Review

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Posted Date: 21 December 2023

doi: 10.20944/preprints202312.1642.v1

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Review

Shrews (*Soricidae*) and Viruses Identified in Shrews

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Abstract: Shrews (*Soricidae*) are common small wild mammals with a significant overlap in their habitats with humans and domestic animals. Currently, viruses from 24 families have been identified in shrews, including *Adenoviridae*, *Arenaviridae*, *Arteriviridae*, *Astroviridae*, *Bornaviridae*, *Caliciviridae*, *Circoviridae*, *Coronaviridae*, *Filoviridae*, *Flaviviridae*, *Hantaviridae*, *Hepadnaviridae*, *Hepeviridae*, *Nairoviridae*, *Orthoherpesviridae*, *Paramyxoviridae*, *Parvoviridae*, *Phenuiviridae*, *Picornaviridae*, *Polyomaviridae*, *Poxviridae*, *Rhabdoviridae*, *Sedoreoviridae*, and *Spinareoviridae*, which pose potential threats to humans and domestic animals. This review compiled fundamental information about shrews and provided a comprehensive summary of the viruses that have been detected in shrews, with the aim to facilitating a deeper understanding of shrews and the diversity and risks of their viruses for researchers and the general public.

Keywords: shrew; virus; diversity; domestic animal; human

1. Introduction of Shrews (*Soricidae*)

Shrews are usually termed long-nosed mice, but they are not rodents. The largest species of shrews, *Suncus murinus* (Asian house shrews) (Figure 1), attains a length of approximately 15 cm and a weight of around 100 g, while *Suncus etruscus* (Etruscan shrews) could represent the smallest extant terrestrial mammals, measuring a mere 3.5 cm in length and weighing approximately 1.8 g [1].

Figure 1. Three Asian house shrews we raised in a barrel with soil.

In taxonomy, shrews are closer in phylogenetics to hedgehogs and moles than to rodents. They are taxonomically classified within the family *Soricidae* in the order *Eulipotyphla*. Currently, *Soricidae* encompasses three subfamilies, 26 genera, and 376 recognized species (Table 1, Figure 2). The three subfamilies are *Crocidurinae* (white-toothed shrews), *Soricinae* (red-toothed shrews), and *Myosoricinae* (African shrews). These three subfamilies comprise nine genera with 210 species, 14 genera with 148 species, and three genera with 18 species, respectively. The genus *Crocidura* in the subfamily *Crocidurinae* is the largest genus in *Soricidae* and covers 172 species. The genus *Sorex* is the largest genus in *Soricidae* and covers 77 species. The common names of some shrew species are listed in Table 2.

Table 1. Geographic and viral distribution of 26 shrew genera.

Shrew Genus	**Geographical Distribution**	**Viral Distribution (Shrew Host Species Were Given in Parentheses)**
Crocidura in the subfamily *Crocidurinae* covers 172 species	Distributed across all tropical and temperate regions of Africa, Europe, and Asia, from northern South Africa to Europe, and across the entire eastern part of Asia, extending to the Malay Archipelago	Langya virus (*Crocidura shantungensis, Crocidura lasiura*); Gamak virus and Daeryong virus (*Crocidura shantungensis, Crocidura lasiura*); Melian virus (*Crocidura grandiceps*); Denwin virus (*Crocidura russula*); Beilong virus (*Crocidura shantungensis*); Bowé virus (*Crocidura douceti*); Imjin virus (*Crocidura lasiura*); Jeju virus (*Crocidura lasiura*); Seoul virus (*Crocidura lasiura*); Azagny virus (*Crocidura obscurior*); Bufavirus (*Crocidura hirta*); Lamusara virus (*Crocidura sp.*); Lamgora virus (*Crocidura sp.*); Erve virus (*Crocidura russula*); Thiafora virus (*Crocidura spp.*); Usutu virus (*Crocidura sp.*); Olivier's shrew virus 1 (*Crocidura olivieri guineensis*); lymphocytic choriomeningitis virus (*Crocidura goliath*); Borna disease virus (*Crocidura leucodon*); Ljungan virus (*Crocidura leucodon*); Monkeypox virus (*Crocidura spp.*); Shrew herpesviruses (*Crocidura spp.*); Mokola virus (*Crocidura spp.*); rabbit hemorrhagic disease virus 2b (*Crocidura russula*); Shrew orthoreovirus (*Crocidura hirta*)
Suncus in the subfamily *Crocidurinae* covers 18 species	Distributed in all continents except Oceania	Thottapalayam virus (*Suncus murinus*); Rotavirus A (*Suncus murinus*); Porcine Bocavirus G4 (*Suncus murinus*); adeno-associated virus (*Suncus murinus*); Japanese encephalitis virus (*Suncus murinus*); *Suncus murinus* hepacivirus (*Suncus murinus*); rat pegivirus (*Suncus murinus*); Wenzhou virus (*Suncus murinus*); torque teno virus (*Suncus murinus*); astroviruses (*Suncus murinus*); severe fever with thrombocytopenia syndrome virus (*Suncus murinus*); hepatitis E virus (*Suncus murinus*); shrew hepatitis B virus (*Suncus murinus*); Asian house shrew adenovirus (*Suncus murinus*); Cencurut virus (*Suncus murinus*); Wénchéng shrew virus (*Suncus murinus*)
Sylvisorex in the subfamily *Crocidurinae* covers 12 species	Distributed in Africa	Ebola virus (*Sylvisorex ollula*); Unnamed shrew adenovirus (*Sylvisorex sp.*)
Diplomesodon in the subfamily *Crocidurinae* covers 1 species	Distributed in Caspian region	No viruses have been identified in this shrew genus
Feroculus	Distributed in southern Sri Lanka and southern India	No viruses have been identified in this shrew genus

in the subfamily *Crocidurinae* covers 1 species		
Paracrocidura in the subfamily *Crocidurinae* covers 3 species	Distributed in Burundi, the Democratic Republic of the Congo, Rwanda, Uganda, Gabon, the Central African Republic, and Equatorial Guinea in Africa	No viruses have been identified in this shrew genus
Ruwenzorisorex in the subfamily *Crocidurinae* covers 1 species	Distributed in Found in Burundi, the Democratic Republic of the Congo, Rwanda, and Uganda	No viruses have been identified in this shrew genus
Scutisorex in the subfamily *Crocidurinae* covers 1 species	Distributed in the Republic of the Congo	No viruses have been identified in this shrew genus
Solisorex in the subfamily *Crocidurinae* covers 1 species	Distributed in Sri Lanka and southern India	No viruses have been identified in this shrew genus
Sorex in the subfamily *Soricinae* covers 77 species	Distributed Eurasia and North America	Ninorex virus (*Sorex minutus*); Lena mobatvirus (*Sorex caecutiens, Sorex roboratus*); Asikkala virus (*Sorex minutus*); Asikkala virus (*Sorex minutus*); Kenkeme virus (*Sorex roboratus*); Seewis virus (*Sorex araneus*); Yakeshi virus (*Sorex unguiculatus*); Altai virus (*Sorex araneus*); Artybash virus (*Sorex caecutiens*); Artybash virus (*Sorex caecutiens*); Ash River virus (*Sorex cinereus*) Jemez Springs virus (*Sorex monticolus*); Puumala virus (*Sorex araneus*); Qian hu shan virus (*Sorex cylindricauda*); common shrew coronavirus Tibet-2014 (*Sorex araneus*); Ljungan Virus (*Sorex antinorii*); Hepatitis A virus (*sorex araneus*); human polyomavirus 12 (*sorex araneus, sorex coronatus, sorex minutus*); cowpox virus (*Sorex araneus*); tick-borne encephalitis virus (*Sorex araneus*)
Anourosorex in the subfamily *Soricinae* covers 4 species	Distributed in China, Taiwan, India, and Indochina	Cao Bang virus (*Anourosorex squamipes*); Lianghe virus (*Anourosorex squamipes*); Xinyi virus (*Anourosorex yamashinai*)
Blarinella in the subfamily *Soricinae* covers 3 species	Distributed in India, China, and Myanmar	Camp Ripley virus (*Blarina brevicauda*); Powassan virus type 2 (*Blarina brevicauda*)
Neomys in the subfamily *Soricinae* covers 3 species	Distributed in Europe and northern Asia	Boginia virus (*Neomys fodiens*)
Blarina in the subfamily *Soricinae* covers 4 species	Distributed in North America	No viruses have been identified in this shrew genus
Cryptotis	Distributed in North America and Central America	No viruses have been identified in this shrew genus

