Nairoviridae

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Edited by: Jens H. Kuhn and Stuart G. Siddell
Posted: July 2020

Summary

Members of the family Nairoviridae produce enveloped virions containing genomes consisting of three negative-sense, single-stranded RNA segments totalling 17.1–22.8 kb (S: 1.7–2.1 kb; M: 4.4–6.3 kb; L: 11.2–14.4 kb) (Table 1. Nairoviridae). Nairoviruses are classified into three genera (Orthonairovirus, Shaspivirus, and Striwavirus). These viruses are maintained in arthropods or transmitted by ticks among mammals, birds, or bats. The most important nairovirus with public-health impact is Crimean-Congo hemorrhagic fever virus, which is tick-borne and endemic in much of Asia, Africa, Southern and Eastern Europe. The most significant nairovirus with veterinary importance is Nairobi sheep disease virus, which is also tick-borne and causes lethal hemorrhagic gastroenteritis in small ruminants in Africa and India.

Table 1. Nairoviridae. Characteristics of members of the family Nairoviridae

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Typical member</td>
<td>Dugbe virus [S segment: AF434161; M segment: M94133; L segment: U15018], species Dugbe orthonairovirus, genus Orthonairovirus</td>
</tr>
<tr>
<td>Virion</td>
<td>Enveloped, spherical virions 80–120 nm in diameter with heterodimer surface spikes</td>
</tr>
<tr>
<td>Genome</td>
<td>Three single-stranded, negative-sense RNA molecules, S, M, and L of about 2 kb, about 5 kb, and about 12 kb, respectively</td>
</tr>
<tr>
<td>Replication</td>
<td>Cytoplasmic. The nucleocapsid protein (N) encapsidates the genomic RNA forming ribonucleoprotein (RNP) complexes with the viral RNA-directed RNA polymerase (RdRP)-containing large protein (L). Anti-genomic RNAs are generated and serve as templates for synthesis of nascent RNP complexes containing genomic RNA</td>
</tr>
<tr>
<td>Translation</td>
<td>From capped mRNAs that lack poly(A) termini. The 5′-cap structure is derived from cellular mRNAs via cap-snatching</td>
</tr>
<tr>
<td>Host range</td>
<td>Birds, humans, rodents, hares, shrews, ruminants, bats, ticks (Orthonairovirus); spider vector (Shaspivirus) or water strider vector (Striwavirus) with unknown host range</td>
</tr>
<tr>
<td>Taxonomy</td>
<td>Realm Riboviria, kingdom Orthornavirae, phylum Negarnaviricota, subphylum Polyploviricota, class Ellioviricetes, order Bunyavirales; three genera including 17 species</td>
</tr>
</tbody>
</table>

45 viruses are united in 17 species and three genera in the Nairoviridae family. The genera within the family form monophyletic clades based on RdRP, glycoprotein (GP), and N protein phylogeny. Genomes of viruses from all three genera have a similar genome architecture. Within the Orthonairovirus genus viruses have variable host ranges.

Avian Host

Genus Orthonairovirus. Five of the 14 species within this genus include viruses that have been isolated from birds or from ticks collected from birds: Crimean-Congo hemorrhagic fever orthonairovirus, Dera Ghazi Khan orthonairovirus, Hughes orthonairovirus, Sakhalin orthonairovirus, and Tamdy orthonairovirus.

Mammalian Host

Genus Orthonairovirus. Of the 14 species within this genus, viruses from all but two species (Hughes orthonairovirus and Sakhalin orthonairovirus) have been detected in mammals. Of those members with known vectors, most viruses are transmitted by ticks to mammalian hosts, such as bats, hares, rodents, and ungulates. Infections of their mammalian hosts are generally asymptomatic. An exception is Nairobi sheep disease virus (NSDV; species Nairobi sheep disease orthonairovirus), a tick-borne virus that occasionally causes lethal hemorrhagic
gastroenteritis in small ruminants in Africa and India. One orthonairovirus, Crimean-Congo hemorrhagic fever virus (CCHFV, species Crimean-Congo hemorrhagic fever orthonairovirus), can infect humans and cause severe and frequently fatal disease. Although rare, Dugbe virus (DUGV, species Dugbe orthonairovirus), NSDV, and possibly Erve virus (ERVEV, species Thiafora orthonairovirus) infect non-lethal disease in humans. Tamdy virus (TAMV) was linked to a self-limiting acute fever that resolves in 5–7 days (Lvov et al., 1984b, Lvov 1994). The genus includes two species, Keterah orthonairovirus and Kasokero orthonairovirus, whose members have only been isolated from bats, and one species, Thiafora orthonairovirus, whose members have only been isolated from shrews (Walker et al., 2015).

