

# Template for Taxonomic Proposal to the ICTV Executive Committee

## Creating Species in an existing genus

Code  To designate the following as species in the genus:

belonging to the family<sup>°</sup>:

*Human coronavirus NL63*

AY518894

AY518894

<sup>†</sup> Assigned by ICTV officers

<sup>°</sup> leave blank if inappropriate or in the case of an unassigned genus

~~Author(s) with e-mail address(es) of the Taxonomic Proposal~~

Dr. W.J.M. Spaan (Chair of the SG)  
w.j.m.spaan@lumc.nl

Dr. Lia van der Hoek  
[c.m.vanderhoek@amc.uva.nl](mailto:c.m.vanderhoek@amc.uva.nl)

### Old Taxonomic Order

Order            Nidovirales  
Family            Coronaviridae  
Genus             Coronavirus  
Type Species  
Species in the Genus

**Group 1 coronaviruses: transmissible gastroenteritis 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

### New Taxonomic Order

Order  
Family  
Genus  
Type Species                                    Type 1b  
Species in the Genus

**Group 1 coronaviruses: transmissible gastroenteritis virus; canine coronavirus; feline coronavirus; human coronavirus 229E; human coronavirus NL63; porcine epidemic diarrhoea virus; bat coronavirus**  
Tentative Species in the Genus  
Unassigned Species in the family

The SG approved the proposal during the last study group meeting In Colorado Springs

## 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 NL63 (HCoV-NL63) of this proposal is a Group 1 coronavirus, subgroup 1b. This is based on comparative sequence analysis and phylogenetic analysis.

The genome of HCoV-NL63 consists of 27,553 nucleotides and a poly-A tail. Short untranslated regions (UTRs) of 286 and 287 nucleotides are present at the 5' and 3' termini, respectively. The 1a and 1b genes encode the RNA polymerase and proteases that are essential for virus replication. A potential pseudoknot structure is present at position 12,439, which may provide the -1 frameshift signal to translate the 1b polyprotein. Genes predicted to encode the S, E, M and N proteins are found in the 3' part of the genome. The hemagglutinin-esterase gene, which is present in some group 2 coronaviruses, is not present in HCoV-NL63. One accessory ORF - ORF3 - is located between the S and E genes. The highest similarity with other coronaviruses is found in the 1b gene and the amino acid identity with its closest relative (HCoV-229E) is 81%. For all other regions the amino acid identity is less (range 43 - 81%). To show that HCoV-NL63 is a new member of the Group 1 coronaviruses, phylogenetic analysis was performed using the nucleotide sequence of the 1a, 1b, S, M and N genes. For each gene analyzed, HCoV-NL63 clustered with the group 1 coronaviruses. The 1a, 1b and S genes of HCoV-NL63 are most closely related to those of HCoV-229E. However, further inspection revealed a subcluster of HCoV-NL63, HCoV-229E and PEDV (subgroup 1b of Group 1). Phylogenetic analysis could not be performed for the ORF3 and E genes because the regions were too variable or too small for analysis, respectively. Bootscan analysis by the Simplot software version 2.5 found no signs of recombination with other coronaviruses.

## List of created Species in the genus

*Human coronavirus NL63*

## References

- van der Hoek L. Pyrc K. Jebbink MF. Vermeulen-Oost W. Berkhout RJ. Wolthers KC. Wertheim-van Dillen PM. Kaandorp J. Spaargaren J. Berkhout B. Identification of a new human coronavirus. **Nature Medicine** 2004 10:368-373
- Pyrc K. Jebbink M. Berkhout B. van der Hoek L. Genome structure and transcriptional regulation of human coronavirus NL63. **Virology Journal** 2004, 1:7

## Annexes: