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:

Assignment of human, simian and bat pegiviruses (previously described as GBV-A, GBV-C, and GBV-D) as members of a new Genus (*Pegivirus*) within the *Flaviviridae.*

Authors: Jack T. Stapleton, Jens Bukh, A. Scott Muerhoff, Steven Foung, and Peter Simmonds.

Code assigned:	***2012.011a-dV***	(to be completed by ICTV officers)

Short title: Assign human, simian and bat pegiviruses (previously described as GBV-A, GBV-C, and GBV-D) to be species in a new genus, *Pegivirus*, family *Flaviviridae*

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

Author(s) with e-mail address(es) of the proposer:

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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)	The Flavivirus Study Group has seen and approved this submission

ICTV-EC or Study Group comments and response of the proposer:

Not applicable

Date first submitted to ICTV:	June, 12th, 2012
Date of this revision (if different to above):	July 30, 2012

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	***2012.011aV***	(assigned by ICTV officers)

To create two new species within:

Genus:	***Pegivirus*** (new)
Subfamily:	-
Family:	***Flaviviridae***
Order:	-

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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Pegivirus A *Pegivirus B*	U22303 GU566734

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

Pegivirus A

Proposed members of the species, *Pegivirus A* are monophyletic and show < 50% nucleotide (55% amino acid) sequence divergence between aligned sequences from the polyprotein from each other. However all differ by >50% nucleotide (>55% amino acid) divergence from other members of this genus. Pegiviruses to be assigned to this species (Pegivirus A) originate from primate host species (humans, chimpanzees and several New World monkey species). The sequence U22303 has been assigned the type member of the species as this was the first pegivirus to be described for this species.

Pegivirus B

One complete genome of the proposed species, *Pegivirus B* infecting the bat species *Pteropus giganteus* has been characterized to date. This sequence differs by >50% nucleotide (>55% amino acid) divergence from all proposed members of the primate-derived *Pegivirus A* species that originate from primate host species (humans, chimpanzees and several New World monkey species)

The sequence GU566734 has been assigned the type member of the species as this was the first pegivirus to be described for this species.

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2012.011bV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Flaviviridae***
Order:	

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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2012.011cV***	(assigned by ICTV officers)

To name the new genus: *Pegivirus*

Assigning the type species and other species to a new genus

Code	***2012.011dV***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Pegivirus A	Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

Please enter here the TOTAL number of species (including the type species) that the genus will contain:

Currently two, *Pegivirus A* (primate) and *Pegivirus B* (Bat). The assignment of further species to be discussed by the authors and the Flavivirus Study group and a separate proposal submitted.

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

Members of the proposed genus *Pegivirus* are phylogenetically distinct from the three assigned genera with the *Flaviviridae* (*Hepacivirus, Flavivirus and Pestivirus*) forming a separate monophyletic cluster on analysis of homologous genes, such as those for the RNA polymerase (Appendix; Fig 1) and helicase. Members of the proposed genus additionally share a number of genome features, such as an absence of an identified core protein coding region and possession of an internal ribosomal entry site structurally distinct from those of hepaciviruses and pestiviruses (Fig. 2). All members of the genus described to date share an ability to persist in their natural hosts and lack any identified pathogenicity. The rationale is detailed in the attached article summarizing this proposal (J.Gen.Virol., 92:233-246, 2011).

The proposed genus was tentatively identified in the 9th ICTV Report.

Origin of the new genus name:

"Pe" for persistent and "g" for "G" virus, in historical reference to GB virus and hepatitis G virus.