Genus Orthonairovirus. This genus has virus members that replicate in hard (ixodid) and soft (argasid) ticks.

Arthropod Host

Genus Shaspivirus. This genus currently has one virus member, Shāyáng spider virus 1 (SySV-1), which was detected in spiders of 3 species (Li et al., 2015).

Genus Striwavirus. This genus currently has one virus member, Sānxiá water strider virus 1 (SxWSV-1), which was detected in gerrid water striders (Li et al., 2015).

Virion

Morphology

Only known for members of the genus Orthonairovirus. Orthonairovirions are spherical in shape, 80–120 nm in diameter, the membrane envelope is decorated with GP spikes composed of G and G (Figure 1. Nairoviridae). Isolated ribonucleoprotein (RNP) complexes are composed of individual segment genomic RNA encapsidated in nucleoprotein (N). The nucleoproteins of Hazara virus (HAZV), kupe virus (KUPEV), Erve virus (ERVEV) and Crimean-Congo hemorrhagic fever virus (CCHFV) show structural conservation within the head domain of N (Surtees et al., 2015, Wang et al., 2015).

Physicochemical and physical properties

Only known for members of the genus Orthonairovirus. The virion Mr is 300×10^6 to 400×10^6 and has an S of 350–500. Virion buoyant densities in sucrose and CsCl are 1.16–1.18 and 1.20–1.21 g cm⁻³, respectively. Virions are sensitive to heat, lipid solvents, detergents and formaldehyde.

Nucleic acid

Nairoviruses contain three negative-sense, single-stranded RNA segments. The three genomic segments are designated L (large), M (medium), and S (small). The viral mRNAs are not polyadenylated and contain a 5′-methylated cap and 10–18 non-templated nucleotides at the 5′-end that are derived from host cell mRNAs. Further information is only known for members of the genus Orthonairovirus. Orthonairoviruses contain the
RNA segments in circular forms formed by non-covalent binding of the complementary and conserved 3'- and 5'-terminal sequences (9 nt). The Mr of the genome ranges from 4.8×10^6–8×10^6 and accounts for 1–2% of the weight of the virion.

Proteins

Nairoviruses express 4 structural proteins (Table 2. Nairoviridae). The most abundant structural protein in a nairovirion is N (encoded by the S segment), which encapsidates the nairoviral genomic segments. The least abundant protein is L (encoded by the L segment), which mediates viral genome replication and transcription. Two glycoproteins, G_N and G_C, are encoded by the M segment. Specifics are only known for members of the genus Orthonairovirus.

Table 2. Nairoviridae. Location and function of orthonairovirus structural proteins.

<table>
<thead>
<tr>
<th>Protein</th>
<th>Location, mass, and function</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glycoprotein (GP)</td>
<td>Structural virion protein consisting of two subunits (G_N 30–45 kD, G_C 72–84 kD). Produced via proteolytic cleavage from the orthonairoviral genome-encoded precursor GPC. Cleavage produces G_N, G_C, and non-structural glycoproteins. Inserts into virion membranes as GP spikes composed of G_N and G_C. As a putative class I fusion protein, GP mediates cell-surface and internal receptor binding, virion-cell membrane fusion and, thereby cell entry.</td>
</tr>
<tr>
<td>Large protein (L)</td>
<td>Structural virion protein (250–450 kD) with RdRP, helicase, and endoribonuclease domains. Component of the RNP inside virions. Oligomerizes and mediates transcription and replication of orthonairoviral RNA segments. Contains an ovarian tumor family-like domain (OTU) that is conserved among all orthonairoviruses. Mediates cap-snatching for viral mRNA capping.</td>
</tr>
</tbody>
</table>

Lipids

Not reported.

