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:	***2010.023a-dV***	(to be completed by ICTV officers)

Short title: A new genus and three new species in the subfamily *Coronavirinae*
(e.g. 6 new species in the genus *Zetavirus*)

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

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

Raoul J. de Groot and Alexander E. Gorbalenya

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)	Submission on behalf of the Coronavirus Study Group. Authors are CSG members (R.J de Groot, Chair)

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

Date first submitted to ICTV:
Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

Code	***2010.023aV***	(assigned by ICTV officers)

To create new species within:

Genus:	***Deltacoronavirus* (new)**
Subfamily:	***Coronavirinae***
Family:	***Coronaviridae***
Order:	***Nidovirales***

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Bulbul coronavirus HKU11	**[FJ376619]**
Thrush coronavirus HKU12	**[FJ376621=NC_011549]**
Munia coronavirus HKU13	**[FJ376622=NC_011550]**

Reasons to justify the creation and assignment of the new species:
According to the demarcation criteria as outlined in Module 3 and agreed upon by the Coronavirus Study Group, the new coronaviruses isolated from Bulbul, Thrush and Munia are representatives of separates species. They share less than 90% sequence identity both with members of existing coronavirus species and among themselves in the coronaviridae-wide conserved key replicase domains defined in module 3.

MODULE 3: **NEW GENUS**

Code	***2010.023bV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Coronavirinae***
Family:	***Coronaviridae***
Order:	***Nidovirales***

naming a new genus

Code	***2010.023cV***	(assigned by ICTV officers)

To name the new genus: *Deltacoronavirus*

Assigning the type species and other species to a new genus

Code	***2010.023dV***	(assigned by ICTV officers)

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

Bulbul coronavirus HKU11

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

3

Reasons to justify the creation of a new genus:

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

In rooted phylogenetic trees generated for the RdRp and helicase of the coronaviruses, the new coronaviruses isolated from Bulbul, Thrush and Munia group together and form a distinct cluster well separated from the three clusters already recognized as genera (*Alpha*-, *Beta*- and *Gammacoronavirus*) (see appendix, Module 9). Moreover, each of the new viruses shares less than 46% sequence identity with any other established member of the subfamily in the replicase domains (this threshold determined by Lauber and Gorbalenya (*in preparation*) serves as coronavirus genus demarcation criterion). Based upon these facts, we propose to establish three new species (*Bulbul coronavirus HKU11, Thrush coronavirus HKU12, Munia coronavirus HKU13*) to be united in a new genus *Deltacoronavirus.*

Origin of the new genus name:

Coronavirus genera are indicated according to the Greek alphabet.

Reasons to justify the choice of type species:

Bulbul coronavirus HKU11 was first to be isolated. None of the three new coronaviruses has been studied in great detail.

Species demarcation criteria in the new genus:

Demarcation criteria for genera and species

Only coronaviruses for which a complete genome sequence is available are to be considered for taxonomy according to the following demarcation criteria:

- Established and newly identified members of the family *Coronaviridae* are assigned to a subfamily and genus on the basis of rooted phylogeny and calculation of pair-wise evolutionary distances for the following *Coronaviridae*-wide conserved domains in replicase polyprotein pp1ab: ADRP, nsp5 (3CL^{pro}), nsp12 (RdRp), nsp13 (Hel), nsp14 (ExoN), nsp15 (NendoU) and nsp16 (O-MT). This procedure, developed by Lauber and Gorbalenya (*in preparation*), at present unambiguously identifies 23 distinct non-overlapping clusters (with the largest intra-cluster distance being smaller than the smallest inter-cluster distance): 20 coronaviruses, 2 toroviruses, 1 bafinivirus), the three new coronavirus species included. Likewise, this procedure recognizes higher-rank clusters corresponding to genus and subfamily levels.
- Phylogenetic outliers assigned to the family *Coronaviridae* may be considered representatives of a new genus when they do not cluster with any of the current genera and share less than 46% sequence identity in the aforementioned conserved replicase domains with any other established member of the family.
- Viruses that share more than 90% aa sequence identity in the conserved replicase domains are considered to belong to the same species. This 90% identity threshold serves as the sole species demarcation criterion.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Woo PC, Lau SK, Lam CS, Lai KK, Huang Y, Lee P, Luk GS, Dyrting KC, Chan KH, Yuen KY (2009). Comparative analysis of complete genome sequences of three avian coronaviruses reveals a novel group 3c coronavirus. J. Virol. 2009 83(2):908-17.

Annex:

Fig. 1. Phylogenetic relationships among the members of the subfamily *Coronavirinae*. A rooted Neighbour-Joining tree was generated from amino acid sequence alignments of RdRp and helicase domains with equine torovirus Berne as outgroup. The tree reveals four main monophyletic clusters corresponding to genera *Alpha*-, *Beta*- and *Gammacoronavirus* and an envisaged new genus *Deltacoronavirus* (color-coded).