



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:	2011.002aV	(to be completed by ICTV officers)
Short title: New names for 2 species in the genus <i>Iotatorquevirus</i> (family <i>Anelloviridae</i>) (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 2 <input type="checkbox"/> 3 <input type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/> 6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input checked="" type="checkbox"/> 9 <input checked="" type="checkbox"/>	

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)

Anelloviridae – Circoviridae SG

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

Date first submitted to ICTV: **28 / 01 / 2011**
Date of this revision (if different to above):
Next revision – deletion of proposal to change change of proposed species name from *Torque teno sus virus 3* to *Torque teno sus virus 2*, in line with changes to 2010.005aV, which now will name this species *Torque teno sus virus k2*.

MODULE 8: **NON-STANDARD**

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

Code	2011.002aV	(assigned by ICTV officers)
Title of proposal: New names for 2 species in the genus <i>Iotatorquevirus</i> (family <i>Anelloviridae</i>)		

Text of proposal	GenBank sequence accession number(s) of reference isolate:
In the genus <i>Iotatorquevirus</i> , change the name of species <i>Torque teno sus virus 1</i> to <i>Torque teno sus virus 1a</i>	AB076001
In the genus <i>Iotatorquevirus</i> , change the name of species <i>Torque teno sus virus 2</i> to <i>Torque teno sus virus 1b</i>	AY823990

Reasons to justify the taxonomic changes:

Sequences belonging to the family *Anelloviridae* harbor a high degree of genetic diversity in humans and in some animal species as well.

Anellovirus sequences identified in swine are currently described by two distinct genera, *Iotatorquevirus* and *Kappatorquevirus*, according to demarcation criteria defined previously:

Genus *Iotatorquevirus* comprises two type species:

- *Torque teno sus virus 1* (virus name abbreviation TTSuV1) AB076001

- *Torque teno sus virus 2* (TTSuV2) AY823990

A proposal was made in mid-2010 (2010.005) in order to create a novel genus, *Kappatorquevirus*, with a highly divergent type species:

- *Torque teno sus virus 3* (TTSuV3) AY823991

This has since been modified to *Torque teno sus virus k2*.

The purpose of this proposal is to modify names of two species.

The new proposed names are:

In genus *Iotatorquevirus*:

- *Torque teno sus virus 1a* (TTSuV1a) AB076001

- *Torque teno sus virus 1b* (TTSuV1b) AY823990

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

- Biagini, P. (2009). Classification of TTV and related viruses (anelloviruses). *Curr Top Microbiol Immunol* 331, 21-33.
- Corey, M., Macera, L, Segalés, J. & Kekarainen, T. (2010). Genetic variability and phylogeny of Torque teno sus virus 1 (TTSuV1) and 2 (TTSuV2) based on complete genomes. *Vet Microbiol*, in press.
- Huang, Y.W., Ni, Y.Y., Dryman, B.A. & Meng, X.J. (2010). Multiple infection of porcine Torque teno virus in a single pig and characterization of the full-length genomic sequences of four U.S. prototype PTTV strains: implication for genotyping of PTTV. *Virology* 396, 289-297.
- Okamoto, H. (2009). TT viruses in animals. *Curr Top Microbiol Immunol* 331, 35-52.

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.

Host: Domestic pig.

Sequences: anellovirus sequences identified in this host.

A phylogenetic tree (p-distance / Neighbor-joining method) is shown (Figure 1); based on full ORF1 nt sequences available currently.

Cut-off values for sequence divergence are: species > 35%, genera > 56% (current criteria demarcating species and genera in the family *Anelloviridae*).

A detailed phylogenetic analysis was provided previously for the description of genus *Iotatorquevirus*.

Figure 1. Neighbor-joining phylogenetic tree built with ORF1-nt sequences.

(Type species are marked with an asterisk).