Carbohydrates

Not reported.

Genome organization and replication

Nairoviruses encode three different proteins, in the virus-complementary sense RNA: S RNA encodes N, the M RNA encodes the viral GP precursor (GPC), and the L RNA encodes the large protein L, which has RNA-directed RNA polymerase, helicase, and endonuclease domains (Figure 2. Nairoviridae). Based on experimental evidence from CCHFV, nairoviral glycoproteins (G_N and G_C) and non-structural glycoproteins of unknown function are derived by co-translational and post translational cleavage from an intracellular GP precursor (GPC) by cellular proteases (Bergeron et al., 2015, Sanchez et al., 2006, Vincent et al., 2003).

![Figure 2. Nairoviridae. Schematic representation of nairovirus genome organization.](image)

Specifics are only known for members of the genus Orthonairovirus. Orthonairovirus infection starts with attachment to unknown cell-surface receptors and entry via the endosomal route (Garrison et al., 2013, Simon et al., 2009) (Figure 3. Nairoviridae). Viral fusion with the host cell results in early or late endosomal release, depending on the virus, of the virion RNP complex into the cytoplasm. This pH-dependent fusion event likely requires the previous participation of an intracellular receptor (Garrison et al., 2013, Shtanko et al., 2014). During primary transcription the virion-associated large protein (L) generates uncapped antigenomic RNA which are then capped using host-cell derived capped primers (Holm et
al., 2018). L and S segment-transcribed mRNAs are translated by free ribosomes. M segment-transcribed mRNA is translated by membrane-bound ribosomes, co-translationally cleaved to yield G₀ and G₂ and non-structural glycoproteins and glycosylated by nascent envelope proteins. The synthesis of the antigenome RNA by the RdRP domain of the L protein serves as a template for genomic RNA replication. Secondary transcription amplifies the synthesis of mRNA and genome replication. During morphogenesis, G₀ and G₂ accumulate in the Golgi, are terminally glycosylated, modified host membranes are acquired, and virions bud into the Golgi cisternae (Booth et al., 1991, Rwambo et al., 1996).

Figure 3. Nairoviridae. Lifecycle of nairoviruses. (1) Virion attachment; (2) virion uptake; (3) virion-cell membrane fusion; (4) transcription; (5) translation; (6) replication; (7) virion assembly; and (8) virion egress.

Biology

Most viruses within this family are transmitted by ticks; a few viruses have been isolated from biting midges, horseflies, and mosquitoes, although the role of these hosts in virus transmission is not proven. One virus has been found by sequencing of RNA in spiders, one virus by sequencing of RNA in water striders, and one virus has been found by sequencing RNA in millipedes. Specifics are only known for members of the genus Orthonairovirus. Most orthonairoviruses are capable of alternately replicating in vertebrates and arthropods, and cause little or no cytopathogenicity in their invertebrate hosts. The viruses within this genus are transmitted by different species of hard (Ixodidae) and soft (Argasidae) ticks. Although a few viruses have been isolated from biting midges, horseflies, and mosquitoes, the role of these hosts in virus transmission is not proven. Transovarial, transstadial, and venereal transmission have been demonstrated for CCHFV. In general, the viruses of the same species have strictly limited range of the arthropod vectors and occupy a specific ecological niche. The range of vertebrate hosts is mainly determined by the ecology of their vectors and includes mammals, birds, and bats. The orthonairoviruses that are vectored by soft ticks infect rodents, birds, and bats, while species vectored by hard ticks infect mammals (small ruminants, hares, human, etc.) and birds. Among orthonairoviruses, only CCHFV is known as an important human pathogen causing severe form of haemorrhagic fever. However, there are several reports that Issyk-kul virus (L'vov et al., 1984a), Tamdy virus (L'vov et al., 1984b, Lvov 1994), Dugbe virus (Burt et al., 1996), and NSDV, can also cause mild febrile illness in humans.
Antigenicity

Only known for members of the genus *Orthonairovirus*. One or both of the envelope glycoproteins display hemagglutinating and neutralizing antigenic determinants. Complement-fixing antigenic determinants are principally associated with the nucleoprotein.

