



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.

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

Example:	Borna disease virus 1 (U04608), species <i>Mammalian 1 orthobornavirus</i> , genus <i>Orthobornavirus</i>
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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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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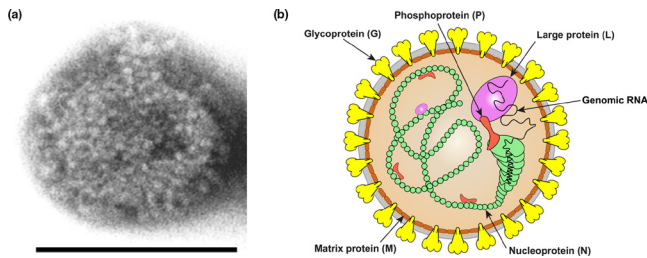


Fig. 1. (a) Electron micrograph of a Borna disease virus 1 particle. Scale bar, 100 nm. Courtesy of Dr M. Eickmann. (b) Illustration of an orthobornavirus particle. Grey - bilaminar lipid envelope.

(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. Bornaviruses form a family in the haploviricotine order *Mononegavirales*,

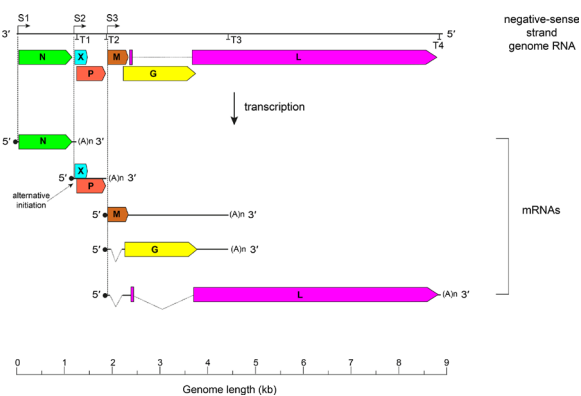


Fig. 2. Orthobornavirus genome organization and transcripts. Dashed lines - introns. ORFs (depicted on the negative-sense strand) encode N, nucleoprotein; X, accessory protein; P, phosphoprotein; M, matrix protein; G, glycoprotein; L, large protein containing an RdRP domain. S, transcription initiation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

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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