in the subfamily *Soricinae* covers 30 species		
Chimarrogale in the subfamily *Soricinae* covers 6 species	Distributed in Asia	No viruses have been identified in this shrew genus
Chodsigoa in the subfamily *Soricinae* covers 8 species	Distributed in Asia	No viruses have been identified in this shrew genus
Episoriculus in the subfamily *Soricinae* covers 4 species	Distributed in Asia	No viruses have been identified in this shrew genus
Nectogale in the subfamily *Soricinae* covers 1 species	Distributed in India and China	No viruses have been identified in this shrew genus
Nesiotites in the subfamily *Soricinae* covers 2 species	Distributed in Europe and North Africa	No viruses have been identified in this shrew genus
Soriculus in the subfamily *Soricinae* covers 1 species	Distributed in Asia	No viruses have been identified in this shrew genus
Megasorex in the subfamily *Soricinae* covers 1 species	Distributed in the United States and Mexico	No viruses have been identified in this shrew genus
Notiosorex in the subfamily *Soricinae* covers 4 species	Distributed in the United States and Mexico	No viruses have been identified in this shrew genus
Myosorex in the subfamily *Myosoricinae* covers 14 species	Distributed in Africa	Kilimanjaro virus (*Myosorex geata*); Uluguru virus (*Myosorex zinki*)
Surdisorex in the subfamily *Myosoricinae* covers 2 species	Distributed in Kenya	No viruses have been identified in this shrew genus
Congosorex in the subfamily *Myosoricinae* covers 2 species	Distributed in Gabon, Central African Republic, Democratic Congo, Cameroon, Tanzania	No viruses have been identified in this shrew genus

Table 2. The common names of some shrew species.

Common Name of Shrews	**Species Name of Shrews**
American water shrew	*Sorex palustris*

Asian house shrews	*Suncus murinus*
Asian lesser white-toothed shrews	*Crocidura shantungensis*
bicolored shrews	*Crocidura leucodon*
Chinese mole shrews	*Anourosorex squamipes*
Doucet's musk shrews	*Crocidura douceti*
dusky shrews	*Sorex monticolus*
Eurasian pygmy shrews	*Sorex minutus*
Eurasian common shrews	*Sorex Araneus*
Eurasian water shrews	*Neomys fodiens*
flat-skulled shrews	*Sorex roboratus*
Geata mouse shrews	*Myosorex geata*
Goliath shrews	*Crocidura goliath*
greater forest shrews	*Sylvisorex ollula*
greater white-toothed shrews	*Crocidura russula*
Kilimanjaro mouse shrews	*Myosorex zinki*
large-headed shrews	*Crocidura grandiceps*
Laxmann's shrews	*Sorex caecutiens*
lesser red musk shrews	*Crocidura hirta*
long-clawed shrews	*Sorex unguiculatus*
masked shrews	*Sorex cinereus*
Millet's shrews	*Sorex coronatus*
northern short-tailed shrews	*Blarina brevicauda*
Olivier's shrews	*Crocidura olivieri guineensis*
stripe-backed shrews	*Sorex cylindricauda*
Taiwanese mole shrews	*Anourosorex yamashinai*
Ussuri white-toothed shrews	*Crocidura lasiura*
Valais shrews	*Sorex antinorii*
West African pygmy shrews	*Crocidura obscurior*

