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

Code[†] 2006.010V.04 To designate the following as species in the genus:

coronavirus

belonging to the family° : ***coronaviridae***

Human coronavirus HKU1 (HCoV-HKU1)

AY597011

[†] Assigned by ICTV officers

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

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Old Taxonomic Order

Order **Nidoviales**

Family *coronavridae*

Genus *coronavirus*

Type Species

Species in the Genus

Group 1 coronaviruses: transmissible gastronenteritis virus; canine coronavirus; feline coronavirus; human coronavirus 229E; 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

Tentative Species in the Genus

Unassigned Species in the family

New Taxonomic Order

Order

Family

Genus

Type Species Type 2a

Species in the Genus

Group 2a coronaviruses: murine hepatitis virus; bovine coronavirus; canine respiratory coronavirus; porcine haemagglutinating encephalomyelitis virus; human coronavirus OC43; human coronavirus HKU1

Group 2b coronavirus: SARS-coronavirus.

Tentative Species in the Genus

Unassigned Species in the family

ICTV-EC comments and response of the SG

The coronavirus study group has approved this proposal during its last SG meeting in 2005

Species demarcation criteria in the genus

Currently all coronaviruses are within one genus, *Coronavirus*, 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.

Species demarcation criteria within the genus have never been defined by the Study Group. A coronavirus can be recognized as being a species on the basis of its known natural host and by its sequence distance, compared to the members of the *Coronavirus* Genus.

Argumentation to justify the designation of new species in the genus

Human coronavirus HKU1(HCoV-HKU1) of this proposal is a Group 2 coronavirus, subgroup 2a. This is based on comparative sequence analysis and phylogenetic analysis.

The genome of HCoV-HKU1 is a 29,926-nucleotide, polyadenylated RNA. The G+C content is 32%. Genomic analysis reveals that CoV-HKU1 is a group 2a coronavirus. The genome organization of CoV-HKU1 concurs with those of other coronaviruses, with the characteristic gene order 5'-replicase, S, E, M, N-3', short untranslated regions in both 5' and 3' ends, 5' conserved coronavirus core leader sequence, putative TRS upstream of multiple ORFs, and conserved pseudoknot in the 3' untranslated region. HCoV-HKU1 contains characteristic features of subgroup 2a coronaviruses, including the presence of HE, ORF 4, and N2. However, the proteins of HCoV-HKU1 formed distinct branches in the phylogenetic trees, indicating that HCoV-HKU1 is a distinct member within the group and is not very closely related to any other known members of group 2 coronaviruses. Other unique features of HCoV-HKU1 include a deletion of about 800 bp between the replicase ORF 1b and the HE ORF. Upstream to PL1^{pro} in ORF 1a, there are 14 tandem copies of a 30-base repeat that codes for a highly acidic

List of created Species in the genus

Human coronavirus HKU1

References

Woo PC, Lau SK, Chu CM, Chan KH, Tsoi HW, Huang Y, Wong BH, Poon RW, Cai JJ, Luk WK, Poon LL, Wong SS, Guan Y, Peiris JS, Yuen KY. Characterization and complete genome sequence of a novel coronavirus, coronavirus HKU1, from patients with pneumonia.
J Virol 2005:884-95.

Annexes: