



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	2008.085- 126V	(to be completed by ICTV officers)			
Short title: Revision of the family Coronaviridae (e.g. 6 new species in the genus <i>Zetavirus</i> ; re-classification of the family <i>Zetaviridae</i> etc.)					
Modules attached (please check all that apply):	1 <input type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input checked="" type="checkbox"/>	4 <input checked="" type="checkbox"/>	5 <input checked="" type="checkbox"/>
	6 <input checked="" type="checkbox"/>	7 <input checked="" type="checkbox"/>			

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The proposers are members of the Coronavirus Study Group.

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

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MODULE 3: **NEW SUBFAMILY**

Code	2008.085V
To create a new Subfamily assigned as follows:	
Family:	<i>Coronaviridae</i>
Order:	<i>Nidovirales</i>

Code	2008.086V
To name the new Subfamily: <i>Coronavirinae</i>	

Code	<i>see below</i>
To assign the following genera to the new subfamily: <i>Alphacoronavirus (new), Betacoronavirus (new), Gammacoronavirus (new)</i>	

Code	
To assign the following species to be unassigned in the new subfamily (i.e. within the subfamily but not assigned to any genus): Not applicable	

Argument to justify the creation of a new Subfamily:

The *Coronaviridae* (order *Nidovirales*) comprises a group of evolutionary related enveloped (+)strand RNA viruses of vertebrates. With respect to genome size (27-31 kb), they are the largest RNA viruses identified so far. Presently, the family *Coronaviridae* is bi-generic and comprised of the genera *Coronavirus* and *Torovirus*.

The proposed taxonomic revision of the *Coronaviridae* and the organization of the to-be-established subfamily *Coronavirinae* (Fig. 1) is based upon rooted phylogeny and pair-wise comparisons using *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab (nsp3, ADP-ribose 1''-phosphatase (ADRP); nsp5, 3C-like main proteinase (3CL); nsp12, RNA dependent RNA polymerase (RdRp); nsp13, superfamily 1 helicase with N-terminal Zn-binding domain (Z+Hel); nsp14, 3'-to-5' exoribonuclease (ExoN), nsp15, uridylate-specific endoribonuclease (NendoU); nsp16, ribose-2'-O-methyltransferase (O-MT), see Annexes, Fig. 2) and using the (coronavirus) structural proteins S, E, M and N (González *et al.*, 2003; Gorbalenya *et al.*, 2006, 2008). Note that toro- and bafiniviruses lack an E protein and that their structural proteins S, M and N show very little sequence similarity to each other and nearly no similarity to those of coronaviruses.

In rooted trees, the members of the genus *Coronavirus* (i.e. the true coronaviruses) consistently form three distinct monophyletic groups (see Annex, Fig. 3) and in pair-wise comparisons, they form three robust non-overlapping clusters. This phylogenetic constellation is well recognized and in publications these three groups are consistently referred to as phylogroups 1, 2 and 3. However, in view of the recent increase in

Argument to justify the creation of a new Subfamily:

number of newly discovered coronaviruses (and sequence data) and ensuing debates and confusion in the literature concerning coronavirus taxonomy, it is crucial to develop a frame-work for consistent classification and to establish definite genus and species demarcation criteria.

The *inter*-group pair-wise amino acid identity scores for the true coronaviruses are comparable to those calculated for structural and non-structural proteins of different genera in other RNA virus families (e.g. *Potyviridae*, *Picornaviridae*) (González *et al.*, 2003). Based on this *defacto* criterion, we propose to convert phylogroups 1 through 3 into genera designated *Alpha*-, *Beta* and *Gammacoronavirus*, respectively.

The establishment of these new genera necessitates the allocation of the genus *Torovirus* either to a new family or subfamily (the evolutionary distance between the corona- and torovirus clusters is much larger and of a different order than that between the coronavirus phylogroups; González *et al.*, 2003). Corona- and toroviruses (including the bafiniviruses) have diverged considerably, but are still more closely related to each other than to other known members of the *Nidovirales* (*Roni*- and *Arteriviridae*). There is ample support from numerous analyses that among the four nidovirus clusters, coronaviruses and the toro/bafiniviruses must have a monophyletic origin (Gorbalenya, 2008). We therefore propose to create in the family *Coronaviridae* two new subfamilies, *Coronavirinae* (to accommodate the three new genera *Alpha*-, *Beta* and *Gammacoronavirus*) and *Torovirinae* (to accommodate the genera *Torovirus* and *Bafinivirus*).

Origin of the new Subfamily name:

The name *Coronavirinae* is obviously derived from the established name of this group of viruses (coronaviruses)

References:

González *et al.* (2003) A comparative sequence analysis to revise the current taxonomy of the family *Coronaviridae*. *Arch. Virol.* 148: 2207–2235

Gorbalenya *et al.* (2006) Nidovirales: evolving the largest RNA virus genome. *Virus Res.* 117: 17-37

Gorbalenya (2008) Genomics and evolution of the *Nidovirales*. *In: "Nidoviruses"* (Perlman, Gallagher, Snijder, eds.), p. 15-28, ASM Press, Washington, DC.

Schütze *et al.* (2006) Characterization of White bream virus reveals a novel genetic cluster of nidoviruses. *J. Virol.* 80:11598-609

Ziebuhr (2008) Coronavirus replicative proteins. *In: "Nidoviruses"* (Perlman, Gallagher, Snijder, eds.), p. 65-81, ASM Press, Washington, DC.

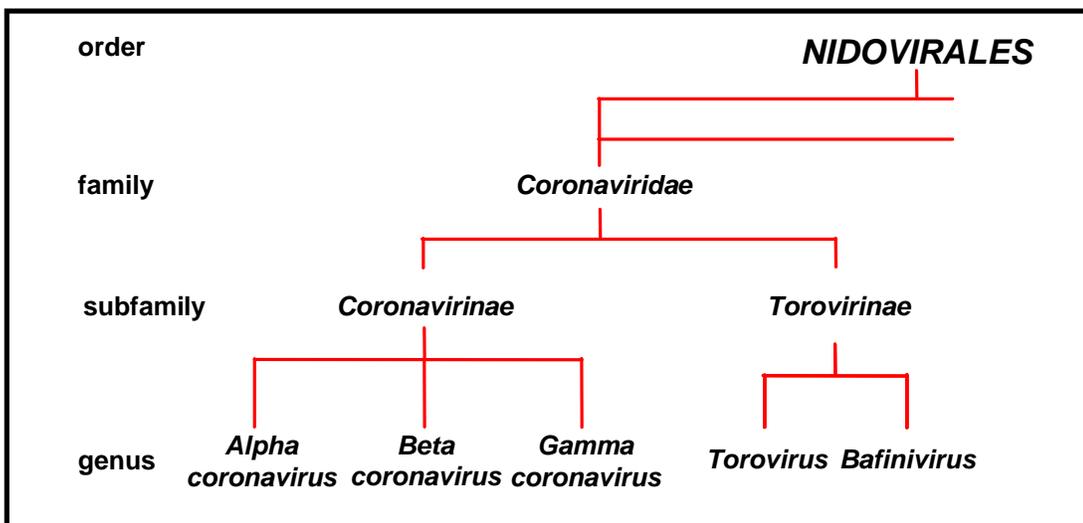
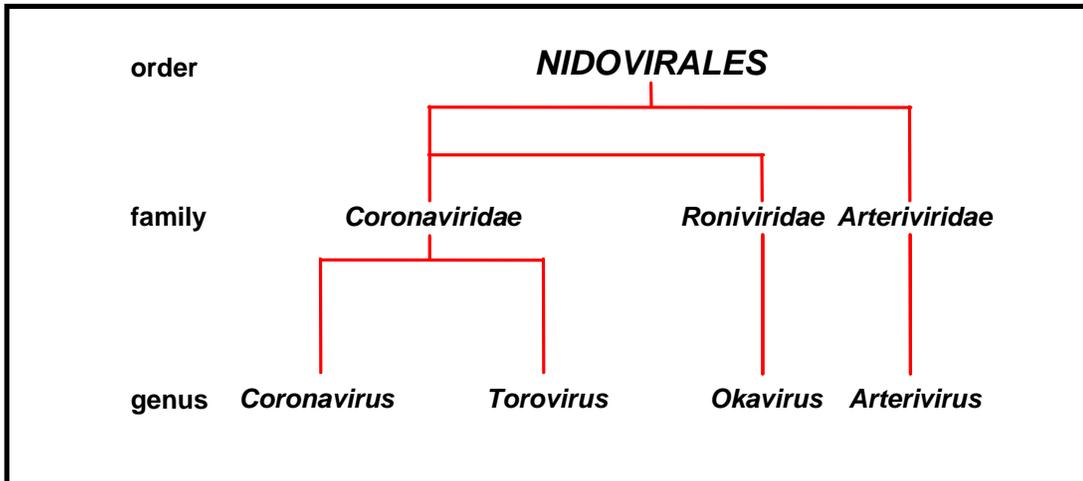


Fig. 1. Current taxonomic organization of the *Nidovirales* (top) and envisaged revision of the family *Coronaviridae* (bottom).