Reasons to justify the choice of type species:

Pegivirus A contains the well characterized viruses (epidemiologically, genetically and clinically)

from a range of primates, including viruses from New World primates (formerly described as GBV-A), humans (formerly GBV-C or hepatitis G virus) and homologues infecting chimpanzees and Old World monkey species.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

Species form monophyletic groups on comparison of conserved homologous genes such as those coding for the viral RNA-dependent RNA polymerase and helicase or complete genome sequences. Aligned polyprotein sequences from different species show >50% nucleotide (55% amino acid) sequence divergence from each other, although this threshold may be subject to minor revision as further variants are genetically characterized in the future. Currently proposed species contain viruses infecting different hosts (*Pegivirus A*: primates; *Pegivirus B*: bats; Fig. 3) and it is possible or likely that such host associations will remain as further pegiviruses are characterized. However, host range is not a primary attribute for species assignment.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

We are attaching the following reference

References:

Stapleton JT, Foung S, Muerhoff AS, Bukh J, Simmonds P. The GB viruses: a review and proposed re-classification as Pegiviruses. *J Gen Virol*, **92**:233-246, 2011.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

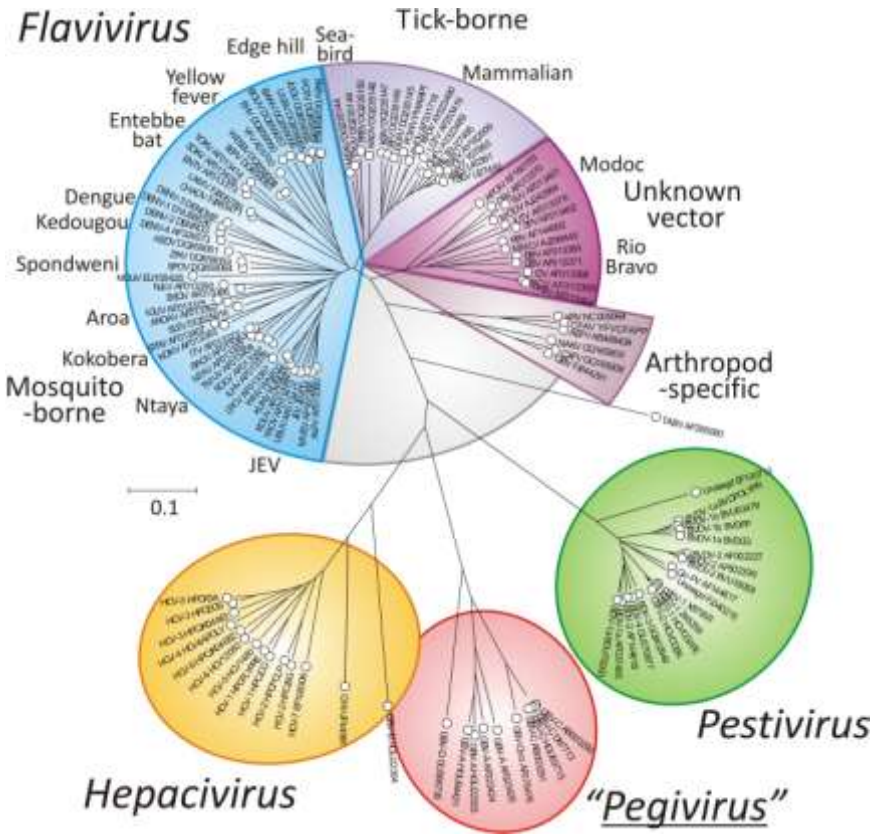

Fig. 1. Phylogeny of the conserved sequences in the RdRp (NS5 or NS5B) of classified members of the family *Flaviviridae*. Partial gene sequences (292 aa, positions 7704-8550 numbered as in the HCV-1 genome, AF011751) from the representative strains listed in each table. CLUSTALW was used to create a multiple alignment for the aa sequences which was verified by alignment of the known motifs in the region. An unrooted phylogenetic tree was constructed from the sequence alignment by neighbor-joining of (uncorrected) amino acid p-distances using the MEGA version 4.1 package. The proposed genus "*Pegivirus"* is underlined.