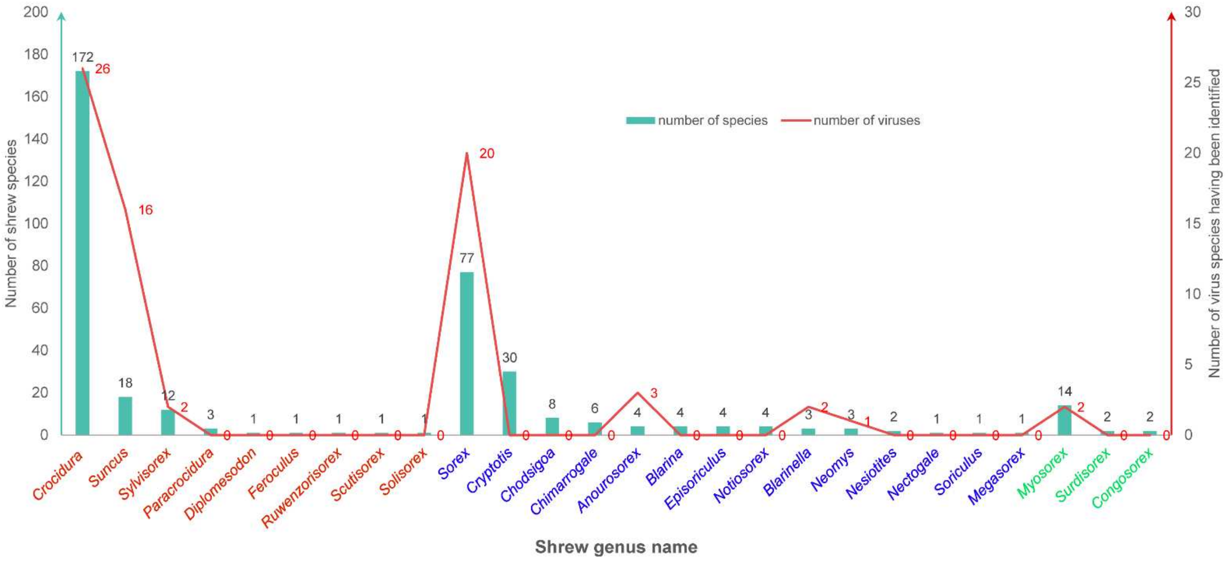

Figure 2. Numbers of known host species and known virus species in each shrew genus. The genera shown in red, blue, and green colors belongs to the subfamilies of *Crocidurinae* (white-toothed shrews), *Soricinae* (red-toothed shrews), and *Myosoricinae* (African shrews), respectively.

It is worth emphasizing that tree shrews, otter shrews, elephant shrews, West Indies shrews, and marsupial shrews are not shrews, because they do not fall within the *Soricidae* family [2].

Shrews are distributed globally across major tropical and temperate landmasses (Table 1), with notable exceptions in New Guinea, Australia, and New Zealand, where indigenous shrew populations are absent. In South America, shrews are confined to the northern Andes region and were introduced during the Great American Interchange.

In behaviors, shrews have a lifespan of 12 to 30 months, and they exhibit a relatively high metabolic rate, higher than some mammals of similar body sizes. Consequently, shrews have a relatively large food intake. Shrews do not hibernate but can enter a torpid state. During the winter, many shrews undergo significant changes in morphology, with body weight decreasing by 30% to 50%, and both skeletal and organ sizes noticeably shrinking [3]. Shrews are mostly found in cool and humid environments, with many being terrestrial, while some are semi-aquatic or burrowing. They may be active during both day and night or primarily nocturnal. Shrews are typically solitary creatures, coming together only for mating purposes.

In reproduction, female shrews can give birth to as many as 10 litters each year. In tropical regions, they are capable of mating year-round, while in temperate regions, they cease reproduction during the winter. The gestation period for shrews ranges from 17 to 32 days. Female shrews can become pregnant again within one to two days after giving birth and can lactate and nurse their offspring during pregnancy [4].

Shrews possess two characteristics distinct from most mammals. Firstly, certain shrew species secrete venom [5], which contains various compounds. For example, the venom of American short-tailed shrews can kill 200 mice when administered intravenously. Some shrews in China also produce venom. Secondly, similar to bats and toothed whales, some shrews are capable of echolocation [6]. Currently, two genera, namely *Sorex* (long-tailed shrews) and *Blarina* (blarina shrews) possess echolocation abilities. Species within these two genera include Eurasian water shrews (*Neomys fodiens*), northern short-tailed shrews (*Blarina brevicauda*), and American water shrews (*Sorex palustris*), among others [7].

The viruses in shrews have exhibited a high diversity, and many viruses in shrews have not been identified [8]. Currently, as detailed below and summarized in Figure 2 and Table 3, viruses from 24 families have been identified in shrews, including *Adenoviridae*, *Arenaviridae*, *Arteriviridae*, *Astroviridae*, *Bornaviridae*, *Caliciviridae*, *Circoviridae*, *Coronaviridae*, *Filoviridae*, *Flaviviridae*, *Hantaviridae*, *Hepadnaviridae*, *Hepeviridae*, *Nairoviridae*, *Orthoherpesviridae*, *Paramyxoviridae*, *Parvoviridae*, *Phenuiviridae*, *Picornaviridae*, *Polyomaviridae*, *Poxviridae*, *Rhabdoviridae*, *Sedoreoviridae*, and *Spinareoviridae*.

