Picornavirus Taxonomy: Seventh ICTV Report, Species, and Other Issues

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Abstract

The Seventh Report of the International Committee of Taxonomy of Viruses (ICTV) is to be published this year, and will contain a description of the Picornavirus, that, not surprisingly, will be more detailed than that in last report submitted in 1993, and will represent what is currently understood about these viruses. The Committee has agreed with ICTV that this poster should be a general overview of the main conclusions reached in the Fifth ICTV Report, with particular reference to the fifth ICTV Report. The report can be obtained free of charge from the ICTV. The poster is printed on a biodegradable material. The Committee is not responsible for any opinions or conclusions expressed in this poster.

Names and assignments approved since the last ICTV Report

Parvovirinae

The name of the new genus, human parvovirus, is provisionally named Hominiviruses. They are no longer parvoviruses, but the new family is not yet defined. A new genus is provisionally named Erythropoietic parvovirus, for the PEV-1 sequence; Philip Marvil for the AEV sequence; Jianhong Peng for the PEV-8 and PEV-9 sequences; and Ian Clarke for the PEV-7 sequence. The new genus name will change, but superimposed above serotypes will be the new taxonomic level of species, for which we have had to invent several names like Hepatitis A virus, Hepatitis B virus, Hepatitis C virus, etc.

Acknowledgements

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References


Agenda for Eurovir ‘98

1. Agree on a comprehensive species list of enteroviruses and rhinoviruses

2. Propose taxonomic assignments, and where necessary genus names, for...

Fig. 1. Schematic diagram showing the genome layout and size of picornavirus genes. The 5.8S rRNA, VP1, VP2, VP3, VP4, 3A, 2C, and 3C regions are shown.

Fig. 2. Neighbor-joining tree of the P1 capsid region based on amino acid similarity matrices. Alignments and trees were produced using Clustal X, version 1.83.

Fig. 3. Neighbor-joining tree of the partial 3D polymerase region based on amino acid similarity matrices. Alignments and trees were produced using Clustal X, version 1.83.

Fig. 4. Neighbor-joining tree of the partial 3D polymerase region based on amino acid similarity matrices. Alignments and trees were produced using Clustal X, version 1.83.

Fig. 5. Neighbor-joining tree of the partial 3D polymerase region based on amino acid similarity matrices. Alignments and trees were produced using Clustal X, version 1.83.