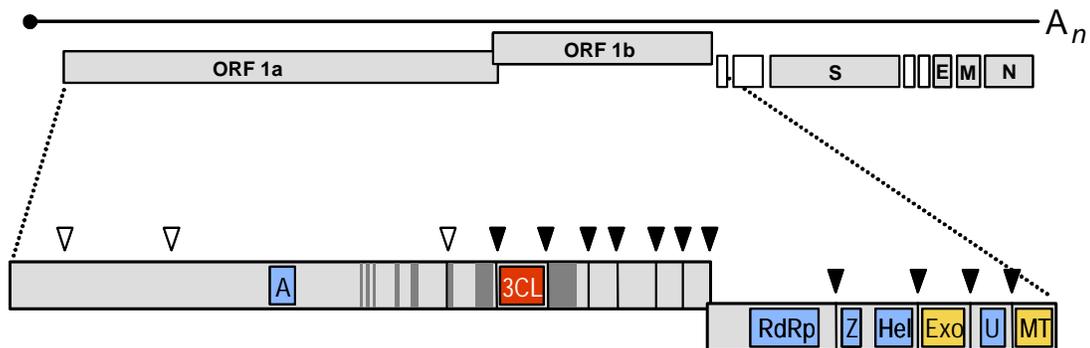


Fig. 2. Coronavirus genome organization and domain organization of replicase polyprotein pp1ab using MHV as an example (upper panel) Grey boxes indicate genes for the replicase polyproteins pp1a and pp1ab and for the structural proteins S, E, M and N. White boxes indicate niche-specific optional accessory genes. (lower panel) Replicase domains conserved in all *Coronaviridae* are indicated: A, ADRP; Exo, ExoN; U, NendoU; MT, O-MT (Gorbalenya, 2006; Ziebuhr, 2008).

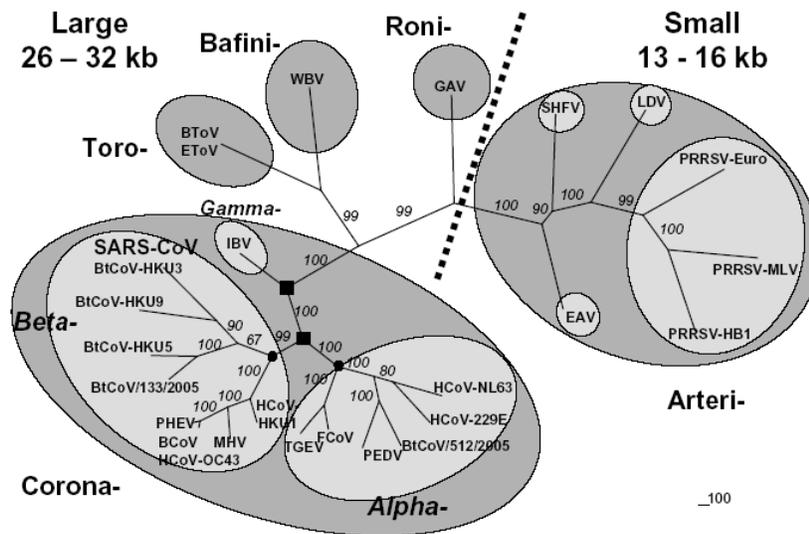


Fig. 3. Nidovirales phylogeny. Unrooted maximum parsimonious tree -inferred from multiple nucleotide alignments of the RdRp-Hel region- depicting the evolutionary relationships between the five major groups of nidoviruses (Corona-, Toro-, Bafini-, Roni- and Arteriviruses) and between the envisaged genera *Alpha-*, *Beta-* and *Gammacoronavirus* and *Toro-* and *Bafinivirus*. Adapted from Gorbalenya (2008).

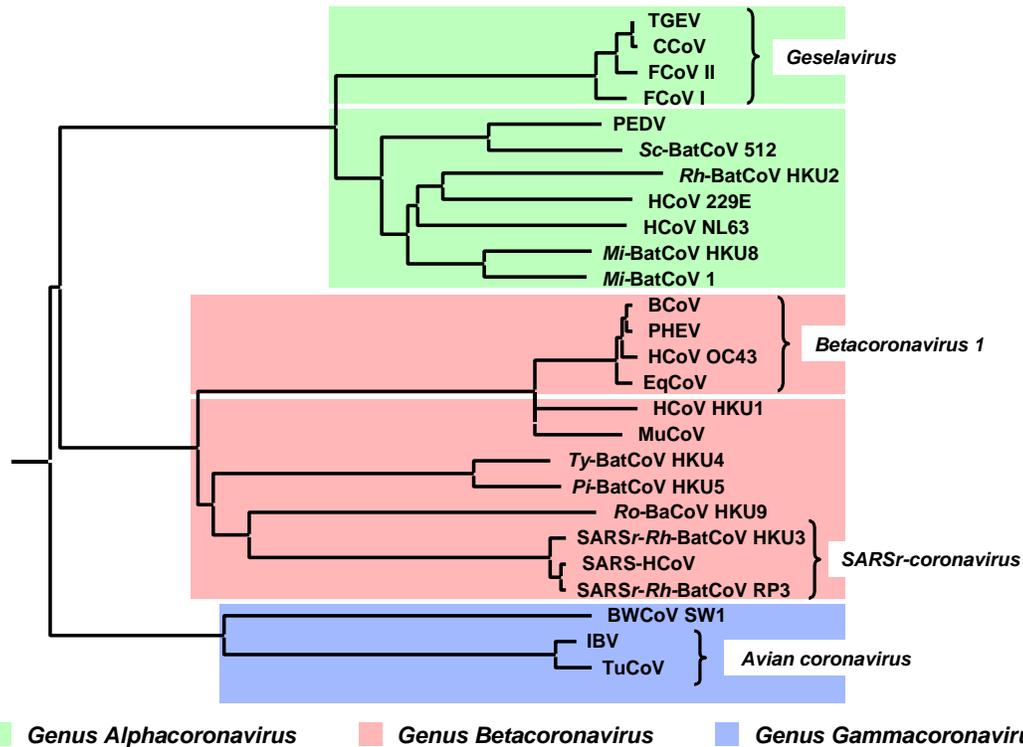


Fig. 4. Rooted Neighbour-Joining tree inferred from multiple amino acid alignments of the RdRp, illustrating the relationships between the proposed coronavirus genera and between the viruses lumped in the new species *Alphacoronavirus 1*, *Betacoronavirus 1*, *Severe acute respiratory syndrome-related coronavirus* and *Avian Coronavirus*.