Derivation of names

*Nairoviridae*: from Nairobi (Kenya) where Nairobi sheep disease virus was first isolated, and *vridae*, suffix for a family.

Genus demarcation criteria

The availability of at least coding-complete sequences of all genome segments may be sufficient for nairovirus classification in the absence of a cultured isolate.

Demarcation of genera is based upon considerations of their phylogenetic relationships, significant differences in member virus genome architecture, virion antigenicity, and virus ecology (e.g., host range, pathobiology, and transmission patterns). Three genera have been established to date.

Relationships within the family

Phylogenetic relationships across the family have been estimated using maximum likelihood trees generated from complete and partial protein sequences (Figure 4. *Nairoviridae*).
Figure 4A. Nairoviridae. Midpoint-rooted maximum likelihood phylogenetic trees inferred from (A - above) S, (B - Figure 4B) M, and (C - Figure 4C) L protein sequences. Three separate alignments, one for each segment’s coding sequence, were first aligned using MUSCLE version 3.8.425 (Edgar 2004) and manually curated in Geneious R9 (Kearse et al., 2012). Maximum likelihood trees were estimated with an exhaustive search (-slow), WAG amino acid substitution model (Whelan and Goldman 2001), 20 Γ-rate categories, and 1,000 bootstrap replications using FastTree 2.1 (Price et al., 2010). Tree rooting and visualization was done in FigTree (Rambaut 2020).

Species with more than four representative sequences in a monophyletic clade were collapsed for simplicity. Bootstrap support values are shown at tree nodes as a percentage and only if greater than 70%. Tree branches are scaled by amino acid substitutions per site. GenBank accession numbers for nucleotide sequences are shown at tree tips. Circles at tips are colour-filled according to species; open circles indicate unclassified viruses. The Rondônia virus sequences are incomplete.

These phylogenetic trees and corresponding sequence alignments are available to download from the Resources page.
Figure 4B. Nairoviridae. Midpoint-rooted maximum likelihood phylogenetic trees inferred from M protein sequences. See Figure 4A. Nairoviridae legend for full details. These phylogenetic trees and corresponding sequence alignments are available to download from the Resources page.
Figure 4C. Nairoviridae. Midpoint-rooted maximum likelihood phylogenetic trees inferred from L protein sequences. See Figure 4A. Nairoviridae legend for full details. These phylogenetic trees and corresponding sequence alignments are available to download from the Resources page.

Relationships with other taxa

Nairoviruses are most closely related to Wuhan millipede virus 2 (WhMV-2; Wupedeviridae) and, more distantly, to members of the families Arenaviridae and Mypoviridae (Wolf et al., 2018).

Related, unclassified viruses

Additional unclassified nairoviruses that are probable members of existing genera are listed under individual genus descriptions.
<table>
<thead>
<tr>
<th>Virus Name</th>
<th>Accession Numbers</th>
<th>Abbreviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beiji nairovirus</td>
<td>S: MG880115; L: MG880120</td>
<td></td>
</tr>
<tr>
<td>Blattodean nairo-related virus OKIAV321</td>
<td>Not available (Käfer et al., 2019)</td>
<td></td>
</tr>
<tr>
<td>Finch Creek virus</td>
<td>L: EU267169</td>
<td>FINCV</td>
</tr>
<tr>
<td>Grotenhout virus</td>
<td>S: KY700683; L: KY700684</td>
<td></td>
</tr>
<tr>
<td>Norway nairovirus 1</td>
<td>S: MF141045; L: MF141044</td>
<td></td>
</tr>
<tr>
<td>Pacific Coast tick nairovirus</td>
<td>S: KU933935; M: KU933934; L: KU933933</td>
<td></td>
</tr>
<tr>
<td>Pustyn virus</td>
<td>S: KT007143; L: KT007142</td>
<td></td>
</tr>
<tr>
<td>South Bay virus</td>
<td>S: KJ746878; L: KJ746877</td>
<td>SBV</td>
</tr>
<tr>
<td>Xinzhōu spider virus</td>
<td>S: KM817762; M: KM817729; L: KM817702</td>
<td>XSV</td>
</tr>
</tbody>
</table>

Virus names and virus abbreviations are not official ICTV designations.

