



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**

<b>Code assigned:</b>	<b>2015.017aM</b>	(to be completed by ICTV officers)			
<b>Short title:</b> One (1) new species, <i>Porcine parainfluenza virus 1</i> , in the genus <i>Respirovirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input type="checkbox"/>	10 <input checked="" type="checkbox"/>

**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 <a href="http://www.ictvonline.org/subcommittees.asp">http://www.ictvonline.org/subcommittees.asp</a> . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	
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**ICTV Study Group comments (if any) and response of the proposer:**

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Date first submitted to ICTV:

June 15, 2015

Date of this revision (if different to above):

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

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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	<b>2015.017aM</b>	(assigned by ICTV officers)
<b>To create 1 new species within:</b>		
Genus:	<b><i>Respirovirus</i></b>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:	<b><i>Paramyxovirinae</i></b>	
Family:	<b><i>Paramyxoviridae</i></b>	
Order:	<b><i>Mononegavirales</i></b>	
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>
<i>Porcine parainfluenza virus 1</i>	porcine parainfluenza virus 1 strain S206N	JX857409

**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

Porcine parainfluenza virus 1 (PPIV-1) is a newly described virus identified in nasopharyngeal and rectal swab samples from infected pigs (Lau *et al.*, *Journal of General Virology* (2013), **94**, 2184–2190). The complete genome is 15,396 nt in length, complying with the ‘rule of six’ seen with all respiroviruses. Phylogenetic analyses of three isolates using the N gene sequence and the L protein sequence (Appendix, Module 10) showed that PPIV-1 was most closely related to, but distinct from, human parainfluenza virus 1 and Sendai virus. While PPIV-1 shares many common features with the respiroviruses it contains two features that distinguish it from the other respiroviruses. Firstly, unlike HPIV-1, PPIV-1 demonstrates mRNA editing in the phosphoprotein gene. Secondly, PPIV-1 is unique among respiroviruses in having two G residues instead of three to five G residues following the A6 run at the P gene editing site. On the basis of the overall genome features, the phylogenetic analyses and the distinguishing features associated with the phosphoprotein gene porcine parainfluenza virus 1 is proposed as a member of a new species in the *Respirovirus* genus of the subfamily *Paramyxovirinae*, family *Paramyxoviridae*.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