MODULE 4: NEW GENUS

Code	2008.087V
To create a new genus assigned as follows:	
Subfamily:	<i>Coronavirinae</i>
Family:	<i>Coronaviridae</i>
Order:	<i>Nidovirales</i>

Code	2008.088V
To name the new genus: <i>Alphacoronavirus</i>	

Code	2008.089V
To assign the following as species in the new genus:	
<ul style="list-style-type: none"> • <i>Alphacoronavirus 1</i> (new) (comprised of existing species FCoV, CCoV, TGEV) • <i>Human coronavirus 229E</i> (existing; to be removed from genus <i>Coronavirus</i>) • <i>Human coronavirus NL63</i> (existing; to be removed from genus <i>Coronavirus</i>) • <i>Porcine epidemic diarrhea virus</i> (existing; to be removed from genus <i>Coronavirus</i>) • <i>Rhinolophus bat coronavirus HKU2</i> (new) • <i>Scotophilus bat coronavirus 512/05</i> (new) • <i>Miniopterus bat coronavirus 1</i> (new) • <i>Miniopterus bat coronavirus HKU8</i> (new) 	

Code	2008.090V
To designate the following as the type species in the new genus:	
<i>Alphacoronavirus 1</i>	

Argument to justify the creation of a new genus:

The proposed revision of the family *Coronaviridae* and the organization of the to-be-established subfamily *Coronavirinae* is based upon rooted phylogeny and pair-wise comparisons using *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab as well as the structural proteins S, E, M and N (González *et al.*, 2003; Gorbalenya *et al.*, 2006, 2008). In rooted trees, the proposed genera *Alpha-*, *Beta-* and *Gammacoronavirus* consistently form three distinct monophyletic groups (see Annex, Fig. 1) and in pair-wise comparisons, they form three robust non-overlapping clusters. The *inter*-group pair-wise scores for coronaviruses are comparable to those calculated for structural and non-structural proteins of different genera in other RNA virus families (e.g. *Potyviridae*, *Picornaviridae*) (González *et al.*, 2003). Based on this *defacto* criterion, we propose to convert phylogroups 1 through 3 into genera designated *Alpha-*, *Beta* and *Gammacoronavirus*, respectively.

Argument to justify the creation of a new genus:

The 90% aa sequence identity threshold now proposed as a *species* demarcation criterion within each genus has been determined from the analysis of pair-wise aa distances in seven conserved replicase domains (nsp3 ADRP, nsp5 (3CLpro), nsp12 (RdRp), nsp13 (He11), nsp14 (ExoN), nsp15 (NendoU) and nsp16 (O-MT)) of 156 viruses in the *Coronaviridae* (Gorbalenya *et al.*, *in preparation*). In this analysis, 20 distinct groups (17 coronaviruses, 2 toroviruses, 1 bafinivirus) are unambiguously recognized as non-overlapping clusters (with the largest intra-cluster distance being smaller than the smallest inter-cluster distance). Of these clusters, 8 fall into the envisaged genus *Alphacoronavirus*, each of which is now proposed to represent a distinct alphacoronavirus species (*Alphacoronavirus 1*, *Human coronavirus 229E*, *Human coronavirus NL63*, *Porcine epidemic diarrhea virus*, *Rhinolophus bat coronavirus HKU2*, *Scotophilus bat coronavirus 512/05*, *Miniopterus bat coronavirus 1*, *Miniopterus bat coronavirus HKU8*; see Annex, Figs. 3, 4).

Origin of the new genus name:

The naming of coronavirus genera is according to the Greek alphabet.

The viruses grouped in currently recognized genera form distinct monophyletic clusters, but do not share other obvious traits (host tropism, organ tropism, type of disease) to suggest a common denominator. Hence, the CSG proposes to use a neutral nomenclature, which would intuitively follow the unofficial (but widely accepted) nomenclature: phylogroup 1: *Alphacoronavirus*; phylogroup 2: *Betacoronavirus*; phylogroup 3: *Gammacoronavirus*.

Argument to justify the choice of type species:

Alphacoronavirus 1 is a new species to be established, comprising a group of closely related viruses of domestic animals (FCoV, CCoV, TGEV). Their replication, epidemiology and pathogenesis has been studied in far greater detail than for other members of this genus. In fact, TGEV was the first coronavirus for which reverse genetics methodology based upon a full-length cDNA clone was developed (Almazán *et al.*, 2000).

Species demarcation criteria in the genus:

Only coronaviruses for which a complete genome sequence is available will be considered for taxonomy. Established and newly identified coronaviruses are assigned to one of the genera (*Alpha-*, *Beta-*, *Gammacoronavirus*) on the basis of rooted phylogeny and pair-wise comparisons using the *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab (ADRP, nsp5 (3CLpro), nsp12 (RdRp), nsp13 (He11), nsp14 (ExoN), nsp15 (NendoU) and nsp16 (O-MT)). Phylogenetic outliers that do not cluster with any of the three currently recognized groups (genera) may be considered representatives of a new genus.

Species demarcation criteria

- Members of a given *Alphacoronavirus* species share greater than 90% amino acid identity in the seven replicase polyprotein pp1ab domains conserved in the *Coronaviridae*.
- A newly identified coronavirus may be considered a new species in the genus

Species demarcation criteria in the genus:

***Alphacoronavirus* when it shares less than 90% amino acid identity in the pp1ab domains with other alphacoronaviruses and possesses a unique set of accessory genes (i.e. different from those in already existing *alphacoronavirus* species).**

References:

Almazán *et al.* (2000) Engineering the largest RNA virus genome as an infectious bacterial artificial chromosome. *Proc. Natl. Acad. Sci. U.S.A.* 97: 5516-5521.

González *et al.* (2003) A comparative sequence analysis to revise the current taxonomy of the family *Coronaviridae*. *Arch. Virol.* 148: 2207–2235

Gorbalenya *et al.* (2006) Nidovirales: evolving the largest RNA virus genome. *Virus Res.* 117: 17-37

Gorbalenya (2008) Genomics and evolution of the *Nidovirales*. In: “Nidoviruses” (Perlman, Gallagher, Snijder, eds.), p. 15-28, ASM Press, Washington, DC.

Annexes:

MODULE 5: NEW SPECIES

Code	2008.091V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Alphacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Alphacoronavirus 1

Argument to justify the creation of the new species:

A new species, *Alphacoronavirus 1*, is proposed to accommodate previously established *Alphacoronavirus* species of swine, cats and dogs (TGEV, FCoV, CCoV). Sequence identity between these viruses in the key replicase 1ab domains (>96%) is well above the species demarcation threshold (90%), i.e. too high to justify their inclusion as separate coronavirus species.

References:

- Almazán *et al.* (2000) Engineering the largest RNA virus genome as an infectious bacterial artificial chromosome. *Proc. Natl. Acad. Sci. U.S.A.* 97: 5516-5521.**
- Decaro *et al.* (2007) Molecular characterisation of the virulent canine coronavirus CB/05 strain. *Virus Res.* 125: 54-60.**
- Decaro *et al.* (2008) Genomic RNA sequence of canine coronavirus, *unpublished*.**
- Dye and Siddell (2005) Genomic RNA sequence of feline coronavirus strain FIPV WSU-79/1146. *J. Gen. Virol.* 86; 2249-2253.**
- Dye and Siddell (2007) Genomic RNA sequence of feline coronavirus strain FCoV C1Je. *J. Feline Med. Surg.* 9:202-13.**
- Haijema *et al.* (2005) Feline infectious peritonitis virus strain 79-1146, complete genome. **AY994055****
- Tekes *et al.* (2008) Genome organization and reverse genetic analysis of a type I feline coronavirus. *J. Virol.* 82: 1851-1859.**

MODULE 5: NEW SPECIES

Code	2008.092V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Alphacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Rhinolophus bat coronavirus HKU2

Argument to justify the creation of the new species:

On the basis of rooted phylogeny and pair-wise comparisons using the *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab, *Rhinolophus bat coronavirus HKU2* must be assigned to genus *Alphacoronavirus*. It has a unique genome organization and its sequence identity with other alphacoronaviruses in the key replicase 1ab domains is well below the species demarcation threshold (90%), while the current diversity of its four isolates is very limited (>99% aa identity). We therefore propose *Rhinolophus bat coronavirus HKU2* to be included in the genus *Alphacoronavirus* as a separate species.