### Member taxa

- Orthonairovirus
- Shaspivirus
- Striwavirus
**Genus: Orthonairovirus**

**Distinguishing features**

The consensus terminal nucleotide sequences of the L, M, and S genome segments are typically characterized by a genus-specific 5′ genomic segment terminus 5′-UCUCAAAGA-3′ and 3′ genomic segment terminus of 5′-UCUUUGAGA-3′; however several members of the *Orthonairovirus* genus have termini that differ by one nucleotide. Glycoprotein (GP) subunits G₉ and G₉ and non-structural proteins are encoded as a precursor polyprotein by the M RNA. Genetic reassortment has been demonstrated between viruses belonging to the same species but not between members of different species. Of the 15 species within this genus, viruses of all but two species (*Hughes orthonairovirus* and *Sakhalin orthonairovirus*) have been detected in mammals. Of those members with known vectors, the majority of viruses within this genus are transmitted by ticks to mammalian hosts or birds. Some viruses are transmitted transovarially in arthropods.

**Virion**

See discussion under family description.

**Genome organization and replication**

The orthonairovirus genome consists of three single-stranded, negative-sense RNA molecules, termed S (small), M (medium), and L (large). These RNAs encode three different proteins: S RNA encodes N, the M RNA encodes the viral glycoprotein precursor (GPC), and the L RNA encodes the large protein (L) with its RNA-directed RNA polymerase (RdRP) domain in the virus-complementary sense RNA (Figure 1. *Orthonairovirus*).

**Biology**

See discussion under family description.

**Derivation of names**

*Orthonairovirus*: from the Ancient Greek ὀρθός (*orthós*), meaning upright or straight and Nairobi, from Nairobi (Kenya) where Nairobi sheep disease virus was first isolated, and virus, suffix for a genus.

**Species demarcation criteria**

Demarcation of genera is based upon considerations of phylogeny, significant differences in member virus genome architecture, virion antigenicity, and virus ecology (e.g., host range, pathobiology, and transmission patterns).

**Phylogenetic relationships**

Phylogenetic relationships across the genus have been estimated using maximum likelihood trees generated from complete and partial protein sequences (Figure 4. Nairoviridae).

**Member Species**

<table>
<thead>
<tr>
<th>★ Exemplar isolate of the species</th>
<th>Species</th>
<th>Virus name</th>
<th>Isolate</th>
<th>Accession number</th>
<th>RefSeq number</th>
<th>Available sequence</th>
<th>Virus Abbrev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>★ Artashat orthonairovirus</td>
<td>Artashat virus</td>
<td>LEIV-10898Az</td>
<td>L: KP792744; M: KP792745; S: KP792746</td>
<td>L: NC_043440; M: NC_043442; S: NC_043441</td>
<td>Complete coding genome</td>
<td>ARTSV</td>
<td></td>
</tr>
<tr>
<td>★ Chim orthonairovirus</td>
<td>Chim virus</td>
<td>LEIV-858Uz</td>
<td>L: KP792711; M: KP792712; S: KP792713</td>
<td>L: NC_043434; M: NC_043436; S: NC_043435</td>
<td>Complete coding genome</td>
<td>CHIMV</td>
<td></td>
</tr>
<tr>
<td>★ Crimea-Congo hemorrhagic fever orthonairovirus</td>
<td>Crimean-Congo hemorrhagic fever virus</td>
<td>IbAr10200</td>
<td>L: AY389361; M: AF467768; S: U88410</td>
<td>L: NC_005301; M: NC_005300; S: NC_005302</td>
<td>Complete genome</td>
<td>CCHFV</td>
<td></td>
</tr>
<tr>
<td>★ Dera Ghazi Khan orthonairovirus</td>
<td>Dera Ghazi Khan virus</td>
<td>JD254</td>
<td>L: KU343151; M: KU343152; S: KU343153</td>
<td>L: NC_034520; M: NC_034510; S: NC_034501</td>
<td>Partial genome</td>
<td>DGKV</td>
<td></td>
</tr>
</tbody>
</table>