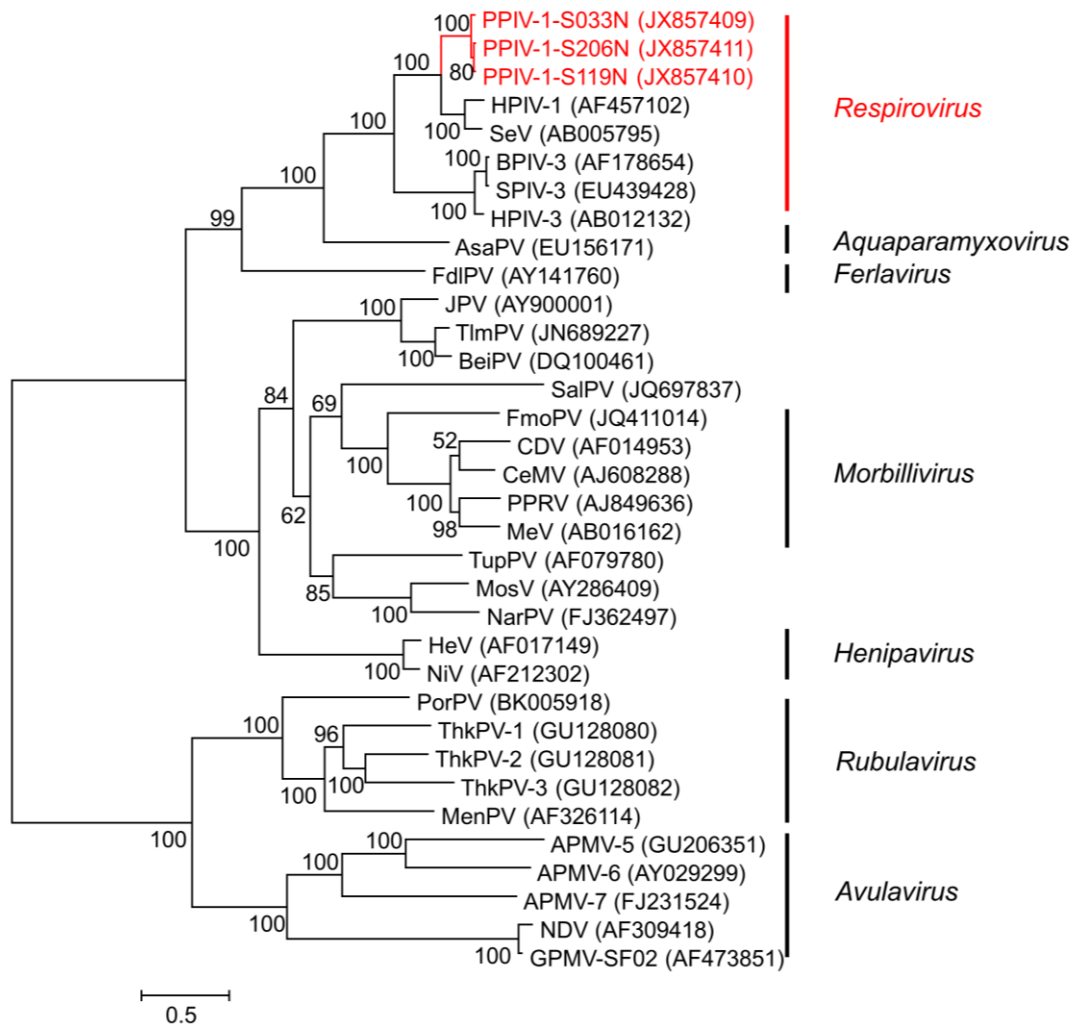
**References:**

Lau SK, Woo PC, Wu Y, Wong AY, Wong BH, Lau CC, Fan RY, Cai JP, Tsoi HW, Chan KH, Yuen KY.. Identification and characterization of a novel paramyxovirus, porcine parainfluenza virus 1, from deceased pigs. *Journal of General Virology* (2013), **94**, 2184–2190.