References:

Lau *et al.* (2007) Complete genome sequence of bat coronavirus HKU2 from Chinese horseshoe bats revealed a much smaller spike gene with a different evolutionary lineage from the rest of the genome. *Virology* 367:428-39.

Woo *et al.* (2006) Molecular diversity of coronaviruses in bats. *Virology* 20:180-187.

Annexes:

MODULE 5: **NEW SPECIES**

Code	2008.093V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Alphacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Scotophilus bat coronavirus 512

Argument to justify the creation of the new species:

On the basis of rooted phylogeny and pair-wise comparisons using the *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab, *Scotophilus bat coronavirus 512* must be assigned to genus *Alphacoronavirus*. It has a unique genome organization and sequence identity with other alphacoronaviruses in the key replicase 1ab domains is well below the species demarcation threshold (90%). We therefore propose *Scotophilus bat coronavirus 512* to be included in the genus *Alphacoronavirus* as a separate species.

References:

Tang *et al.* (2006) Prevalence and genetic diversity of coronaviruses in bats from China. *J. Virol.* 80:7481-90.

Annexes:

(see Figs. 3, 4).

MODULE 5: **NEW SPECIES**

Code	2008.094V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Alphacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Miniopterus bat coronavirus 1

Argument to justify the creation of the new species:

Two genomic sequences are available for *Miniopterus bat coronavirus 1* (*Mi-BatCoV1A* and *Mi-BatCoV1B*; isolated from two distinct *Miniopterus* spp). On the basis of rooted phylogeny and pair-wise comparisons using the *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab, *Miniopterus bat coronavirus 1* must be assigned to genus *Alphacoronavirus*. It has a unique genome organization and sequence identity with other alphacoronaviruses in the key replicase 1ab domains is well below the species demarcation threshold (90%), while the current diversity of its two isolates is very limited (>96% aa identity). We therefore propose *Miniopterus bat coronavirus 1* to be included in the genus *Alphacoronavirus* as a separate species.

References:

Poon *et al.* (2005) Identification of a novel coronavirus in bats. *J. Virol.* 79: 2001-2009.

Chu *et al.* (2008) Genomic characterizations of bat coronaviruses (1A, 1B and HKU8) and evidence for co-infections in *Miniopterus* bats. *J. Gen. Virol.* 89: 1282-1287.

Annexes:

See Figs. 3 and 4.

MODULE 5: **NEW SPECIES**

Code	2008.095V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Alphacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Miniopterus bat coronavirus HKU8

Argument to justify the creation of the new species:

On the basis of rooted phylogeny and pair-wise comparisons using the *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab, *Miniopterus bat coronavirus HKU8* must be assigned to genus *Alphacoronavirus*. It has a unique genome organization and sequence identity with other alphacoronaviruses in the key replicase 1ab domains is well below the species demarcation threshold (90%). We therefore propose *Miniopterus bat coronavirus HKU8* to be included in the genus *Alphacoronavirus* as a separate species.

References:

Chu *et al.* (2008) Genomic characterizations of bat coronaviruses (1A, 1B and HKU8) and evidence for co-infections in *Miniopterus* bats. *J. Gen. Virol.* 89: 1282-1287.

Woo *et al.* (2006) Molecular diversity of coronaviruses in bats. *Virology* 20:180-187.

Annexes:

See Figs. 3 and 4.

MODULE 4: **NEW GENUS**

Code	2008.096V
To create a new genus assigned as follows:	
Subfamily:	<i>Coronavirinae</i>
Family:	<i>Coronaviridae</i>
Order:	<i>Nidovirales</i>

Code	2008.097V
To name the new genus: <i>Betacoronavirus</i>	

Code	2008.98V
To assign the following as species in the new genus:	
<ul style="list-style-type: none"> • <i>Betacoronavirus 1</i> (new) (comprised of existing species BCoV, HCoV-OC43, ECoV, HCoV, PHEV and of canine respiratory coronavirus, CrCoV) • <i>Murine coronavirus</i> (new) (comprised of existing species <i>Murine hepatitis virus</i>, <i>Rat coronavirus</i> and <i>puffinosis virus</i>) • <i>Human coronavirus HKU1</i> (existing; to be removed from genus <i>Coronavirus</i>) • <i>Rousettus bat coronavirus HKU9</i> (new) • <i>Tylonycteris bat coronavirus HKU4</i> (new) • <i>Pipistrellus bat coronavirus HKU5</i> (new) • <i>Severe acute respiratory syndrome-related coronavirus (SARSr-CoV)</i> (new) (comprised of existing species <i>Severe acute respiratory syndrome coronavirus</i> and newly discovered SARS-related <i>Rhinolophus BatCoV</i>) 	

Code	2008.99V
To designate the following as the type species in the new genus:	
<i>Murine coronavirus</i>	

Argument to justify the creation of a new genus:

The proposed revision of the family *Coronaviridae* and the organization of the to-be-established subfamily *Coronavirinae* is based upon rooted phylogeny and pair-wise comparisons using *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab as well as the structural proteins S, E, M and N (González *et al.*, 2003; Gorbalenya *et al.*, 2006, 2008). In rooted trees, the proposed genera *Alpha-*, *Beta-* and *Gammacoronavirus* consistently form three distinct monophyletic groups (see Annex, Fig. 1) and in pair-wise comparisons, they form three robust non-overlapping clusters. The *inter*-group pair-wise scores for coronaviruses are comparable to those calculated for structural and non-structural proteins of different genera in other RNA virus families (e.g. *Potyviridae*, *Picornaviridae*) (González *et al.*, 2003). Based on this *defacto*

Argument to justify the creation of a new genus:

critterion, we propose to convert phylogroups 1 through 3 into genera designated *Alpha-*, *Beta* and *Gammacoronavirus*, respectively.

The 90% aa sequence identity threshold now proposed as a *species* demarcation criterion within each genus has been determined from the analysis of pair-wise aa distances in seven conserved replicase domains (nsp3 ADRP, nsp5 (3CLpro), nsp12 (RdRp), nsp13 (He11), nsp14 (ExoN), nsp15 (NendoU) and nsp16 (O-MT)) of 156 viruses in the *Coronaviridae* (Gorbalenya *et al.*, *in preparation*). In this analysis, 20 distinct groups (17 coronaviruses, 2 toroviruses, 1 bafinivirus) are unambiguously recognized as non-overlapping clusters (with the largest intra-cluster distance being smaller than the smallest inter-cluster distance). Of these clusters, 7 fall into the envisaged genus *Betacoronavirus*, each of which is now proposed to represent a distinct betacoronavirus species (*Betacoronavirus 1*, *Murine coronavirus*, *Human coronavirus HKU1*, *Rousettus bat coronavirus HKU9*, *Tylonycteris bat coronavirus HKU4*, *Pipistrellus bat coronavirus HKU5*, *Severe acute respiratory syndrome-related coronavirus*; see Figs. 3 and 4).

Origin of the new genus name:

The naming of coronavirus genera is according to the Greek alphabet.

The viruses grouped in currently recognized genera form distinct monophylogenetic clusters, but do not share other common traits (host tropism, organ tropism, type of disease) to suggest a common denominator. Hence, the CSG decided for a neutral nomenclature, which would intuitively follow the unofficial (but widely accepted) nomenclature: phylogroup 1: *Alphacoronavirus*; phylogroup 2: *Betacoronavirus*; phylogroup 3: *Gammacoronavirus*.

Argument to justify the choice of type species:

For the last 30 years, murine coronavirus (mouse hepatitis virus) has been *the* main model in studies on coronavirus replication and pathogenesis. Key aspects of entry, RNA synthesis and viral assembly were first discovered and described for this virus.