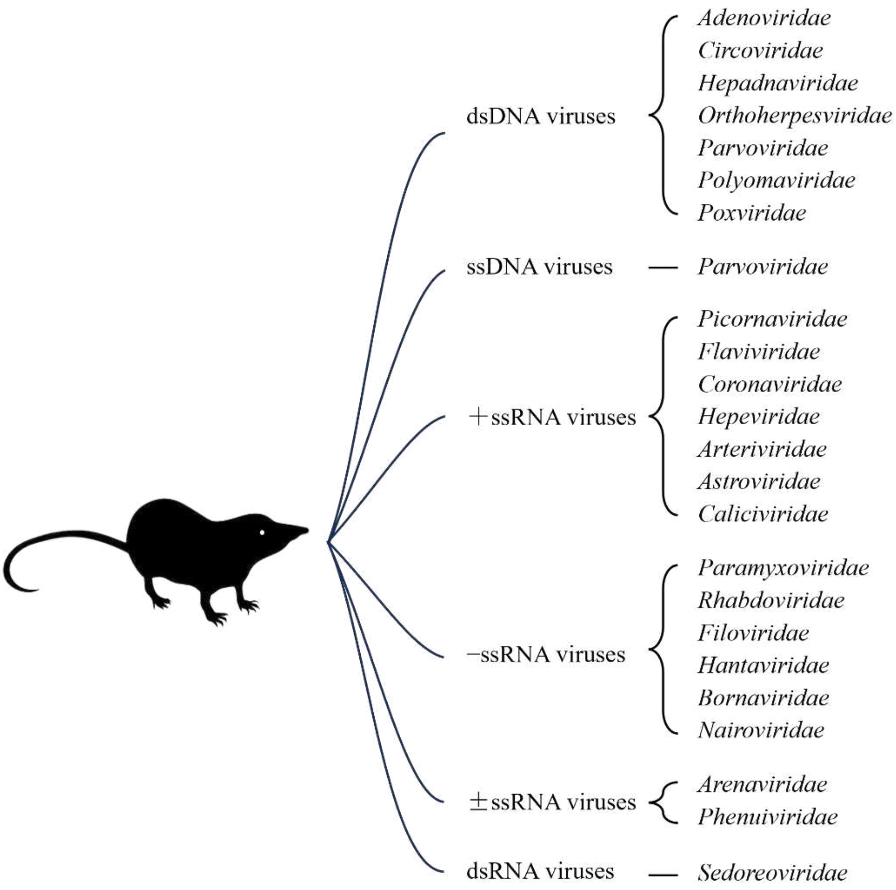

Figure 3. The virus families that contain viruses having been identified in shrews.

2. Paramyxoviruses in *Shrews*

Paramyxoviridae family contains several important viruses that are pathogenic to both humans and livestock. Viruses within this family are enveloped, approximately spherical or pleomorphic in shape, with a diameter of around 150 nm or larger. The genomes of *Paramyxoviridae* viruses consist of single-stranded, negative-sense RNA that is non-segmented, with a length of approximately 15 to 21 kb. These genomes encode six to ten different proteins, including the nucleocapsid protein (NP), phosphoprotein (P), large polymerase protein (L), matrix protein (M), fusion protein (F), and hemagglutinin-neuraminidase protein (HN) [9].

The International Committee on Taxonomy of Viruses (ICTV) currently classifies the *Paramyxoviridae* into 17 genera. The *Paraavulavirus* genus contains two species of avian viruses. The *Henipavirus* genus comprises 10 mammalian viruses, including the pathogenic Hendra virus, Nipah virus, and Langya virus. The *Jeilongvirus* genus includes 15 mammalian viruses, such as J virus and Beilong virus. Currently, seven species of paramyxoviruses have been identified in shrews, with six belonging to the *Henipavirus* genus and one belonging to the *Jeilongvirus* genus.

Langya virus, a member of the *Henipavirus*, was first reported in China in 2022, with shrews potentially serving as its natural reservoir host, detected in two shrew species, *Crocidura lasiura* (Ussuri white-toothed shrews) and *Crocidura shantungensis* (Asian lesser white-toothed shrews). The study identified 35 acute Langya virus cases among patients in Shandong and Henan provinces, manifesting symptoms such as fever (100%), fatigue (54%), cough (50%), loss of appetite (50%), myalgia (46%), nausea (38%), headache (35%), vomiting (35%), thrombocytopenia (35%), leukopenia (54%), and liver (35%) and kidney dysfunction (8%). Research encompassed 25 wild animal species and indicated a high virus infection rate among shrews (71/262 [27%]). Nevertheless, the virus's distribution in shrews and other animals across diverse Chinese regions remains poorly elucidated [10].

Gamak virus and Daeryong virus, both belonging to the *Henipavirus*, which were discovered in South Korea in 2021 from Ussuri white-toothed shrews and Asian lesser white-toothed shrews, respectively. Gamak virus has the ability to infect and replicate in human lung epithelial cell line A549 cells and rapidly induce the secretion of type I/III interferons, ISGs, and pro-inflammatory cytokines from these cells [11].

The viruses Melian virus and Denwin virus, belonging to the *Henipavirus*, were respectively discovered in 2022 in large-headed shrews (*Crocidura grandiceps*) in Guinea and greater white-toothed shrews (*Crocidura russula*) in Belgium. Further studies on their pathogenicity have not been conducted yet [12].