www.ictv.global/report/nairoviridae
### Related, unclassified viruses

<table>
<thead>
<tr>
<th>Virus name</th>
<th>Accession number</th>
<th>Virus abbreviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ahn virus</td>
<td>Not available</td>
<td></td>
</tr>
<tr>
<td>Bakel virus</td>
<td>Not available</td>
<td></td>
</tr>
<tr>
<td>Elïiæøy virus</td>
<td>Not available</td>
<td></td>
</tr>
<tr>
<td>Foula virus</td>
<td>Not available</td>
<td></td>
</tr>
<tr>
<td>Fraser Point virus</td>
<td>Not available</td>
<td></td>
</tr>
<tr>
<td>Garm virus</td>
<td>Not available</td>
<td></td>
</tr>
<tr>
<td>Grimsøy virus</td>
<td>Not available</td>
<td></td>
</tr>
<tr>
<td>Inner Farne Island virus</td>
<td>Not available</td>
<td></td>
</tr>
<tr>
<td>Island of May virus</td>
<td>Not available</td>
<td></td>
</tr>
</tbody>
</table>

Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
<table>
<thead>
<tr>
<th>Virus name</th>
<th>Sources</th>
<th>Abbreviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kachemak Bay virus</td>
<td>Not available (Ritter and Feltz 1974)</td>
<td>KBV</td>
</tr>
<tr>
<td>Kao Shuan virus</td>
<td>Not available (Ooherty et al., 1976)</td>
<td>KSV</td>
</tr>
<tr>
<td>Meram virus</td>
<td>S: MN972596*; M: MN972595*; L: MN972594* (Ergünay et al., 2020)</td>
<td></td>
</tr>
<tr>
<td>Mykines virus</td>
<td>Not available (Nuttall et al., 1986)</td>
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</tr>
<tr>
<td>Nàyǔn tick nairovirus</td>
<td>S: KP141755</td>
<td>NTNV</td>
</tr>
<tr>
<td>Omo virus</td>
<td>Not available (Rodhain et al., 1985)</td>
<td>OMOV</td>
</tr>
<tr>
<td>Paramushir virus</td>
<td>S: MH124636; M: MH124635; L: MH124634</td>
<td>PARV</td>
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<tr>
<td>Pathum Thani virus</td>
<td>Not available (Bishop et al., 1980)</td>
<td>PTHV</td>
</tr>
<tr>
<td>Pretoria virus</td>
<td>Not available (Converse et al., 1975)</td>
<td>PREV</td>
</tr>
<tr>
<td>Puffin Island virus</td>
<td>Not available (Gould et al., 1983)</td>
<td>PIV</td>
</tr>
<tr>
<td>Rondônia virus</td>
<td>S: MN560621*; M: MN560623*; L: MN560626*</td>
<td></td>
</tr>
<tr>
<td>Vinegar Hill virus</td>
<td>S: MF176883; M: MF176882; L: MF176881</td>
<td>VINHV</td>
</tr>
</tbody>
</table>

Virus names and virus abbreviations are not official ICTV designations.

*Not currently released. The Meram sequence are available in the sequence alignments on the Resources page.

*Coding region sequences incomplete.
**Genus: Shaspivirus**

**Distinguishing features**

Shāyáng spider virus 1 (SySV-1) is the only known shaspivirus and was detected in spiders.

**Virion**

Virions are unknown

**Nucleic acid**

Based on sequence homology, shaspiviruses have three negative-sense single-stranded RNA segments (Li et al., 2015).

**Genome organization and replication**

The S segment encodes the nucleoprotein (N), the M segment encodes the glycoprotein precursor (GPC), and the L segment encodes the large protein (L) containing an RdRP domain (Figure 1.Shaspivirus).