Species demarcation criteria in the genus:

Only coronaviruses for which a complete genome sequence is available will be considered for taxonomy. Established and newly identified coronaviruses are assigned to one of the genera (*Alpha-*, *Beta-*, *Gammacoronavirus*) on the basis of rooted phylogeny and pair-wise comparisons using the *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab (nsp3 ADRP, nsp5 (3CLpro), nsp12 (RdRp), nsp13 (He11), nsp14 (ExoN), nsp15 (NendoU) and nsp16 (O-MT)). Phylogenetic outliers that do not cluster with any of the three currently recognized groups (genera) may be considered representatives of a new genus.

Species demarcation criteria

- Members of a given *Betacoronavirus* species share greater than 90% amino acid identity in the seven replicase polyprotein pp1ab domains conserved in the *Coronaviridae*.
- A newly identified coronavirus may be considered a new species in the genus *Betacoronavirus* when it shares less than 90% amino acid identity in the pp1ab

Species demarcation criteria in the genus:

domains with other betacoronaviruses and possesses a unique set of accessory genes (i.e. different from those in already existing *Betacoronavirus* species).

References:

González *et al.* (2003) A comparative sequence analysis to revise the current taxonomy of the family *Coronaviridae*. *Arch. Virol.* 148: 2207–2235

Gorbalenya *et al.* (2006) Nidovirales: evolving the largest RNA virus genome. *Virus Res.* 117: 17-37

Gorbalenya (2008) Genomics and evolution of the *Nidovirales*. In: “Nidoviruses” (Perlman, Gallagher, Snijder, eds.), p. 15-28, ASM Press, Washington, DC.

Annexes:

MODULE 5: NEW SPECIES

Code	2008.100V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Betacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Betacoronavirus 1

Argument to justify the creation of the new species:

A new species, *Betacoronavirus 1*, is proposed to accommodate previously established *Betacoronavirus* species of humans, cattle, swine and horses (*Human enteric coronavirus*; *Human coronavirus OC43*; *Bovine coronavirus*; *Porcine hemagglutinating encephalomyelitis virus*; *Equine coronavirus*) and a newly recognized virus of dogs (canine respiratory coronavirus; Erles *et al.*, 2007). For those viruses for which a complete genome sequence is available (all except *Human enteric coronavirus* and canine respiratory coronavirus), sequence identity in the key replicase 1ab domains (>96%) is well above the species demarcation threshold (90%), i.e. too high to justify their inclusion as separate coronavirus species.

References:

Chouljenko *et al.* (2001) Comparison of genomic and predicted amino acid sequences of respiratory and enteric bovine coronaviruses isolated from the same animal with fatal shipping pneumonia. *J. Gen. Virol.* 82: 2927-2933.

Erles *et al.* (2007) Isolation and sequence analysis of canine respiratory coronavirus. *Virus Res.* 124: 78-87.

St-Jean *et al.* (2004) Human Respiratory Coronavirus OC43: Genetic Stability and Neuroinvasion. *J. Virol.* 78: 8824-8834.

Vijgen *et al.* (2005) Complete genomic sequence of human coronavirus OC43: molecular clock analysis suggests a relatively recent zoonotic coronavirus transmission event. *J. Virol.* 79: 1595-1604

Vijgen *et al.* (2006) Evolutionary History of the Closely Related Group 2 Coronaviruses: Porcine Hemagglutinating Encephalomyelitis Virus, Bovine Coronavirus, and Human Coronavirus OC43. *J. Virol.* 80: 7270-7274.

Annexes:

MODULE 5: NEW SPECIES

Code	2008.101V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Betacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Murine coronavirus

Argument to justify the creation of the new species:

A new species, *Murine coronavirus*, is proposed to accommodate previously established *Betacoronavirus* species of mice (*Murine hepatitis virus*), rats (*Rat coronavirus*) and allegedly from puffins (*puffinosis virus*; almost certainly a murine coronavirus variant isolated from mouse brain). Only for *Murine hepatitis virus* complete genome sequences are available. Its sequence identity with other betacoronaviruses in the key replicase 1ab domains is below the species demarcation threshold (90%), while the current diversity of its six strains is very limited (>97% aa identity).

References:

Leparc-Goffart *et al.* (1997) Altered pathogenesis of a mutant of the murine coronavirus MHV-A59 is associated with a Q159L amino acid substitution in the spike protein. *Virology* 239: 1-10.

Baker *et al.* (2007) MHV-JHM complete assembled genome sequence and the PATRIC-BRC project (<https://patric.vbi.vt.edu>), NC_006852

Coley *et al.* (2005) Recombinant mouse hepatitis virus strain a59 from cloned, full-length cDNA replicates to high titers in vitro and is fully pathogenic in vivo. *J. Virol.* 79: 3097-3106

Sarma *et al.* (2001) Mouse hepatitis virus type-2 infection in mice: an experimental model system of acute meningitis and hepatitis. *Exp. Mol. Pathol.* 71: 1-12.

Annexes:

See Figs. 3 and 4.

MODULE 5: NEW SPECIES

Code	2008.102V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Betacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Rousettus bat coronavirus HKU9

Argument to justify the creation of the new species:

On the basis of rooted phylogeny and pair-wise comparisons using the *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab, *Rousettus bat coronavirus HKU9* must be assigned to genus *Betacoronavirus*. It has a unique genome organization and sequence identity with other betacoronaviruses in the key replicase 1ab domains is below the species demarcation threshold (90%), while the current diversity of its four isolates is relatively limited (>93% aa identity) although the greatest among the coronavirus species. We therefore propose *Rousettus bat coronavirus HKU9* to be included in the genus *Betacoronavirus* as a separate species.

References:

Woo *et al.* (2007) Comparative analysis of twelve genomes of three novel group 2c and group 2d coronaviruses reveals unique group and subgroup features. *J. Virol.* 81: 1574-1585.

Annexes:

See Figs. 3 and 4.

MODULE 5: **NEW SPECIES**

Code	2008.103V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Betacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Tylonycteris bat coronavirus HKU4

Argument to justify the creation of the new species:

On the basis of rooted phylogeny and pair-wise comparisons using the *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab, *Tylonycteris bat coronavirus HKU4* must be assigned to genus *Betacoronavirus*. It has a unique genome organization and sequence identity with other betacoronaviruses in the key replicase 1ab domains is well below the species demarcation threshold (90%), while the current diversity of its three isolates is very limited (>99% aa identity). We therefore propose *Tylonycteris bat coronavirus HKU4* to be included in the genus *Betacoronavirus* as a separate species.

References:

Tang *et al.* (2006) Prevalence and genetic diversity of coronaviruses in bats from China. *J. Virol.* 80:7481-90.

Woo *et al.* (2006) Molecular diversity of coronaviruses in bats. *Virology* 351:180-187.

Woo *et al.* (2007) Comparative analysis of twelve genomes of three novel group 2c and group 2d coronaviruses reveals unique group and subgroup features. *J. Virol.* 81: 1574-1585.

Annexes:

See Figs. 3 and 4.

MODULE 5: NEW SPECIES

Code	2008.104V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Betacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Pipistrellus bat coronavirus HKU5

Argument to justify the creation of the new species:

On the basis of rooted phylogeny and pair-wise comparisons using the *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab, *Pipistrellus bat coronavirus HKU5* must be assigned to genus *Betacoronavirus*. It has a unique genome organization and sequence identity with other betacoronaviruses in the key replicase 1ab domains is well below the species demarcation threshold (90%), while the current diversity of its three isolates is very limited (>99% aa identity). We therefore propose *Pipistrellus bat coronavirus HKU5* to be included in the genus *Betacoronavirus* as a separate species.

References:

Woo *et al.* (2006) Molecular diversity of coronaviruses in bats. *Virology* 20:180-187.

Woo *et al.* (2007) Comparative analysis of twelve genomes of three novel group 2c and group 2d coronaviruses reveals unique group and subgroup features. *J. Virol.* 81: 1574-1585.

Annexes:

See Figs. 3 and 4.

