This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

**Part 1:** **TITLE, AUTHORS, etc**

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| **Code assigned:** | ***2018.008P*** | | (to be completed by ICTV officers) |
| **Short title:** One new species in the genus *Prunevirus*. | | | |
|  | | | |
| **Author(s):** | | | |
| Stella Veerakone, Lia W. Liefting, Joe Tang, Lisa I. Ward | | | |
| **Corresponding author with e-mail address:** | | | |
| Stella Veerakone, stella.veerakone@mpi.govt.nz | | | |
| **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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | *Beta*-, *Gamma*-, and *Deltaflexiviridae* Study Group (SG Chair: Ioannis Tzanetakis) | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
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|  | | | |
| Date first submitted to ICTV: | | | May 8th 2018 |
| Date of this revision (if different to above): | | |  |

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| **ICTV-EC comments and response of the proposer:** |
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**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
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**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module: 2018.008P.N.v1.Prunevirus\_sp.xlsx** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:  A novel prunevirus was isolated from *Actinidia chinensis* using high throughput sequencing (HTS) of total RNA (Veerakone et al, 2018). The complete genome sequence of the novel *Actinidia* virus consists of 8,192 nucleotides (nt) (GenBank accession number MF440375), excluding the 3ʹ poly (A) tail. The genome organization is similar to that of the pruneviruses (Marais et al. 2015), with four ORFs coding for the conserved domains described for that genus (Figure 1). ORF1 (nt 66-6074) encodes a putative replicase (REP) of 2,002 amino acids (aa), ORF2 (nt 6067-7407) encodes a 30K type putative movement protein (MP) of 446 aa, ORF3 (nt 6983-7651), which overlaps ORF2 by 424 nt, encodes a putative coat protein (CP) of 222 aa, and ORF4 (nt 7653-8126) encodes a putative nucleic acid binding protein (NB) of 157 aa. The 5’ and the 3’ UTRs are 65 and 66 nt long, respectively.  Comparison of the novel *Actinidia* virus REP, MP and CP aa sequences showed highest aa identity (47.1%, 52.3% and 63.5%, respectively) to the corresponding proteins of caucasus prunus virus (CPrV), a member of the genus *Prunevirus* (Figure 2)*.* On the full sequence pairwise comparison, the new virus shares 56% nt identity with CPrV. This is well below the threshold determined by the ICTV for species demarcation. Therefore, the novel *Actinidia* virus is proposed as a protype of a new species in the genus *Prunevirus* for which the name *Actinidia seed borne latent virus* (ASbLV) is proposed.   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing.   Members of the genus *Prunevirus* should have the same genomic organization (gene number and gene order). Species that belong to this genus have a filamentous virion with four open reading frames (ORFs). As for other genera in the family *Betaflexiviridae*, isolates of different species should have less than 72% nucleotide identity (or 80% amino acid identity) between their respective coat protein (CP) or replicase genes (Adams et al, 2004). ASbLV shows ~47% Pol and ~63% CP aa identity values to its closest relative.     * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

**Figure 1.** Genome organisation of *Actinidia seed borne latent virus* (ASbLV). The locations of the replicase (REP), movement protein (MP), coat protein (CP) and nucleic acid binding protein (NB) and their amino acid sizes are indicated.



**Figure 2.**  Phylogenetic analysis of recognized members in the family *Betaflexiviridae* based on the deduced amino acid sequences of the coat protein. Branches with more than 70% bootstrap support from 1000 replicates are shown. Abbreviations of virus names: red clover vein mosaic virus (RCVMV), garlic common latent virus (GarCLV), apple stem pitting virus (ASPV), grapevine rupestris stem pitting-associated virus (GRSpaV), cherry necrotic rusty mottle virus (CNRMV), cherry green ring mottle virus (CGRMV), banana mild mosaic virus (BanMMV), banana virus X (BanVX), sugarcane striate mosaic-associated virus (SCSMaV), apple stem grooving virus (ASGV), cherry virus A (CVA), carrot Ch virus 1 (CChV-1), carrot Ch virus 2 (CChV-2), citrus leaf blotch virus (CLBV), diuris virus A (DiVA), diuris virus B (DiVB), apricot vein clearing associated virus (AVCaV), caucasus prunus virus (CPrV), potato virus T (PVT), apple chlorotic leaf spot virus (ACLSV), cherry mottle leaf virus (ChMLV), peach mosaic virus (PcMV), actinidia virus A (AcVA), actinidia virus B (AcVB). Position of ASbLV is indicated in bold and with a red star.

| **References:** |
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| Veerakone S, Liefting LW, Tang J, Ward LI (2018) The complete nucleotide sequence and genome organization of a novel *Betaflexiviridae* from *Actinidia chinensis*. Archives of Virology 163:1367-1370.  Marais A, Faure C, Mustafayev E, Candresse T (2015) Characterization of new isolates of *Apricot vein clearing-associated virus* and of a new *Prunus*-infecting virus: Evidence for recombination as a driving force in *Betaflexiviridae* evolution. PLoS ONE 10:e0129469.  Adams MJ, Antoniw JF, Bar-Joseph M, Brunt AA, Candresse T, Foster GD, Martelli GP, Milne RG, Zavriev SK, Fauquet CM (2004) The new plant virus family *Flexiviridae* and assessment of molecular criteria for species demarcation. Arch Virol 149:1045-1060 |