Template for Taxonomic Proposal to the ICTV Executive Committee Creating Species in an existing genus

| Code 2006.011V.04 | To designate the following as species in the genus: | | | | |
|-------------------|---|--|--|--|--|
| | coronavirus | | | | |
| | belonging to the family°: <i>Coronaviridae</i> | | | | |
| | Equine coronavirus (ECoV) | | | | |
| | | | | | |

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Old Taxonomic Order

Order Nidovirales
Family Coronaviridae
Genus Coronavirus

Type Species Murine hepatitis virus

Species in the Genus

Group 1 coronaviruses: transmissible gastronenteritis virus; canine coronavirus; feline coronavirus; human coronavirus 229E; human coronavirus NL63; porcine epidemic diarrhoea virus; bat coronavirus.

Group 2 coronaviruses: murine hepatitis virus; bovine coronavirus; canine respiratory coronavirus; porcine haemagglutinating encephalomyelitis virus; human coronavirus OC43; SARS-coronavirus.

Group 3 coronaviruses: avian infectious bronchitis virus; turkey coronavirus.

Tentative Species in the Genus Unassigned Species in the family

New Taxonomic Order

Order

Family

Genus

Type Species

Species in the Genus

Group 2 coronaviruses: murine hepatitis virus; bovine coronavirus; canine respiratory coronavirus; porcine haemagglutinating encephalomyelitis virus; human coronavirus OC43; SARS-coronavirus; equine coronavirus

Tentative Species in the Genus Unassigned Species in the family

[†] Assigned by ICTV officers

[°] leave blank if inappropriate or in the case of an unassigned genus

| ICTV-EC comments and response of the SG |
|--|
| Study group has approved taxonomic proposal for equine coronavirus during the last SG meeting in Colorado Springs 2005 |
| Species demarcation criteria in the genus |
| Currently all coronaviruses are within one genus, <i>Coronavirus</i> , which is divided into three Groups, 1, 2 and 3. The structural proteins of the species of one Group have <40% amino acid identity with the corresponding structural proteins of species in other Groups. |
| The EqCoV-NC99, isolated from a diarrheic foal, should be considered a group 2 coronavirus because of its antigenic relatedness to the BCoV and non-relatedness to group 1 or group 3 coronaviruses (Guy et al 2000) and because of its genomic sequence similarities to other group 2 coronaviruses (Table 1 and references therein). |
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| |

Argumentation to justify the designation of new species in the genus

Table 1. % amino acid sequence identity between EqCoV and other group 2 coronaviruses.

| Protein | % amino acid sequence identity between EqCoV and other group 2 coronaviruses ^a | | | | | |
|--|---|------------|-----------|---------|---------|--|
| Trotein | BCoV-Mebus | HECoV-4408 | HCoV-OC43 | HEV-67N | MHV-A59 | |
| first 96 aa of 246-aa nsp 1 (p28) ^b | 75.0 | 75.0 | 73.9 | 75.0 | 45.8 | |
| HE protein ^b | 72.7 | 73.2 | 72.9 | 72.7 | - | |
| S protein ^b | 80.1 | 80.7 | 81.5 | 76.8 | 62.8 | |
| 12.7 kDa protein ^b | 83.6 | 82.7 | 81.8 | 86.4 | 50.4 | |
| E protein ^b | 90.6 | 90.6 | 91.8 | 92.9 | 62.8 | |
| M protein ^b | 91.8 | 91.8 | 88.7 | 88.7 | 84.5 | |
| N protein ^c | 91.8 | 91.3 | 90.4 | 89.6 | 71.5 | |

^a GenBank Accession numbers: EqCoV, AY316300, AF251144; BCoV-Mebus, U00735; HECoV-4408, AY316299, L07747, L07748; HCoV-OC43, NC005147; HEV-67N, AF481863; MHV-A59, NC001846.

Although isolated from the equine species, extensive host susceptibility studies have not been done to determine host range. Yet, it is clear from sequence analyses (Table 1 and references therein) and enzyme studies on the hemagglutinin-esterase (Smits et al 2005) that the equine coronavirus, while more closely related to the bovine coronavirus-Mebus strain, human respiratory coronavirus-OC43 strain, human enteric coronavirus-4408 strain, and the porcine hemagglutinating encephalomyelitis virus-67N strain than the mouse hepatitis virus strains, the rat coronavirus strains or the puffinosis virus strains, it is quite distant from other group 2 coronaviruses.

^b Data from Wu et al, 2003

^c Data from Guy et al, 2000

List of created Species in the genus

| Equine coronavirus (ECoV) | | | | |
|---------------------------|--|--|--|--|
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References

Guy JS, Breslin JJ, Breuhaus B, Vivrette S, Smith LG. Characterization of a coronavirus isolated from a diarrheic foal. J Clin Microbiol. 2000 Dec;38(12):4523-6.

Smits SL, Gerwig GJ, van Vliet AL, Lissenberg A, Briza P, Kamerling JP, Vlasak R, de Groot RJ. Nidovirus sialate-O-acetylesterases: evolution and substrate specificity of coronaviral and toroviral receptor-destroying enzymes. J Biol Chem. 2005 Feb 25;280(8):6933-41. Epub 2004 Oct 26.

Wu HY, Guy JS, Yoo D, Vlasak R, Urbach E, Brian DA. Common RNA replication signals exist among group 2 coronaviruses: evidence for in vivo recombination between animal and human coronavirus molecules. Virology. 2003 Oct 10;315(1):174-83.

Annexes:

None