MODULE 5: NEW SPECIES

Code	2008.105V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Betacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Severe acute respiratory syndrome-related coronavirus

Argument to justify the creation of the new species:

A new species, *Severe acute respiratory syndrome-related coronavirus*, is proposed to replace and extend the existing *Betacoronavirus* species *severe acute respiratory syndrome coronavirus* of humans and animals (palm civets, raccoon dogs, Chinese ferret badger and bats). This new species should include not only viruses directly linked to the 2003 outbreak in the human population and virtually identical animal isolates (Guan *et al.*, 2003; Li *et al.*, 2005), but also more distantly-related viruses, like *SARS-Rh-BatCoV HKU3*, *SARSr-Rh-BatCoV* and *SARSr-Rh-BatCoV 273* that were recently isolated from bats (Lau *et al.*, 2005; Tang *et al.*, 2006). All these viruses, 29 in total, share >97% aa sequence identity in the key replicase 1ab domains (i.e. well above the species demarcation threshold of 90%).

References:

Guan *et al.* (2003) Isolation and characterization of viruses related to the *Severe acute respiratory syndrome* coronavirus from animals in southern China. *Science* 302: 276-278

Li *et al.* (2005) Bats are natural reservoirs of *Severe acute respiratory syndrome*-like coronaviruses. *Science* 310:676-679

Lau *et al.* (2005) Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats. *Proc. Natl. Acad. Sci. U.S.A.* 102: 14040-14045

Tang *et al.* (2006) Prevalence and genetic diversity of coronaviruses in bats from China. *J. Virol.* 80:7481-7490

Annexes:

See Figs. 3 and 4.

MODULE 4: **NEW GENUS**

Code	2008.106V
To create a new genus assigned as follows:	
Subfamily:	<i>Coronavirinae</i>
Family:	<i>Coronaviridae</i>
Order:	<i>Nidovirales</i>

Code	2008.107V
To name the new genus: <i>Gammacoronavirus</i>	

Code	2008.108V
To assign the following as species in the new genus:	
<ul style="list-style-type: none"> • <i>Avian coronavirus</i> (new) (comprised of existing species <i>infectious bronchitis virus</i>, <i>turkey coronavirus</i>, <i>pheasant coronavirus</i>, <i>duck coronavirus</i>, <i>goose coronavirus</i>, <i>pigeon coronavirus</i>) • <i>Beluga Whale coronavirus SW1</i> (new) 	

Code	2008.109V
To designate the following as the type species in the new genus:	
<i>Avian coronavirus</i>	

Argument to justify the creation of a new genus:

The proposed revision of the family *Coronaviridae* and the organization of the to-be-established subfamily *Coronavirinae* is based upon rooted phylogeny and pair-wise comparisons using *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab as well as the structural proteins S, E, M and N (González *et al.*, 2003; Gorbalenya *et al.*, 2006, 2008). In rooted trees, the proposed genera *Alpha-*, *Beta-* and *Gammacoronavirus* consistently form three distinct monophyletic groups (see Figs. 3 and 4) and in pair-wise comparisons, they form three robust non-overlapping clusters. The *inter*-group pair-wise scores for coronaviruses are comparable to those calculated for structural and non-structural proteins of different genera in other RNA virus families (e.g. *Potyviridae*, *Picornaviridae*) (González *et al.*, 2003). Based on this *defacto* criterion, we propose to convert phylogroups 1 through 3 into genera designated *Alpha-*, *Beta* and *Gammacoronavirus*, respectively.

The 90% aa sequence identity threshold now proposed as a *species* demarcation criterion within each genus has been determined from the analysis of pair-wise aa

Argument to justify the creation of a new genus:

distances in seven conserved replicase domains (nsp3 ADRP, nsp5 (3CLpro), nsp12 (RdRp), nsp13 (Hel1), nsp14 (ExoN), nsp15 (NendoU) and nsp16 (O-MT)) of 156 viruses in the *Coronaviridae* (Gorbalenya *et al.*, *in preparation*). In this analysis, 20 distinct groups (17 coronaviruses, 2 toroviruses, 1 bafinivirus) are unambiguously recognized as non-overlapping clusters (with the largest intra-cluster distance being smaller than the smallest inter-cluster distance). Of these clusters, 2 fall into the envisaged genus *Gammacoronavirus*, each of which is now proposed to represent a distinct gammacoronavirus species (*Avian coronavirus* and *Beluga Whale coronavirus SW1*; see Fig. 4).

Origin of the new genus name:

The naming of coronavirus genera is according to the Greek alphabet.

The viruses grouped in currently recognized genera form distinct monophyletic clusters, but do not share other common traits (host tropism, organ tropism, type of disease) to suggest a common denominator. Hence, the CSG decided for a neutral nomenclature, which would intuitively follow the unofficial (but widely accepted) nomenclature: phylogroup 1: *Alphacoronavirus*; phylogroup 2: *Betacoronavirus*; phylogroup 3: *Gammacoronavirus*.

Argument to justify the choice of type species:

Infectious bronchitis virus (*Avian coronavirus*) is the current type species of the family *Coronaviridae*; it was the first coronavirus to be discovered and the first coronavirus to have its genome sequenced to completion.

Species demarcation criteria in the genus:

Only coronaviruses for which a complete genome sequence is available will be considered for taxonomy. Existing and newly identified coronaviruses are assigned to one of the genera (*Alpha-*, *Beta-*, *Gammacoronavirus*) on the basis of rooted phylogeny and pair-wise comparisons using the *Coronaviridae*-wide conserved domains in replicase polyprotein pp1a (nsp3 ADRP, nsp5 (3CLpro), nsp12 (RdRp), nsp13 (Hel1), nsp14 (ExoN), nsp15 (NendoU) and nsp16 (O-MT)). Phylogenetic outliers that do not cluster with any of the three currently recognized groups (genera) may be considered representatives of a new genus.

Species demarcation criteria

- Members of a given *gammacoronavirus* species share greater than 90% amino acid identity in the seven replicase polyprotein pp1ab domains conserved in the *Coronaviridae*.
- A newly identified coronavirus may be considered a new species in the genus *Gammacoronavirus* when it shares less than 90% amino acid identity in the pp1ab domains with other gammacoronaviruses and possesses a unique set of accessory genes (i.e. different from those in already existing *gammacoronavirus* species).

References:

References:

Mihindukulasuriya *et al.* (2008) Identification of a novel coronavirus from a beluga whale by using a panviral microarray. *J. Virol.* 82:5084-5088

González *et al.* (2003) A comparative sequence analysis to revise the current taxonomy of the family *Coronaviridae*. *Arch. Virol.* 148: 2207–2235

Gorbalenya *et al.* (2006) Nidovirales: evolving the largest RNA virus genome. *Virus Res.* 117: 17-37

Gorbalenya (2008) Genomics and evolution of the *Nidovirales*. In: “Nidoviruses” (Perlman, Gallagher, Snijder, eds.), p. 15-28, ASM Press, Washington, DC.

Annexes:

MODULE 5: **NEW SPECIES**

Code	2008.110V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Gammacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Avian Coronavirus

Argument to justify the creation of the new species:

A new species, *Avian coronavirus*, is proposed to accommodate *Infectious Bronchitis virus* of fowl and other existing coronavirus species of birds (*Turkey coronavirus*; *Duck coronavirus*; *Goose coronavirus*; *Pheasant coronavirus*; *Pigeon coronavirus*). Sequence identity between *infectious bronchitis virus* and *Turkey coronavirus* in the key replicase 1ab domains is >94%, well above the species demarcation threshold (90%); for *Duck coronavirus*; *Goose coronavirus*; *Pheasant coronavirus*; *Pigeon coronavirus* only partial sequences are available; given that they are already existing species, we tentatively assign them to *Avian coronavirus* based on their apparent relatedness to IBV and TuCoV. This assignment will be reevaluated once full genome sequences become available for the respective coronaviruses.