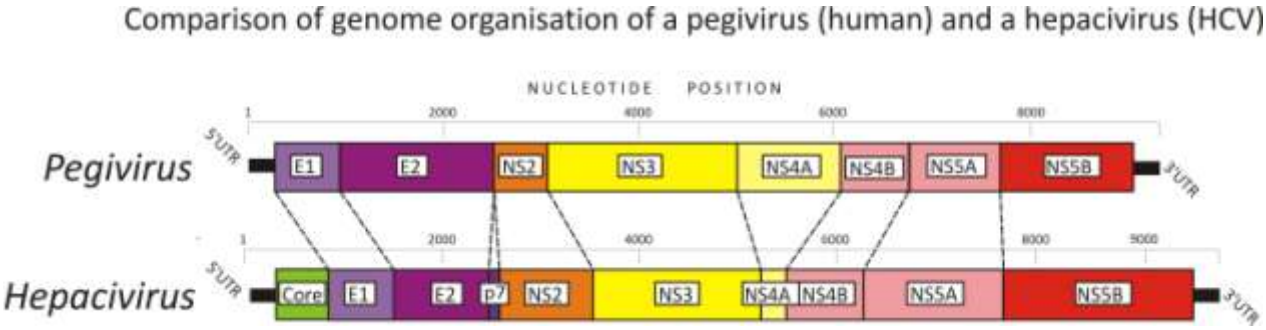

Fig. 2. Comparison of gene components of a pegivirus (human) with an hepacivirus (HCV)., showing the lack of a core protein homologue in pegiviruses and often markedly different sizes of predicted cleaved proteins.

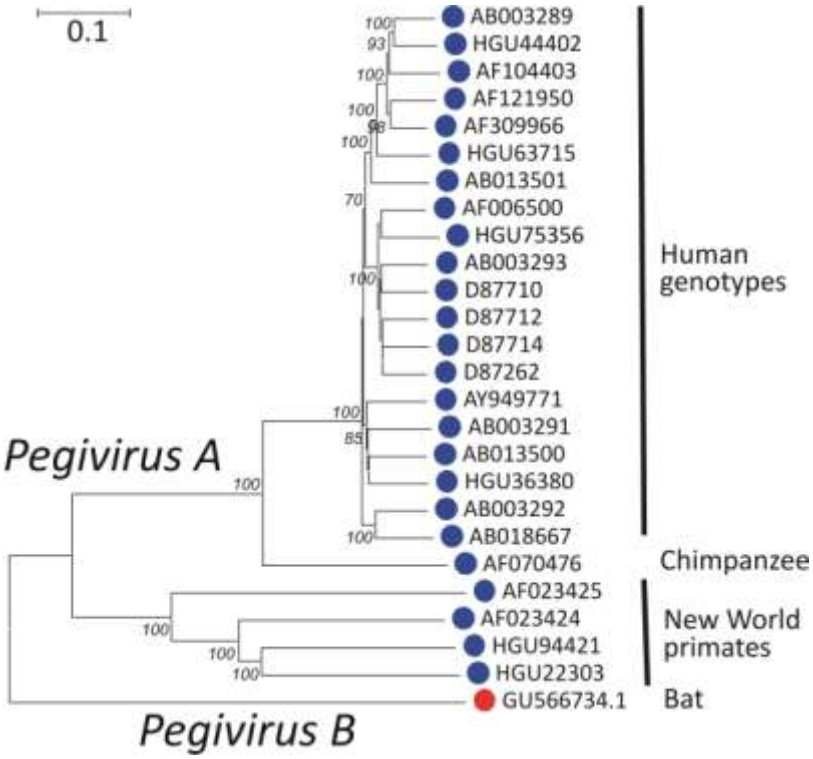

Fig. 3. Phylogeny of aligned nucleotide sequences of the polyprotein of members of the proposed genus, *Pegivirus.*. MUSCLE v. 3.8 was used to create a multiple alignment for translated amino acid sequences from which an unrooted phylogenetic tree was constructed by neighbour-joining of maximum composite likelihood nucleotide distances (MEGA version 5.0). The proposed assignment of members of the genus into *Pegivirus A* (primate-derived; blue filled circles) and *Pegivirus B* (bat-derived; red filled circles) is shown. .