Ninorex virus, belonging to the *Henipavirus*, were respectively discovered in 2023 in *Sorex minutus* in Belgian. Further studies on their pathogenicity have not been conducted yet [13].

Beilong virus, belonging to the *Jeilongvirus*, has also been detected in shrews, although it was initially found in rodents. A study conducted between September 2013 and May 2019, covering eleven provinces in China, examined small mammals. The PCR testing showed a positivity rate of 28.57% (2/7) in the Asian lesser white-toothed shrews and 17.57% (13/74) in the *Suncus murinus*. Currently, there is no evidence of human infection with Beilong virus, but its potential risk to humans and livestock should not be underestimated [14].

3. Hantaviruses in Shrews

Hantaviridae family includes many pathogenic viruses for both humans and animals. These viruses are enveloped and are typically spherical or tubular, with a diameter ranging from 120 to 160 nm. The viral genome is a single-stranded negative-sense RNA virus (−ssRNA) with a size ranging from approximately 10,000 to 15,000 nucleotides. It consists of three segments: large (L), medium (M), and small (S), which collectively encode at least four structural proteins [15]. The largest segment (L) of the viral genome encodes an RNA-dependent RNA polymerase (RdRp). The medium segment (M) encodes a glycoprotein precursor (GPC), which is co-translationally cleaved by host cell signal peptidases in the endoplasmic reticulum to produce two envelope glycoproteins (Gn and Gc, or G1 and G2). The small segment (S) encodes the nucleocapsid protein (N), responsible for assembling the viral genomic RNA [16].

Hantaviridae is currently classified into seven genera. The *Orthohantavirus* genus has 38 mammalian viruses, including 15 that are zoonotic. The *Mobatvirus* genus contains 5 animal viruses. The *Thottimvirus* genus contains 2 mammalian viruses.

Lena mobatvirus, belonging to the *Mobatvirus*, was discovered in 2021 in the *Sorex caecutiens* and *Sorex roboratus* in the Siberian and Far Eastern regions of Russia. Its zoonotic potential has not been analyzed [17].

Asikkala virus, belonging to the *Orthohantavirus*, was discovered in 2010 in Eurasian pygmy shrews (*Sorex minutus*) in Finland. Subsequently, partial L segment sequences of three new hantaviruses were obtained in the Czech Republic and Germany. Genetic evolutionary analysis indicated that all of these hantaviruses belong to the Asikkala virus group, originally identified in Finland [18].

Bowé virus, belonging to the *Orthohantavirus*, was discovered in 2012 in the muscle tissue of the Doucet's musk shrews (*Crocidura douceti*) in southwestern Guinea. It shares a common ancestor with the unclassified Tanganya virus, and its zoonotic potential is currently unknown [19].

Cao Bang virus, a member of the *Orthohantavirus*, was discovered in 2006 in the lung tissue of the Chinese mole shrews (*Anourosorex squamipes*) in China. Sequencing of the M and partial S segments revealed that it is genetically distantly related to hantaviruses carried by rodents and other mole shrews hantaviruses. Its zoonotic potential is currently unknown [20].

Imjin virus, a member of the *Orthohantavirus*, was discovered in 2009 in Ussuri white-toothed shrews in South Korea. Its zoonotic potential is currently unknown [21].

Jeju virus, a member of the *Orthohantavirus*, was discovered in 2012 in Ussuri white-toothed shrews on Jeju Island, South Korea. Genetic evolution analysis revealed that it is distantly related to the previously discovered Imjin virus in South Korea, making it a new member of the *Orthohantavirus*. Its zoonotic potential is currently unknown [22].

Kenkeme virus, a member of the *Orthohantavirus*, was discovered in 2010 on *Sorex roboratus* in the northeastern part of the Sakha Republic, Siberia. Sequence analysis of the full-length S segment and partial M and L segments indicated that Kenkeme virus represents a novel *Orthohantavirus* in terms of its genetic makeup and phylogenetic relationship. Kenkeme virus exhibits distinct differences in terms of genetics and phylogeny when compared to other hantaviruses found in Eurasian common shrews, as well as in other rodents, shrews, and moles. Its zoonotic potential is currently unknown [23].

Seewis virus, a member of the *Orthohantavirus*, was discovered in 2006 in Eurasian common shrews (*Sorex araneus*) in Switzerland. Phylogenetic analysis of the complete S segment and partial M and L segments of Seewis virus revealed that it is genetically distant from hantaviruses found in rodents but more closely related to hantaviruses found in shrews. The zoonotic potential of Seewis virus is currently unknown [24].