References:

Bournsnell *et al.* (1987) Completion of the sequence of the genome of the coronavirus avian infectious bronchitis virus. *J. Gen. Virol.* 68: 57-77.

Gomaa *et al.* (2008) Complete genomic sequence of turkey coronavirus. *Virus Res.* 135: 237-246.

Cao *et al.* (2008) Complete nucleotide sequence of polyprotein gene 1 and genome organization of turkey coronavirus. *Virus Res.* 136: 43-49.

Annexes:

MODULE 5: **NEW SPECIES**

Code	2008.111V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Gammacoronavirus</i>	
Subfamily:	<i>Coronavirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

Beluga whale coronavirus SW1

Argument to justify the creation of the new species:

Based upon rooted phylogeny and pair-wise comparisons using the *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab, Beluga whale coronavirus SW1 must be assigned to the genus *Gammacoronavirus*. However, in these domains amino sequence identity with the only other recognized *gammacoronavirus* species, *Avian Coronavirus*, is <67% (i.e. well below the 90% species demarcation threshold).

References:

Mihindukulasuriya *et al.* (2008) Identification of a novel coronavirus from a beluga whale by using a panviral microarray. *J. Virol.* 82:5084-5088

**Annexes:
See Fig. 4.**

MODULE 3: **NEW SUBFAMILY**

Code	2008.112V
To create a new Subfamily assigned as follows:	
Family:	<i>Coronaviridae</i>
Order:	<i>Nidovirales</i>

Code	2008.113V
To name the new Subfamily: <i>Torovirinae</i>	

Code	<i>see below</i>
To assign the following genera to the new subfamily:	
<ul style="list-style-type: none"> ○ <i>Torovirus</i> (existing genus currently in family <i>Coronaviridae</i>) ○ <i>Bafinivirus</i> (new) 	

Code	
To assign the following species to be unassigned in the new subfamily (i.e. within the subfamily but not assigned to any genus):	
<i>Not applicable</i>	

Argument to justify the creation of a new Subfamily:

Presently, the family *Coronaviridae* is bi-generic and comprised of the genera *Coronavirus* and *Torovirus*. If the coronavirus phylogroups 1 through 3 are to be converted into genera, the genus *Torovirus* has to be allocated to a new family or subfamily (the distance between the corona- and torovirus clusters is much larger and of an entirely different order than that between the coronavirus phylogroups; González *et al.*, 2003).

Comparative sequence analysis shows that corona- and toroviruses (including the bafiniviruses) are more closely related to each other than to the other members of the *Nidovirales* (*Roni-* and *Arteriviridae*) (González *et al.*, 2003; Gorbalenya *et al.*, 2006, 2008; Schütze *et al.*, 2006). Further support for the special relationship between corona-, toro- and bafiniviruses comes from the following observations.

Corona-, toro- and bafiniviruses:

- (i) encode the full set of nidovirus pp1ab replicase domains, unlike *Arteriviridae*, which encode only a limited set of domains
- (ii) possess at least four putative membrane domains in pp1a, the relative positions and approximate sizes of which correspond very well. In contrast, the distributions of ronivirus pp1a membrane domains are clearly different.
- (iii) possess an ADP-ribose 1''-phosphatase domain, which is absent in *Arteriviridae* and *Roniviridae*.

Argument to justify the creation of a new Subfamily:

- (iv) Share limited, but distinct sequence similarity in their S proteins

Of all nidovirus clusters, toro- and bafiniviruses are most closely related to each other (Schütze *et al.*, 2006; Fig. 3). Related, however, as they might be, they are quite divergent and distinct in various aspects:

- (i) WBV, the proposed type bafinivirus, does not encode cyclic nucleotide phosphodiesterase, which is conserved in bovine and equine toroviruses;
- (ii) There is a poor sequence conservation between the N-proximal pp1a/pp1ab regions of WBV and toroviruses
- (iii) There is only limited sequence conservation in the S protein
- (iv) There is no obvious sequence conservation in structural proteins M and N
- (v) the natural hosts of toroviruses are mammals, those of WBV are teleosts.

Based upon these considerations, we propose to create in the family *Coronaviridae* two new subfamilies, *Coronavirinae* (to accommodate three new genera *Alpha-*, *Beta* and *Gammacoronavirus*) and *Torovirinae* (to accommodate the genera *Torovirus* and *Bafinivirus*).

Origin of the new Subfamily name:

The name *Torovirinae* is obviously derived from the established name of the first identified representatives of this group (the toroviruses).

References:

González *et al.* (2003) A comparative sequence analysis to revise the current taxonomy of the family *Coronaviridae*. *Arch. Virol.* 148: 2207–2235

Gorbalenya *et al.* (2006) Nidovirales: evolving the largest RNA virus genome. *Virus Res.* 117: 17-37

Gorbalenya (2008) Genomics and evolution of the *Nidovirales*. In: “Nidoviruses” (Perlman, Gallagher, Snijder, eds.), p. 15-28, ASM Press, Washington, DC.

Schütze *et al.* (2006) Characterization of White bream virus reveals a novel genetic cluster of nidoviruses. *J. Virol.* 80:11598-609

Annexes:

See Fig. 3

MODULE 4: NEW GENUS

Code	2008.114V
To create a new genus assigned as follows:	
Subfamily:	<i>Torovirinae</i>
Family:	<i>Coronaviridae</i>
Order:	<i>Nidovirales</i>

Code	2008.115V
To name the new genus: <i>Bafinivirus</i>	

Code	2008.116V
To assign the following as species in the new genus:	
<ul style="list-style-type: none">• <i>White bream virus</i>	

Code	2008.117V
To designate the following as the type species in the new genus:	
<i>White bream virus</i>	

Argument to justify the creation of a new genus:

White bream virus (WBV) is a bacilliform plus-strand RNA virus of fish. Analysis of the nucleotide sequence, organization, and expression of the 26.6-kb genome provided conclusive evidence for a phylogenetic relationship between WBV and nidoviruses. WBV is most closely related to toroviruses. However, as explained above (pp. 28-29) WBV still is a representative of a separate cluster of nidoviruses that significantly diverged from toroviruses (and, even more, from coronaviruses, roniviruses, and arteriviruses). This would justify the introduction of a new genus, *Bafinivirus*, in the subfamily *Torovirinae*, with *White bream virus* as its type species.

Origin of the new genus name:

“Bafini” is an acronym referring to the bacilliform virion morphology of this new cluster of fish nidoviruses (Schütze *et al.*, 2006)

Argument to justify the choice of type species:

White bream virus is the first and so far sole member of this cluster identified and characterized.

Species demarcation criteria in the genus:

So far, no other bafiniviruses have been identified. Newly discovered bafiniviruses will

**Species demarcation criteria in the genus:
be classified according to the species demarcation criteria established for the
coronaviruses.**

References:

Schütze *et al.* (2006) Characterization of White bream virus reveals a novel genetic cluster of nidoviruses. *J. Virol.* 80:11598-609

Gorbalenya *et al.* (2006) Nidovirales: evolving the largest RNA virus genome. *Virus Res.* 117: 17-37

Gorbalenya (2008) Genomics and evolution of the *Nidovirales*. *In: "Nidoviruses"* (Perlman, Gallagher, Snijder, eds.), p. 15-28, ASM Press, Washington, DC.

**Annexes:
See Fig. 3.**

MODULE 5: **NEW SPECIES**

Code	2008.118V	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	<i>Bafinivirus</i>	
Subfamily:	<i>Torovirinae</i>	
Family:	<i>Coronaviridae</i>	
Order:	<i>Nidovirales</i>	

Name(s) of proposed new species:

White bream virus

Argument to justify the creation of the new species:

White bream virus is the first and so far only identified representative of what is evidently a unique cluster of nidoviruses that are most closely related to yet clearly distinct from the toroviruses.

References:

Schütze *et al.* (2006) Characterization of White bream virus reveals a novel genetic cluster of nidoviruses. *J. Virol.* 80:11598-609

Annexes:

See Figs. 3.

