



# ICTV Virus Taxonomy Profile: *Bornaviridae*

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## Abstract

Members of the family *Bornaviridae* produce enveloped virions containing a linear negative-sense non-segmented RNA genome of about 9 kb. Bornaviruses are found in mammals, birds, reptiles and fish. The most-studied viruses with public health and veterinary impact are Borna disease virus 1 and variegated squirrel bornavirus 1, both of which cause fatal encephalitis in humans. Several orthobornaviruses cause neurological and intestinal disorders in birds, mostly parrots. Endogenous bornavirus-like sequences occur in the genomes of various animals. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the family *Bornaviridae*, which is available at [ictv.global/report/bornaviridae](http://ictv.global/report/bornaviridae).

**Table 1.** Characteristics of members of the family *Bornaviridae*

Example:	<b>Borna disease virus 1 (U04608), species <i>Mammalian 1 orthobornavirus</i>, genus <i>Orthobornavirus</i></b>
Virion	Enveloped, spherical virions 90–130 nm in diameter
Genome	Linear negative-sense non-segmented RNA of about 9 kb with three transcription units and at least six ORFs
Replication	Intranuclear. Anti-genomic RNA is generated as a replication intermediate that enables synthesis of progeny genomes. Genomic and anti-genomic RNA molecules are neither capped nor polyadenylated
Translation	From capped polyadenylated mRNA
Host range	Mammals (reservoir: shrews and squirrels; incidental: horses, sheep, humans and other mammals), birds (parrots, finches, aquatic birds), reptiles and fish
Taxonomy	Realm <i>Riboviria</i> , kingdom <i>Orthornavirae</i> , phylum <i>Negarnaviricota</i> , subphylum <i>Haploviricotina</i> , class <i>Monjiviricetes</i> , order <i>Mononegavirales</i> ; several genera and >10 species

## VIRION

Where known, bornavirus virions are spherical in shape with a bimodal size distribution of larger (110–130 nm diameter) and smaller particles (70–90 nm diameter) [1, 2]. Virions are enveloped with 7-nm spikes and are believed to bud from host cell membranes (Table 1, Fig. 1). Entry occurs through binding to unknown cell surface receptors via the endosomal route.

## GENOME

The bornavirus genome consists of a linear negative-sense non-segmented RNA with six open reading frames (ORFs) in the order 3'-N-X/P-M-G-L-5' (*Orthobornavirus*) or 3'-N-X/P-G-M-L-5' (*Carbovirus* and *Cultervirus*) [3–6] that encode, at a minimum, a nucleoprotein (N), small accessory protein (X), phosphoprotein (P), matrix protein (M), surface glycoprotein (G) and large protein

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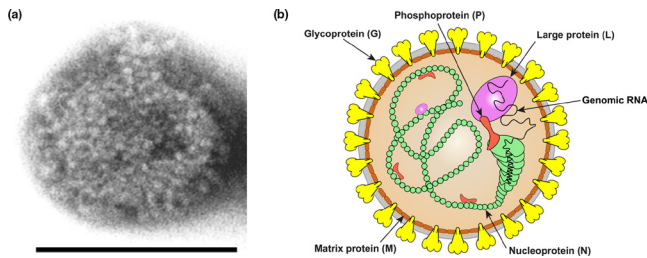
**Keywords:** ICTV Report; *Mononegavirales*; *Bornaviridae*; *Orthobornavirus*; *Cultervirus*; *Carbovirus*; Borna disease virus; bornavirus.

**Abbreviations:** G, surface glycoprotein; L, large protein; M, matrix protein; N, nucleoprotein; P, phosphoprotein; RdRP, RNA-directed RNA polymerase; RNP, ribonucleoprotein; X, small accessory protein.

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**Fig. 1.** (a) Electron micrograph of a Borna disease virus 1 particle. Scale bar, 100 nm. Courtesy of Dr M. Eickmann. (b) Illustration of an orthobornavirus particle. Grey - bilaminar lipid envelope.

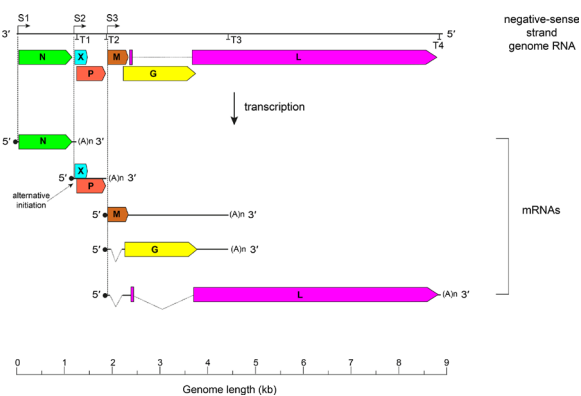
(L) containing RNA-directed RNA polymerase (RdRP), helicase and endonuclease domains.

## REPLICATION

Studies of Borna disease virus 1 indicate that N encapsidates the genomic RNA, forming the viral nucleocapsid, and, together with L and P, forms the ribonucleoprotein (RNP) complex [3]. The genome is transcribed and replicated in the host cell nucleus [7]. Differential use of transcription and termination signals and alternative splicing of polycistronic primary transcripts generate an array of mRNAs (Fig. 2) [8]. Full-length antigenomic positive-sense RNA intermediates are used as templates for generating progeny negative-sense genomic RNA. Nuclear import of viral RNP components after translation of viral mRNA is mediated by their nuclear localization signals; nascent RNPs probably translocate into the cytosol from the nucleus by nuclear export signals [9].

## TAXONOMY

Current taxonomy: [www.ictv.global/taxonomy](http://www.ictv.global/taxonomy). Bornaviruses form a family in the haploviricotine order *Mononegavirales*,



**Fig. 2.** Orthobornavirus genome organization and transcripts. Dashed lines - introns. ORFs (depicted on the negative-sense strand) encode N, nucleoprotein; X, accessory protein; P, phosphoprotein; M, matrix protein; G, glycoprotein; L, large protein containing an RdRP domain. S, transcription initiation site; T, transcription termination site.

most closely related to members of the families *Mymonaviridae*, *Nyamiviridae* and *Xinnoviridae*. Like most other mononegaviruses, bornaviruses (i) have linear negative-sense non-segmented RNA genomes, (ii) have five conserved motifs (A–E) in the amino-acid sequence of their RdRP domain and (iii) produce enveloped virions.

## RESOURCES

Current ICTV Report on the family *Bornaviridae*: [www.ictv.global/report/bornaviridae](http://www.ictv.global/report/bornaviridae).

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### Conflicts of interest

The authors declare that there are no conflicts of interest.

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