Yakeshi virus, a member of the *Orthohantavirus*, was discovered in 2013 on long-clawed shrews (*Sorex unguiculatus*) in China. Lianghe virus, an unclassified virus within the *Orthohantavirus*, was found in Chinese mole shrews (*Anourosorex squamipes*). The zoonotic potential of these viruses is currently unknown [25].

Seoul virus, a member of the *Orthohantavirus*, was first reported in 2014 in Ussuri white-toothed shrews in China. This virus is known to be infectious to humans [26].

Altai virus, an unclassified member of the *Orthohantavirus*, was amplified from the tissue of an Eurasian common shrew in the Altai Republic in 2007. Initially, this virus was classified as Seewis virus, but subsequent findings indicated that it did not align with the host shrew species and geographical location. Through nucleotide pairing comparisons and analysis of a 300-nucleotide region of the L segment, it was confirmed to be a unique Hantavirus species [27].

Artybash virus, an unclassified member of the *Orthohantavirus*, was detected in a very limited manner in the *Sorex caecutiens* captured near Lake Teletskoye in the Altai Republic of Western Siberia in 2006. Initially referred to as the Amga virus, genetic and phylogenetic analysis of both partial and complete genome sequences identified it as a genetic variant of the Artybash virus. Its zoonotic potential remains unknown [28].

Xinyi virus, an unclassified member of the *Orthohantavirus*, was reported in 2016 and discovered in the *Anourosorex yamashinai*. Phylogenetic analysis based on the S segment, M segment, and L segment sequences suggests that Xinyi virus shares a common ancestor with the Cao Bang virus. Their pathogenicity to humans and animals is currently unknown [29].

The unclassified Ash River virus and Jemez Springs virus, both members of the *Orthohantavirus*, were discovered in 2008 on masked shrews (*Sorex cinereus*) and dusky shrews (*Sorex monticolus*) in the United States. Their pathogenicity to humans and animals is currently unknown [30].

The unclassified Camp Ripley virus, a member of the *Orthohantavirus*, was discovered in 2007 in the northern short-tailed shrews in the United States. Its pathogenicity to humans and animals is currently unknown [31].

The unclassified Boginia virus, a member of the *Orthohantavirus*, was reported in 2013 in Eurasian water shrews in Poland. Its pathogenicity to humans and animals is currently unknown [32].

The unclassified Azagny virus, a member of the *Orthohantavirus*, was discovered in 2011 in West African pygmy shrews (*Crocidura obscurior*) in Azagny Park, Côte d'Ivoire. Its pathogenicity to humans and animals is currently unknown [33].

The unclassified Puumala virus, a member of the *Orthohantavirus* genus, was discovered in 2014 in Eurasian common shrews in Finland. Its pathogenicity to humans and animals is currently unknown [34].

The unclassified Kilimanjaro virus and Uluguru virus, members of the *Orthohantavirus*, were discovered in 2014 in the *Myosorex geata* and *Myosorex zinki* in West Africa. Their pathogenicity to humans and animals is currently unknown [35].

The unclassified Qian hu shan virus, a member of the *Orthohantavirus*, was detected in the lung tissue of stripe-backed shrews (*Sorex cylindricauda*) in China in 2014. Its pathogenicity to humans and animals is currently unknown [36].

Thottapalayam virus (TPMV), a member of the *Thottimvirus*, was first isolated in 1965 from Asian house shrews in India. This virus represents the earliest isolation of a hantavirus from shrews [37].

4. Sedoreoviruses in Shrews

The viruses in *Sedoreoviridae* family include numerous pathogens for humans and animals. These viruses lack an envelope, have an icosahedral shape, and measure approximately 60 to 100 nm in diameter [38]. The genome of *Sedoreoviridae* consists of 10 to 12 linear double-stranded RNA segments, with a total length ranging from 18 to 26 kilobase pairs (kp). Individual segments vary in length from 0.6 to 5.8 kp. Each double-stranded positive-sense RNA carries a type 1 cap structure at the 5' end but lacks a 3' polyadenylated tail. Virus RNAs are typically monogenic and feature relatively short 5' and 3' non-coding regions, although some segments may contain a second or third functional open reading frame [39].

Sedoreoviridae is currently classified into six genera. The *Orbivirus* genus contains a total of 22 animal viruses, including 16 mammalian viruses such as Bluetongue virus; the *Rotavirus* genus contains 9 rotaviruses, including 3 that are pathogenic to humans, 3 to birds, and 3 to other mammals.