MODULE 6: **REMOVE and MOVE**

SECTION (a)

Code	2008.119V	(assigned by ICTV officers)
To remove (abolish) the following taxon:		
Genus <i>Torovirus</i>		

Old and new composition of the higher taxon that will be depleted by the removal:

Old composition: family *Coronaviridae*, genera *coronavirus* and *torovirus*

New composition: family *Coronaviridae*, subfamily *Coronavirinae*, genera *Alpha-*, *Beta-* and *Gammacoronavirus* and subfamily *Torovirinae*, genera *Torovirus* and *Bafinivirus*

Argument to justify the removal:

The proposed conversion of the coronavirus phylogroups 1, 2 and 3 into genera (*Alpha-*, *Beta-* and *Gammacoronavirus*, respectively) necessitates the removal of the genus *Torovirus* from the family *Coronaviridae*.

SECTION (b)

Code	2008.120V	(assigned by ICTV officers)
To re-assign the following taxon(s):		
genus <i>Torovirus</i>		

Proposed new position of these taxon(s):

New position: family *Coronaviridae*, subfamily *Torovirinae* (**new**), genus *Torovirus*, species *Bovine torovirus* and *Equine torovirus* (both existing and already assigned to the current genus *Torovirus*)

Argument to justify the re-assignment:

The establishment of the new genera *Alpha-*, *Beta* and *Gammacoronavirus* necessitates the allocation of the genus *Torovirus* either to a new family or subfamily (the distance between the corona- and torovirus clusters is much larger and of a completely different order than that between the coronavirus phylogroups; González *et al.*, 2003). Corona- and toroviruses (including the bafiniviruses) have diverged considerably, but are still more closely related to each other than to other known members of the *Nidovirales* (*Roni-* and *Arteriviridae*). We therefore propose to create in the family *Coronaviridae* two new subfamilies *Coronavirinae* (to accommodate the three new genera *Alpha-*, *Beta* and *Gammacoronavirus*) and *Torovirinae* (to accommodate the genera *Torovirus* and *Bafinivirus*)

References:

González *et al.* (2003) A comparative sequence analysis to revise the current taxonomy

References:

of the family Coronaviridae. *Arch. Virol.* 148:2207-35

Gorbalenya *et al.* (2006) Nidovirales: evolving the largest RNA virus genome. *Virus Res.* 117: 17-37

Gorbalenya (2008) Genomics and evolution of the *Nidovirales*. In: “Nidoviruses” (Perlman, Gallagher, Snijder, eds.), p. 15-28, ASM Press, Washington, DC.

Annexes:

See Figs 1, 3 and 4.

MODULE 6: **REMOVE and MOVE**

SECTION (a)

Code	2008.121V	<i>(assigned by ICTV officers)</i>
<p>To remove (abolish) the following taxa:</p> <p>Species <i>Human enteric coronavirus</i>; <i>Human coronavirus OC43</i>; <i>Bovine coronavirus</i>; <i>Porcine hemagglutinating encephalomyelitis virus</i>; <i>Equine coronavirus</i> (these are to be united in a new species <i>Betacoronavirus 1</i> in a new genus <i>Betacoronavirus</i>)</p> <p>Species <i>Murine hepatitis virus</i>; <i>Puffinosis coronavirus</i>; <i>Rat coronavirus</i> (these are to be united in a new species <i>Murine coronavirus</i> in a new genus <i>Betacoronavirus</i>)</p> <p>Species <i>Transmissible gastroenteritis virus</i>; <i>Canine coronavirus</i>; <i>Feline coronavirus</i> (these are to be united in a new species <i>Alphacoronavirus 1</i> in a new genus <i>Alphacoronavirus</i>)</p> <p>Species <i>Infectious bronchitis virus</i>; <i>Duck coronavirus</i>; <i>Goose coronavirus</i>; <i>Pheasant coronavirus</i>; <i>Pigeon coronavirus</i>; <i>Turkey coronavirus</i> (these are to be united in a new species <i>Avian coronavirus</i> in a new genus <i>Gammacoronavirus</i>)</p> <p>Species <i>Severe acute respiratory syndrome coronavirus</i> (to be united with <i>Severe acute respiratory syndrome-related bat coronavirus</i> in a new species <i>Severe acute respiratory syndrome-related coronavirus</i>)</p>		

Old and new composition of the higher taxon that will be depleted by the removal:

Old composition:

Family: *Coronaviridae*

Genus: *Coronavirus*

Species: *Human enteric coronavirus*; *Human coronavirus OC43*; *Bovine coronavirus*; *Porcine hemagglutinating encephalomyelitis virus*; *Equine coronavirus*; *Human coronavirus HKU1*; *Severe acute respiratory syndrome coronavirus*; *Murine hepatitis virus*; *Puffinosis coronavirus*; *Rat coronavirus*; *Transmissible gastroenteritis virus*; *Canine coronavirus*; *Feline coronavirus*; *Human coronavirus 229E*; *Human coronavirus NL63*; *Porcine epidemic diarrhea virus*; *Infectious bronchitis virus*; *Duck coronavirus*; *Goose coronavirus*; *Pheasant coronavirus*; *Pigeon coronavirus*; *Turkey coronavirus*

New composition:

Family: *Coronaviridae*

Subfamily: *Coronavirinae*

Genus: *Alphacoronavirus*

Species: *Alphacoronavirus 1*; *Human coronavirus NL63*; *Human coronavirus 229E*; *Porcine epidemic diarrhea virus*; *Rhinolophus bat coronavirus HKU2*; *Miniopterus bat coronavirus HKU8*; *Miniopterus bat coronavirus 1*; *Scotophilus bat coronavirus 512*

Genus : *Betacoronavirus*

Species : *Betacoronavirus 1*; *Murine coronavirus*; *Human coronavirus HKU1*; *Rousettus bat coronavirus HKU9*; *Tylonycteris bat coronavirus HKU4*; *Pipistrellus bat coronavirus HKU5*; *Severe acute respiratory syndrome-related coronavirus*

Genus : *Gammacoronavirus*

Species : *Avian coronavirus*; *Beluga whale virus SW1*

Argument to justify the removal:

On the basis of our species demarcation criteria (see above), the coronavirus species that are to be abolished and regrouped are too closely related in genome nucleotide sequence and genome organization to justify their designation as separate species.

SECTION (b)

Code	2008.122V	(assigned by ICTV officers)
To re-assign the following taxa:		
Species <i>Human coronavirus 229E</i>, <i>Human coronavirus NL63</i> and <i>Porcine epidemic diarrhea virus</i> to the genus; <i>Alphacoronavirus</i> and <i>Human coronavirus HKU1</i> to the new genus <i>Betacoronavirus</i>		

Proposed new position of these taxa:

New position: family *Coronaviridae*, subfamily *Coronavirinae* (new), genus *Alphacoronavirus* (new), species *Human coronavirus 229E*, *Human coronavirus NL63*, *Porcine epidemic diarrhea virus*; genus *Betacoronavirus* (new), species *Human coronavirus HKU1*

Argument to justify the re-assignment:

The existing coronavirus species *Human coronavirus 229E*, *Human coronavirus NL63*, *Porcine epidemic diarrhea virus* (previously phylogroup 1) and *Human coronavirus HKU1* (previously phylogroup 2) should be assigned to the new genera *Alpha-* and *Betacoronavirus*, respectively, on the basis of rooted phylogeny and pair-wise comparisons using the *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab.

References:

González *et al.* (2003) A comparative sequence analysis to revise the current taxonomy of the family *Coronaviridae*. *Arch. Virol.* 148:2207-35

Gorbalenya *et al.* (2006) *Nidovirales*: evolving the largest RNA virus genome. *Virus Res.* 117: 17-37

Gorbalenya (2008) Genomics and evolution of the *Nidovirales*. In: "Nidoviruses" (Perlman, Gallagher, Snijder, eds.), p. 15-28, ASM Press, Washington, DC.

Annexes:

See Figs 1, 3 and 4.