circulates in the aphid. Although aphid transmission has not been completely demonstrated for this virus, results so far contrast with the vector of other cheraviruses where nematode transmission has been demonstrated (*Cherry rasp leaf virus*) or is suspected (*Stocky prune virus*) (Candresse et al. 2006). Sequence identities for the two regions mentioned in the demarcation criteria are 67% for the Pol region and 59% for the CPs region with the closest ALSV.

Taken together, these data clearly indicate that CuLV Hol 9/6 should be regarded as a representative isolate of a new cheravirus species, which is illustrated by a phylogenetic analysis (based on the Pro-Pol region).

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Candresse, T., Svanella-Dumas, L. & 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.

Petrzik, K., Pribylova, J., Spak, J. & Havelka, J. (2015) Partial genome sequence of currant latent virus, a new chera-like virus related to Apple latent spherical virus. J Gen Plant Pathol 81, 142-145.

Petrzik, K., Koloniuk, I., Pribylova J. & Spak, J. (2016) Complete genome sequence of currant latent virus (genus Cheravirus, family Secoviridae) Arch Virol 161, 491-493

Annex:

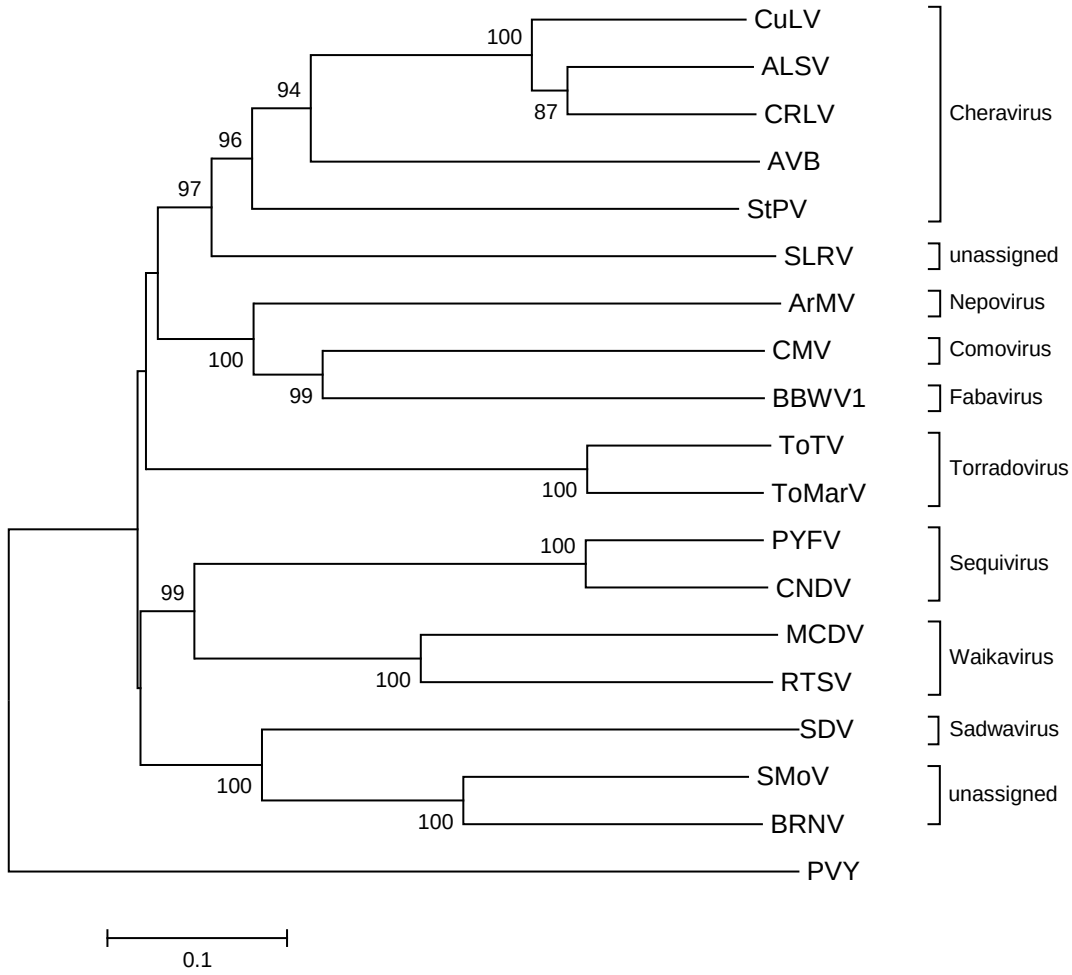
Percentage of amino acid identity of CuLV to the most related cheraviruses

	CoPro	Hel	VPg	Pro	Pol	polyprotein	MP	CP1	CP2	CP3	polyprotein
ALSV	42.1	68.3	59.3	53.6	67.4	64.5	72.1	62.1	56.3	58.9	59.5
CRLV	38.0	66.0	57.8	67.0	66.8	60.2	71.7	55.7	48.9	54.9	58.0

Phylogenetic analysis of the based on the Pro-Pol region

Phylogenetic tree generated by the neighbor-joining method from alignment of the amino acid segment between the “CG” motif of the 3C-like proteinase and the “GDD” motif of the

polymerase. The tree was generated using MEGA5. Numbers on nodes show bootstrap values (1,000 replicates) above 70 %.



Potato virus Y (PVY) a member of the family Potyviridae was used as an outgroup. The bar represents a P distance of 0.1. The GenBank accession numbers used for each virus are as follows: potato virus Y (PVY, NC_001616 = X12456), parsnip yellow fleck virus (PYFV, NC_003628 = D14066), carrot necrotic dieback virus (CNDV, EU980442), maize chlorotic dwarf virus (MCDV, NC_003626 = U67839), rice tungro spherical virus (RTSV, NC_001632 = M95497), yomato torrado virus (ToTV, NC_009013 = DQ388879), yomato marchitez virus (ToMarV, NC_010987 = EF681764), strawberry latent ringspot virus (SLRSV, NC_006964 = AY860978), stocky prune virus (StPV, DQ143874), apple latent spherical virus (ALSV, NC_003787 = AB030940), cherry rasp leaf virus (CRLV, NC_006271 = AJ621357), satsuma dwarf virus (SDV, NC_003785 = AB009958), arracacha virus B (AVB, JQ437415), strawberry mottle virus (SMoV, NC_003445 = AJ311875), black raspberry necrosis virus (BRNV, NC_008182 = DQ344639), arabis mosaic virus (ArMV, NC_006057 = AY303786), cowpea mosaic virus (CPMV, NC_003549 = X00206), broad bean wilt virus 1 (BBWV1, NC_005289 = AB084450).