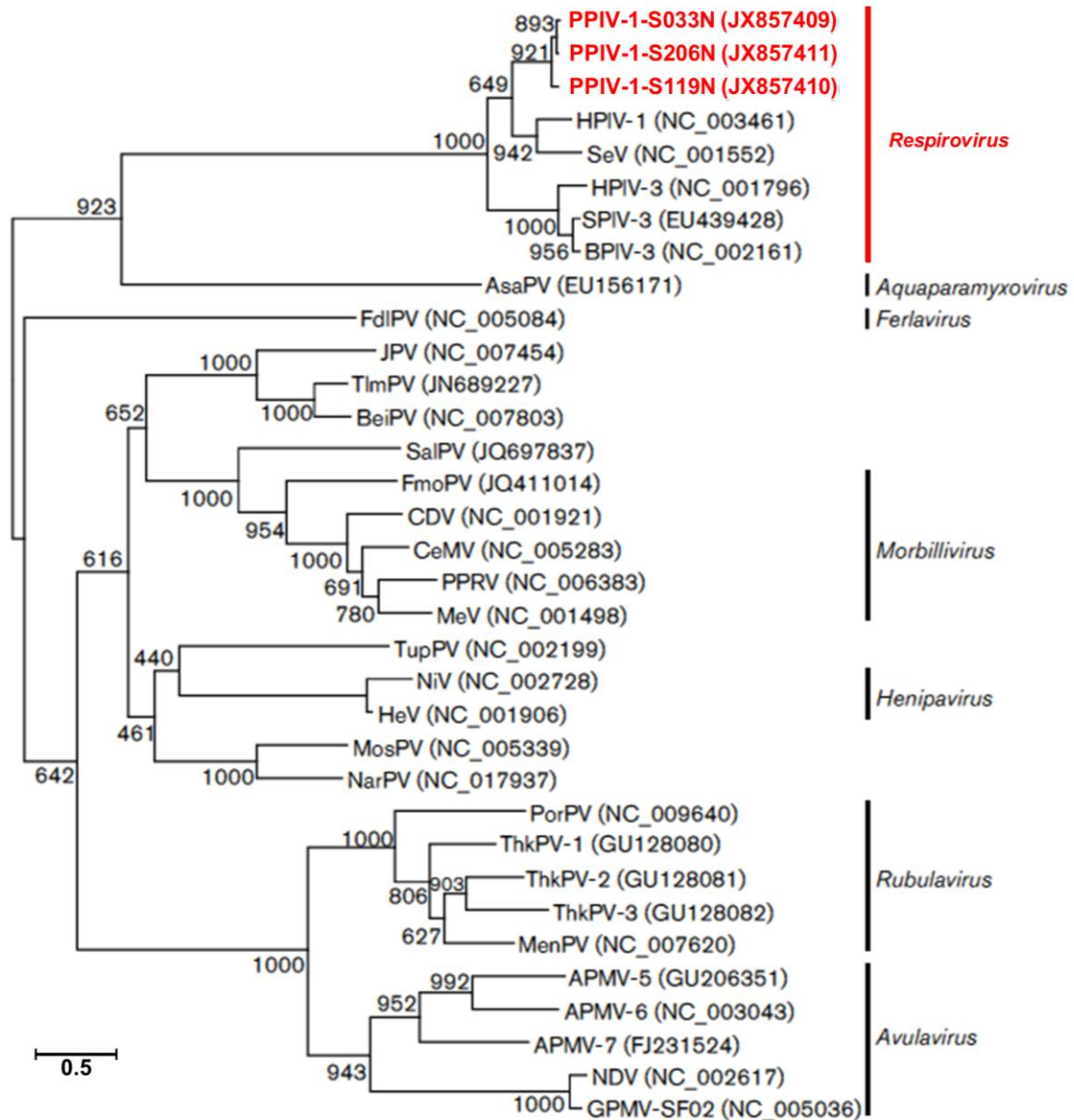
**Annex:**

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.

**A.**



B.



**Figure 1. Phylogenetic relationship of porcine parainfluenzavirus 1 polymerase and members of the family *Paramyxoviridae*, subfamily *Paramyxovirinae*.** The tree was constructed by the maximum-likelihood method with bootstrap values calculated from 1000 trees and rooted on the midpoint. Bar, 0.5 substitutions per site.

A. Phylogenetic analysis of the L proteins of three genomes of porcine parainfluenza virus 1 (highlighted). B. Phylogenetic analysis of the N gene of three isolates of porcine parainfluenza virus 1 (highlighted). HPIV-1, human parainfluenza virus 1; SeV, Sendai virus; BPIV-3, bovine parainfluenza virus 3; HPIV-3, human parainfluenza virus 1; SPIV-3, swine parainfluenza virus 3; AsaPV, Atlantic salmon parainfluenza virus; FdlPV, Fer-de-Lance parainfluenza virus; JPV, J virus; TImPV, Tailam virus; BeiPV, Beilong virus; SalPV, Salem virus; FmoPV, feline morbillivirus; CDV, canine distemper virus; CeMV, cetacean morbillivirus; PPRV, peste-des-petits-ruminants virus; MeV, measles virus; TupPV, Tupaia paramyxovirus; MosPV, Mossman virus; NarPV, Nariva virus; HeV, Hendra virus; NiV, Nipah virus; PorPV, porcine rubulavirus; ThkPV-1–3, Tuhoko virus 1–3; MenPV, Menangle virus; APMV, avian paramyxovirus; NDV, Newcastle disease virus; GPMV, goose paramyxovirus.