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Genus *Torovirus* assigned to the *Coronaviridae*

At its April 1992 mid-term meeting, the Executive Committee of ICTV accepted a proposal from the *Coronaviridae* Study Group that the genus *Torovirus*, previously unassigned to a family, should join the genus *Coronavirus* in the *Coronaviridae*. This was in recognition of the many characteristics shared by these two genera, most of the similarities having come to light only recently with the sequencing of a large part of the genome of Berne virus, the type species and most thoroughly studied torovirus. Both genera comprise viruses which are enveloped and have prominent spikes (S) comprising glycopolypeptides of ~200 kDa which exhibit a coiled-coil structure in the carboxy-terminal, membrane-anchoring half. Each virus possesses an integral membrane protein (M) (~25 kDa) with three membrane-spanning sequences in the amino-terminal half. The genomes are single-stranded, non-segmented, positive-sense RNAs of ~30 kb, the first two-thirds being the gene (number 1) which encodes the presumptive RNA-dependent RNA polymerase. Gene 1 encodes two overlapping open reading frames (ORFs), 1 a and 1 b, ribosomal frameshifting being involved in the translation of the second ORF. Five or more subgenomic mRNAs are generated forming a 3′ co-terminal nested set. Only the 5′ sequence not possessed by the next smaller mRNA is translated. Overall genome organisation is similar, the gene order being 5′-pol-S-M-N-3′, where N is the nucleocapsid protein. There are additional genes, some of which are not common between the two genera and, indeed, not possessed by all members of one genus, e.g., the haemagglutinin-esterase glycoprotein of some coronaviruses.

A number of features require that the coronaviruses and toroviruses should be in separate genera. There is virtually no sequence similarity between the two groups. The N proteins differ greatly in size (~60 kDa for coronaviruses, 18 kDa for toroviruses) and form differently shaped nucleocapsids. The viruses are of similar size, about 130 nm in diameter, the coronaviruses being pleomorphic but roughly spherical in shape, and in negatively-stained preparations toroviruses can look very similar to coronaviruses. However, in ultrathin sections toroviruses exhibit disc-, kidney- or rod shapes. Leaders are present on the 5′ termini of coronavirus mRNAs but these have not been found on Berne virus mRNAs.

It has been suggested that viral taxonomy should also recognise that another genus, *Arterivirus*, has genomic and replication strategy features which resemble those of the enlarged *Coronaviridae*. This genus includes equine arteritis, the type species, lactate dehydrogenase-elevating virus, and Lelystad virus, the causative agent of porcine epidemic abortion and respiratory syndrome. All three are enveloped, with a single-stranded, non-segmented, positive-sense RNA genome which has an organisation similar to that of coronaviruses and toroviruses. A 3′ co-terminal nested set of five or more mRNAs are produced, ribosomal frameshifting is involved in translation of the pol gene and the integral membrane protein has a triple membrane-spanning domain. However, there are several major differences from the other two genera. The arterivirus nucleocapsid is icosahedral, the virions being only 50–70 nm in diameter. The surface glycoprotein is neither prominent nor does it have a coiled-coil structure and comprises a much smaller polypeptide (also M

and N are smaller), than the corona- and torovirus counterparts. The genome is only ~ 13 kb. It was agreed by ICTV at the mid-term meeting that *Arterivirus* should be removed from its previous family, *Togaviridae,* and the *Coronaviridae* Study Group was asked to consider including *Arterivirus* in the *Coronaviridae.*

After much debate, culminating in discussions at the Fifth International Symposium on Coronaviruses in France, September 1992, this possibility did not meet with general approval. Rather, it was considered most appropriate at the present time to place *Arterivirus* in a new family, *Arteriviridae,* and to refer the matter back to the ICTV Executive Committee.

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Agenda

February 24–26, 1993

American Euro Date Update in Infectious Diseases (AED), Vienna, Austria. *Contact:* Mondial Congress, attn. of Mrs. Prinzhorn, Faulmanngasse 4, A-1040 Vienna, Austria, phone + 43 1 588 040, fax + 43 1 587 1268.

March 3–7, 1993

20th Meeting of the European Tumour Virus Group Specialists, Innsbruck, Austria. *Contact:* Dr. M. P. Dietrich, Institute for Hygiene, Leopold-Franzens-University, Fritz-Pregl-Strasse 3, A-6010 Innsbruck, Austria, phone + 43 512 507 2240, fax + 43 512 507 3599.

March 7–9, 1993

Viruses and Virus-like Agents in Disease, Basel, Switzerland. *Contact:* 1993 Congress Secretariat, Allschwilerstrasse 10, P.O. Box, CH-4009 Basel, Switzerland, phone + 41 61 306 1111, fax + 41 61 306 1234.

June 7–11, 1993

9th International Conference on AIDS, 4th STD World Congress, Berlin, Federal Republic of Germany. *Contact:* Dr. H. Zeichhardt, Institute for Clinical and Experimental Virology, Free University of Berlin, Hindenburgdamm 27, D-1000 Berlin 45, Federal Republic of Germany, phone + 49 30 798 3687, fax + 4930 834 3061.

June 13–17, 1993

6th European Congress on Biotechnology, Florence, Italy. *Contact:* ECB6, c/o Organizzazione Internazionale Congressi, Via G. Modena 20, I-50121 Firenze, Italy, phone + 39 55 5000631, fax + 39 55 570227.

June 29–July 1, 1993

FEMS Symposium: The Hepatitis C Virus and Its Infection, Istanbul, Turkey. *Contact:* Dr. Osman Sadi Yenen, Department of Infectious Diseases, Gülhane Military Medical Academy, Haydarpasa, Istanbul, Turkey, phone + 90 1 346 2600/2460, fax + 90 1 130 4409.

July 10–14, 1993

12th Annual Meeting of the American Society for Virology, Davis, California, U.S.A. *Contact:* Dr. George Bruening, Dept. of Plant Pathology, University of California, Davis, CA 95616, U.S.A., phone + 916 752 3474, fax + 916 752 5674.