



ICTV Virus Taxonomy Profile: *Pneumoviridae*

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Abstract

The family *Pneumoviridae* comprises large enveloped negative-sense RNA viruses. This taxon was formerly a subfamily within the *Paramyxoviridae*, but was reclassified in 2016 as a family with two genera, *Orthopneumovirus* and *Metapneumovirus*. Pneumoviruses infect a range of mammalian species, while some members of the *Metapneumovirus* genus may also infect birds. Some viruses are specific and pathogenic for humans, such as human respiratory syncytial virus and human metapneumovirus. There are no known vectors for pneumoviruses and transmission is thought to be primarily by aerosol droplets and contact. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the taxonomy of the *Pneumoviridae*, which is available at www.ictv.global/report/pneumoviridae.

Table 1. Characteristics of the family *Pneumoviridae*

Typical member:	human respiratory syncytial virus-A2 (M74568), species <i>Human orthopneumovirus</i> , genus <i>Orthopneumovirus</i>
Virion	Enveloped, both spherical and filamentous virions with a helical ribonucleoprotein (RNP) core
Genome	Negative-sense unsegmented RNA genomes; from 13.2 to 15.3 kb
Replication	Cytoplasmic. The RNA-dependent RNA polymerase comprises the viral phospho- (P) and large (L) proteins; M2-1 protein is a processivity factor
Translation	The cellular translation machinery translates the capped and poly-adenylated messenger RNAs in the cytoplasm
Host range	Mammals (both genera); birds (avian metapneumovirus)
Taxonomy	Two genera, <i>Orthopneumovirus</i> and <i>Metapneumovirus</i> , which include three and two species, respectively

VIRION

The enveloped virion (Table 1, Fig. 1) contains the RNA genome protected by the nucleocapsid (N) protein in a helical complex with the P and L proteins. Nucleocapsids have a diameter of 13.5 nm and a helical pitch of 6.5 nm. Their atomic structures have been obtained by crystallography and cryo-electron analysis of nucleocapsid structures [1, 2].

Three envelope glycoproteins have receptor attachment [glyco-(G)-protein], fusion (F protein) and ion-channel [small hydrophobic (SH) protein] functions [3].

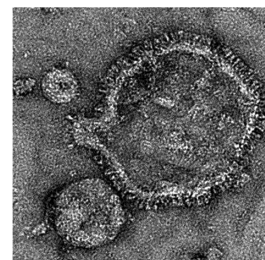


Fig. 1. Electron micrograph of human respiratory syncytial virus. Negative contrast electron micrograph of intact human respiratory syncytial virus (genus *Orthopneumovirus*) (Courtesy of Kyle Dent, Neil Ranson and John Barr, University of Leeds).

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Abbreviations: F, fusion protein; G, glycoprotein; L, large protein; M, matrix protein; N, nucleocapsid; P, phosphoprotein; RNP, ribonucleoprotein; SH, small hydrophobic protein.

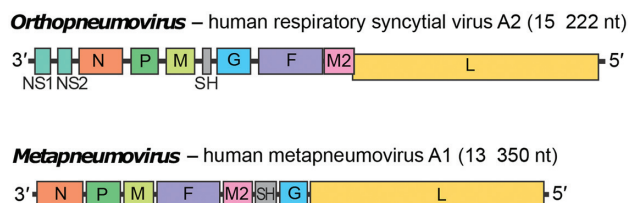


Fig. 2. Genome organization of representative members of the family *Pneumoviridae*. Maps are of genomic RNAs in which each box, drawn approximately to scale, represents a gene encoding a separate mRNA. The M2 mRNA of members of the family *Pneumoviridae* has two overlapping ORFs, M2-1 and M2-2 (not shown). In the genus *Orthopneumovirus*, human respiratory syncytial virus has a gene overlap at M2 and L (staggered boxes).

GENOME

The gene organization of orthopneumoviruses differs from that of metapneumoviruses in the order of the envelope genes; the orthopneumoviruses also possess two genes (NS1 and NS2) upstream of the N gene (Fig. 2) that encode proteins that inhibit the synthesis and action of the host type 1 and type 3 interferon responses and inhibit apoptosis.

Pneumoviruses possess an M2 gene that encodes two proteins, M2-1 and M2-2, from overlapping open reading frames. The highly conserved M2-1 protein enhances virus RNA synthesis through its action as a processivity factor. Expression of the second ORF M2-2 protein utilizes a unique mechanism of reinitiation of translation of the mRNA [4]. The M2-2 protein is involved in the switch of virus RNA synthesis from transcription to replication.

REPLICATION

Transcription of the negative-sense genomic template occurs in the cytoplasm by binding of the P/L (RNA-dependent RNA polymerase) protein complex to the transcription promoter at the 3' end of the template. This generates a set of 8 or 10 sub-genomic positive-sense mRNAs, which are capped and polyadenylated by the activities of the L protein. Transcription is a polar and sequential process that gives rise to a gradient of gene expression. Replication occurs by copying the negative-sense RNA into a full-length positive-sense antigenomic RNA, which is also encapsidated. RNPs are transported to the cellular surface membrane, where budding occurs through the interaction of the matrix (M) protein with both the RNP and the cytoplasmic tails of the glycoproteins, F and G. The F glycoprotein is able to mediate fusion in the absence of a separate viral attachment protein.

PATHOGENICITY

Pneumoviruses are important human pathogens causing extensive infection in young children and are responsible for the majority of cases of bronchiolitis and pneumonia

in this age group [5]. Pneumoviruses may cause acute respiratory infections in other mammalian species. Avian metapneumovirus has been detected in the oviduct and genital tract of turkeys.

TAXONOMY

Phylogenetic analysis of L protein sequences indicates that members of the *Pneumoviridae* represent a distinct clade in the order *Mononegavirales*. The presence of the conserved M2 gene supports their classification into a separate family.

Orthopneumovirus. This genus includes human, rodent and bovine viruses. Members of the *Human orthopneumovirus* species are divided into the co-circulating subgroups A1, A2, B1 and B2. Viruses closely related to murine orthopneumovirus have been isolated from dogs and pigs [6].

Metapneumovirus. This genus consists of viruses infecting human and avian hosts. Members of the *Human metapneumovirus* species are divided into four co-circulating subgroups A1, A2, B1 and B2.

RESOURCES

Full ICTV Online (10th) Report: www.ictv.global/report/pneumoviridae.

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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