

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

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| **Code assigned:** | **2020.029M** |  |
| **Short title:** Create one new genus and 16 new species (*Bunyavirales: Phenuiviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Phenuiviridae* Study Group, ICTV *Tenuivirus* Study Group (co-authors) |

**ICTV study group comments and response of proposer**

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**Submission dates**

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**ICTV-EC comments and response of the proposer**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.029M.R.Phenuiviridae\_1gen16sp.xlsx |

**Abstract**

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| We propose the establishment of one new genus, *Tanzavirus*, including one new species, and 15 additional new species in established genera of the family *Phenuiviridae*. |

**Text of proposal**

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| |  | | --- | | 1. **Create species *Penshurt phlebovirus* and *Corfou phlebovirus* in genus *Phlebovirus***   Two newly sequenced or previously unrecognized viruses have been shown to be closely related to members of the phenuivirid genus *Phlebovirus*. Our analyses indicate that, by applying the established demarcation criterion of <95% amino-acid identity among RNA‑directed RNA polymerase (RdRp) domains, two new phlebovirus species need to be created for these viruses, which we propose to be named *Penshurt phlebovirus* (to accommodate Penshurt virus [[4](#_ENREF_4)] showing 92.66% amino-acid identity to Anhanga virus) and *Corfou phlebovirus* (to accommodate Corfou virus [[2](#_ENREF_2)] showing 94.50% amino‑acid identity to Toros virus). Both viruses have genomes with the typical genomic organization of phleboviruses, consisting of three segments—namely large (L), medium (M), and small (S) encoding the RdRp, a glycoprotein precursor (GPC), and a nucleocapsid (N), respectively—and clustering into the diversity of phleboviruses (Figure 1). In addition, a non‑structural S protein is predicted to be encoded in ambisense orientation on the S‑segment.  Etymology of newly proposed taxa:  Species names have been derived from the respective member virus names.  In parallel to this TaxoProp, an additional four new phlebovirus species are proposed in co‑submitted TaxoProp 2020.022M for Bogoria virus, Embossos virus, Kiborgoch virus, and Perkerra virus.   1. **Create species *Razdan bandavirus* in genus *Bandavirus***   Razdan virus was isolated from *Dermacentor marginatus* ticks in Armenia in 1972 [[1](#_ENREF_1)]. The Razdan virus RdRp is 94.09% identical in amino-acid sequence to that of the tick-borne Bhanja virus. Bhanja virus forms a sister taxon to Razdan virus in phylogenetic analyses (Figure 1). Thus, we propose the creation of a new species, *Razdan bandavirus*, to accommodate Razdan virus.  Etymology of newly proposed taxon:  The species name has been derived from the respective member virus name.   1. **Create species *Coleopteran pidchovirus* in genus *Pidchovirus***   During a metagenomic study investigating insect transcriptomes, the coding-complete genome of Coleopteran phenui-related virus 308 has been recovered from a *Stethorus* sp. pool collected in Australia in 2013 [[7](#_ENREF_7)]. Three segments (L, M, and S) predicted to encode three proteins (RdRp, GPC, and N) have been assembled. The virus forms a sister taxon to Pidgey virus (Figure 1) and thus we propose the creation of a new species, *Coleopteran pidchovirus*, to accommodate this virus.  Etymology of newly proposed taxon:  The species name has been derived from the respective member virus name.   1. **Create species *European wheat striate mosaic tenuivirus* in genus *Tenuivirus***   European wheat striate mosaic virus has been discovered in specimen of *Avena sativa* cv. Pepino collected in Estonia in June 2013. Phylogenetic analyses placed the virus in basal position to rice stripe virus rice hoja blanca virus (Figure 1). The genome organization of European wheat striate mosaic virus and the other viruses consisting of four RNA segments each is identical. We propose establishing a new species, *European wheat striate mosaic tenuivirus*,to accommodate this virus.  Etymology of newly proposed taxon:  The species name has been derived from the respective member virus name.   1. **Create species *Kimberley horwuvirus* and assign to the genus *Horwuvirus***   Fitzroy Crossing tenui-like virus 1 has been detected in *Culex annulirostris* mosquitoes collected in Australia in April 2018 [[10](#_ENREF_10)]. Phylogenetic reconstruction places the virus as a sister taxon to Wǔhàn horsefly virus (Figure 1). The genome of Fitzroy Crossing tenui‑like virus 1 contains four segments encoding an RdRp, glycoproteins, a nucleocapsid and an unknown non-structural protein similar to one encoded by Wǔhàn horsefly virus. We propose establishing a new species, *Kimberley horwuvirus*,to accommodate Fitzroy Crossing tenui-like virus 1.  Etymology of newly proposed taxon:  *Kimberley horwuvirus* has been derived from the geographic region (Kimberley) where the samples have been collected that lead to the discovery of Fitzroy Crossing tenui‑like virus 1.   1. **Create species *Grapevine coguvirus* and in genus *Coguvirus***   The genome of a new virus, Grapevine associated cogu-like virus 1, has been sequenced by HTS from *Plamopara viticola*-infected grapevine leaves collected in Italy in July 2018 [[3](#_ENREF_3)]. Like the genomes of classified coguviruses, the genome of this novel virus consists of three segments, RNA1, RNA2, and RNA3, which are predicted to encode the viral RdRp, putative movement proteins (MPs), and N. The novel virus clusters in basal phylogenetic position to citrus concave gum-associated virus (Figure 1). Thus, we propose the creation of a new species, *Grapevine coguvirus*, to accommodate this virus.  