![Figure 1. Shaspivirus](#)

**Biology**

The original genome sequence of SySV-1 was obtained from brown sailor spiders (Neoscona nautica) (Li et al., 2015). Since no replication competent isolate was obtained, the virus biology is unknown.

**Derivation of names**

*Shaspivirus*: derived from Shāyáng spider virus 1 and *virus*, suffix for a genus.

**Species demarcation criteria**

The genus currently only includes a single species.

**Member species**

<table>
<thead>
<tr>
<th>Species</th>
<th>Virus name</th>
<th>Isolate</th>
<th>Accession number</th>
<th>RefSeq number</th>
<th>Available sequence</th>
<th>Virus Abbrev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Spider</td>
<td>Shāyáng spider virus 1</td>
<td>SYZZ-4</td>
<td>L: KM817676; M: KM817712; S: KM817758</td>
<td>L: NC_031220; M: NC_031218; S: NC_031219</td>
<td>Complete coding genome</td>
<td>SySV-1</td>
</tr>
</tbody>
</table>

Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.

www.ictv.global/report/nairoviridae
**Genus: Striwavirus**

**Distinguishing features**

Sānxiá water strider virus 1 (SxWSV-1) is the only known striwavirus and was detected in gerrid water striders.

**Virion**

Virions are unknown

**Nucleic acid**

Based on sequence homology, striwaviruses contain three negative-sense single-stranded RNA segments (Li et al., 2015).

**Genome organization and replication**

The S segment encodes the N protein, the M segment encodes the glycoprotein precursor (GPC), and the L segment encodes the large protein (L) containing an RdRP domain (Figure 1. *Striwavirus*).

**Biology**

SxWSW-1 was isolated and sequenced from water striders (gerrids) collected in China between 2011 and 2013 (Li et al., 2015). Since no replication competent isolate was obtained, the virus biology is unknown.

**Derivation of names**

*Striwavirus*: derived from Sānxiá water strider virus 1 and *virus*, suffix for a genus.

**Species demarcation criteria**

The genus currently only includes a single species.

**Member species**

<table>
<thead>
<tr>
<th>Species</th>
<th>Virus name</th>
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<th>Virus Abbrev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>★ Strider striwavirus</td>
<td>Sānxiá water strider virus 1</td>
<td>SXSSP01</td>
<td>L: KM817674; M: KM817711; S: KM817737</td>
<td>L: NC_031141; M: NC_031142; S: NC_031143</td>
<td>Complete coding genome</td>
<td>SxWSV-1</td>
</tr>
</tbody>
</table>

Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations.
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Disclaimer

This disclaimer has changed for one author (J.H.K.) since the publication of the JGV Profile. This work was supported in part through Laulima Government Solutions, LLC’s prime contract with the US National Institute of Allergy and Infectious Diseases (NIAID) under Contract No. HHSN272201800013C. JHK performed this work as an employee of Tunnell Government Services (TGS), a subcontractor of Laulima Government Solutions, LLC under Contract No. HHSN272201800013C. This project has been funded in whole or in part with federal funds from the National Cancer Institute, National Institutes of Health, under Contract No. 75N91019D00024, Task Order No. 75N91019F00130 (IC). The content of this publication does not necessarily reflect the views or policies of the Department of Health and Human Services, nor does mention of trade names, commercial products, or organizations imply endorsement by the U.S. Government.
Resources: Nairoviridae

Sequence alignments and tree files:

Figure 4A. Nairoviridae:

Tree file (newick format)
Alignment file (FASTA format)

Figure 4B. Nairoviridae:

Tree file (newick format)
Alignment file (FASTA format)

Figure 4C. Nairoviridae:

Tree file (newick format)
Alignment file (FASTA format)
References: Nairoviridae


Citation: Nairoviridae

A summary of this ICTV Report chapter has been published as an ICTV Virus Taxonomy Profile article in the Journal of General Virology, and should be cited when referencing this online chapter as follows:


Funding support

Support for the preparation of this ICTV Report chapter and associated Journal of General Virology taxonomy profile, was funded by a grant from the Wellcome Trust (WT108418AIA).