ICTV Virus Taxonomy Profile: Belpaoviridae 2021

Beatriz Soriano1, Mart Krupovic2,*, Carlos Llorens1,* and ICTV Report Consortium

Abstract
The family Belpaoviridae comprises metazoan-infecting reverse-transcribing viruses with long terminal repeats, commonly known as Bel/Pao LTR retrotransposons. These viruses share evolutionary history and genes involved in genome replication and virion formation with reverse-transcribing viruses of the families Metaviridae, Pseudoviridae, Retroviridae and Caulimoviridae. These five families form the order Ortervirales. This is a summary of the ICTV Report on the family Belpaoviridae, which is available at ictv.global/report/belpaoviridae.

Table 1. Characteristics of members of the family Belpaoviridae

<table>
<thead>
<tr>
<th>Example</th>
<th>Ascaris lumbricoides Tas virus (Z29712), species Ascaris lumbricoides Tas virus, genus Semotivirus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Virion</td>
<td>Unknown</td>
</tr>
<tr>
<td>Genome</td>
<td>Linear single-stranded RNA of 4–10 kb</td>
</tr>
<tr>
<td>Replication</td>
<td>Replication by reverse-transcription primed by a host-encoded tRNA</td>
</tr>
<tr>
<td>Translation</td>
<td>Genomic RNA is translated into one or more polyproteins</td>
</tr>
<tr>
<td>Host range</td>
<td>Vertebrates, insects and nematodes</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>Realm Riboviria, kingdom Pararnavirinae, phylum Artverviricota, class Revtraviricetes, order Ortervirales; the genus Semotivirus includes &gt;10 species</td>
</tr>
</tbody>
</table>

VIRION
Little is known about the virion morphology of belpaovirids. However, given that belpaovirids encode a Gag polyprotein with nucleocapsid and capsid protein domains homologous to those of other members of the order Ortervirales [1, 2], their replication probably involves the formation of virus-like particles (VLPs), as in the case of retrovirids, metavirids and pseudovirids. Some belpaovirids carry an env-like gene [3], the function of which remains unknown.

GENOME
Members of the family Belpaoviridae have a genomic organization typical of long terminal repeat (LTR) retrotransposons of the family Metaviridae [4], with one to three genes (gag, pol and env) being flanked byLTRs of 0.2–1.2 kb [5], and the whole genome being 4.2–10 kb. Downstream of the 5′-LTR is a non-coding region that corresponds to the first portion of the reverse-transcribed genome, followed by an 18 nt primer-binding site that is complementary to a specific region within the 3′-end of a host tRNA Arg or a tRNA Gly. Upstream of the 3′-LTR is a polypurine tract of about 10 nt, which is responsible for priming the synthesis of the proviral DNA strand. The Gag and Pol polyproteins, encoding respectively the capsid and nucleocapsid domains, and the protease, reverse transcriptase (RT), ribonuclease H and integrase domains, can be encoded by either one continuous or two overlapping gag and pol genes (Table 1, Fig. 1) [6].

REPLICATION
Replication is poorly understood, but, given the similarity in both sequences and functional features, it is assumed to be similar
to that of members of the family Metaviridae [4], in which RT mediates the conversion of a full transcript into a dsDNA that is integrated into the host genome by the integrase protein. The host RNA polymerase II then transcribes the integrated provirus to form new virus RNAs, which are capped and polyadenylated by the corresponding host enzymes. These new viral RNAs are exported to the cytoplasm of the host cell, where Gag and Pol are translated to form immature VLPs. The polyproteins are subsequently processed proteolytically by the viral protease, resulting in VLP maturation. RT then reverse-transcribes the new viral RNAs to dsDNA molecules, which are transported back to the nucleus, where they are inserted into new sites of the host cell genome [7].

**TAXONOMY**

Current taxonomy: [www.ictv.global/taxonomy](http://www.ictv.global/taxonomy). Semotivirus, the only genus in the family, was previously placed in the family Metaviridae, but was removed due to its paraplyetic relationship with other genera of the family Metaviridae. Based on the currently known diversity of belpaovirids, additional species and genera are likely to be introduced into the family Belpaoviridae in the future. Within the order Ortervirales, members of the families Belpaoviridae, Metaviridae and Retroviridae have the same Pol domain order, whereas the integrase is either absent (Caulimoviridae) or located upstream of the protease domain (Pseudoviridae) [8].

**RESOURCES**


GyDB: [http://gydb.org](http://gydb.org)

Repbase: [https://www.girinst.org/repbase](https://www.girinst.org/repbase)

RepetDB: [http://urgi.versailles.inra.fr/repetdb](http://urgi.versailles.inra.fr/repetdb)

RexDB: [http://repeatexplorer.org](http://repeatexplorer.org)

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**Conflicts of interest**

The authors declare that there are no conflicts of interest

**References**