Etymology of newly proposed taxon:  The species name has been derived from the respective member virus name.   1. **Create species *Grapevine laulavirus* 1, *Grapevine laulavirus* 2, and *Grapevine laulavirus* 3 in genus *Laulavirus***   Two previously unknown viruses, named grapevine associated cogu-like viruses 2 and 3, have been sequenced by HTS from *Plamopara viticola*-infected grapevine leaves collected in Italy in July 2018. One year earlier, in 2017, another previously unknown virus has been detected in Esca-diseased grapevine wood tissue and was named grapevine associated cogu-like virus 4. Like laulaviruses the genomes of all three newly discovered viruses contain three segments (RNA1, RNA2, and RNA2) predicted to encode RdRp, putative MPs, and N. All three viruses cluster with Laurel Lake virus (Figure 1). We propose the creation of three new species, *Grapevine laulavirus 2*, *Grapevine laulavirus 3*, and *Grapevine laulavirus 4*, to accommodate these new viruses.  Etymology of newly proposed taxa:  Species names have been derived from the respective member virus names.   1. **Create species *Grapevine rubodvirus* 1 and *Grapevine rubodvirus* 2 in genus *Rubodvirus***   Recently, two viruses have been sequenced by HTS in grapevine [[5](#_ENREF_5)]. Similar to rubodviruses, both viruses encompass tri-segmented genomes each encoding a unique protein: RdRp, nucleocapsid protein (NP), and putative MP. The viruses were named grapevine Garan dmak virus and grapevine Muscat rose virus and show closest sequence identity (60% and 50%, respectively) to members of the genus *Rubodvirus* (Figure 1). Thus, we propose the creation of two new species, *Grapevine rubodvirus 1* and *Grapevine rubodvirus* *2*, to accommodate these viruses.  Etymology of newly proposed taxa:  Species names have been derived from the respective member virus names.   1. **Create species *Narangue mobuvirus* in genus *Mobuvirus***   The recently discovered Narangue virus has been sequenced by HTS from a mosquito of the species *Mansonia titillans* collected in Colombia in April 2016 (unpublished). The virus shares a phylogenetic clade with Mothra virus (Figure 1). Thus, we propose the creation of a new species, *Narangue mobuvirus*, to accommodate this virus.  Etymology of newly proposed taxon:  The species name has been derived from the respective member virus name.   1. **Create species *Kimberley phasivirus* and *Guadaloupe phasivirus* in genus *Phasivirus***   Parry's Creek phasivirus 1 has been discovered in a pooled homogenate of *Culex annulirostris mosquitoes* collected in 2018 in Australia [[10](#_ENREF_10)]. The virus shows 88% amino‑acid identity (RdRp) to Badu virus. A second virus, Guadeloupe mosquito phasivirus, shows 65% amino-acid identity (RdRp) to phasi charoen-like virus and has been discovered in mosquitoes of the genus *Aedes* sp. collected in Guadaloupe in 2017 [[9](#_ENREF_9)]. Both viruses share a phylogenetic clade with phasiviruses (Figure 1) and resemble the typical tri-segmented genome organization. Thus, we propose the creation of the species *Kimberley phasivirus* to accommodate Parry's Creek phasivirus and the species *Guadaloupe phasivirus* to accommodate Guadeloupe mosquito phasivirus.  Etymology of newly proposed taxa:   * *Guadaloupe phasivirus* has been derived from the respective member virus name*.* * *Kimberley phasivirus* has been derived from the geographic region (Kimberley) where the samples have been collected that lead to the discovery of Parry’s Creek phasivirus 1.  1. **Proposed genus *Tanzavirus***   In phylogenetic analyses, the recently discovered Dar es Salaam virus is placed in a solitary position to other phenuivirids (Figure 1). The virus has been recovered by HTS in a human plasma sample collected in Tanzania in 2014 (unpublished). Like phleboviruses, Dar es Salaam virus genome has three segments L, M, and S, that are predicted to encode the RdRp, a GPC, and an NP. Due to the solitary position in phylogenetic analyses we propose establishing a new genus, *Tanzavirus*, including a new (type) species, *Human tanzavirus*, to accommodate this virus.  Species demarcation *criteria:*  We propose defining tanzavirus species demarcation as **<95% identity in the amino acid sequence of the RdRp**: viruses with <95% sequence identity represent unique species.  Etymology of newly proposed taxa:  *Human tanzavirus*: Derived from the host infected by Dar es Salaam virus (humans) and the country in which Dar es Salaam is location (Tanzania).  **Supporting evidence**  **Figure 1.** Maximum-likelihood (ML) phylogeny is based on a MAFFT-alignment of the RNA‑directed RNA polymerase (RdRp) amino-acid sequences of phenuiviruses and phenuivirus‑like sequences using E-INS algorithm. The ML phylogenetic tree was inferred using IQ-TREE [[8](#_ENREF_8)]; the numbers on the nodes represent bootstrap values derived from the ultrafast bootstrap algorithm [[6](#_ENREF_6)]. Trees were inferred under the LG+G+I substitution model. Tree branches are proportional to genetic distances between sequences and the scale bars at the top indicate substitutions per amino acid. For all taxa shown here, the complete genome or complete coding sequence is available at the GenBank nucleotide sequence database. Accession numbers are shown next to the respective virus taxon.  **References**  1. Al'khovskiĭ SV, L'Vov D K, Shchelkanov M, Shchetinin AM, Krasnoslobodtsev KG, Deriabin PG, Samokhvalov EI, Botikov AG, Zakarian VA (2013) [Molecular-genetic characterization of the Bhanja virus (BHAV) and the Razdan virus (RAZV) (*Bunyaviridae*, *Phlebovirus*) isolated from the Ixodes ticks *Rhipicephalus bursa* (Canestrini and Fanzago, 1878) and *Dermacentor marginatus* (Sulzer, 1776) in transcaucasus]. Vopr Virusol 58:14-9. PMID: 24354060.  2. 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