Rotavirus A, belonging to the *Rotavirus*, was detected in Asian house shrews in 2016. This virus can infect humans, causing severe diarrhea in infants and young children. It can also infect domestic and wild mammals as well as birds [40].

Bluetongue virus, a member of the *Orbivirus*, was discovered in an unknown shrew species in Africa in 1994. This virus primarily infects sheep and various ruminant animals, with a very high fatality rate in sheep [41].

5. Parvoviruses in Shrews

The *Parvoviridae* family contains several significant viruses that can cause diseases in humans and animals. Viruses in this family are non-enveloped and typically have small, symmetrical icosahedral shapes with a diameter of approximately 23 to 28 nm [42]. The genome of parvoviruses consists of a linear, non-circular, single-stranded DNA molecule with a length ranging from 4 to 6 kb. The capsid is composed of sixty VP proteins that assemble into a nested arrangement, usually encoded by a single structural gene. This gene includes the entire coding sequence for VP1, which typically ranges from 75 to 100 kDa. Additionally, there are one or more smaller forms (VP2-5) that share a common C-terminal sequence but have varying lengths of N-terminal truncation [43].

Parvoviridae is currently classified into 14 genera. The *Bocaparvovirus* genus encompasses 31 mammalian viruses. The *Dependoparvovirus* genus comprises 13 animal viruses, including 3 avian viruses and 8 mammalian viruses. The *Protoparvovirus* genus includes 18 mammalian viruses, such as canine parvovirus, porcine parvovirus, and 3 human parvoviruses.

Bufavirus, a member of the *Protoparvovirus*, was discovered in the lesser red musk shrews (*Crocidura hirta*) in Zambia in 2015. This virus is capable of infecting humans, primarily causing diarrhea in children [44].

Porcine bocavirus G4, a member of the *Bocaparvovirus*, was discovered in Asian house shrews in 2019 in China. This virus can infect pigs, leading to respiratory and gastrointestinal diseases [45].

Adeno-associated virus (AAV), a member of the *Dependoparvovirus*, was discovered in Asian house shrews in 2020 in China. The Infection status in humans and other animals is unknown [46].

6. Nairoviruses in Shrews

The *Nairoviridae* family includes various significant viruses that are harmful to both humans and animals. Viruses in this family are enveloped, spherical in shape, with a diameter of 80-120 nm. The envelope is covered with glycoproteins Gn and Gc. The isolated ribonucleoprotein (RNP) complex consists of segmented genomic RNA, each wrapped in nucleoprotein (N) [47]. The Nairovirus genome comprises three single-stranded negative-sense RNA molecules, with these three genomic segments labeled as L (large), M (medium), and S (small). These RNAs code for proteins on the viral complementary strands, including N, glycoprotein precursor (GPC), and L (containing RdRp, helicase, and nuclease domains) [48].

Nairoviridae is currently classified into three genera. The *Orthonairovirus* genus comprises 55 animal viruses.

The *Orthonairovirus* Lamusara virus and Lamgora virus were discovered in *Crocidura* sp. in Gabon, Central Africa, in 2022. Their pathogenicity to humans and animals is currently unknown [49].

Erve virus, belonging to the *Orthonairovirus*, was discovered in greater white-toothed shrews in France in 1989. It can infect humans and various domestic animals, leading to neurological symptoms in humans [50].

Thiafora virus, belonging to the *Orthonairovirus*, was discovered in *Crocidura sp.* in Senegal in 2015. Its pathogenicity to humans and animals is currently unknown [51].

Cencurut virus, belonging to the *Orthonairovirus*, was discovered in Asian house shrews in Singapore in 2023. Its pathogenicity to humans and animals is currently unknown [52].

7. Coronaviruses in Shrews

The *Coronaviridae* family includes various significant viruses that are harmful to both humans and animals. Viruses in this family are enveloped and, in the case of the *Orthocoronavirinae* subfamily, have a spherical shape with a diameter of 80 to 160 nm [53]. The shapes of viruses in the other two subfamilies have not yet been determined. The viral genome is non-segmented, single-stranded RNA, approximately 26 to 32 kb in size. The initial part of the coronavirus genome encodes 16 non-structural proteins, while the remaining portion encodes four essential structural proteins: envelope protein (E), spike glycoprotein (S), matrix (M) protein, and nucleocapsid (N) protein [54].

Coronaviridae is currently classified into six genera. The *Alphacoronavirus* genus includes 27 mammalian viruses, including several common human coronaviruses such as Human Coronavirus 229E and Human Coronavirus NL63, as well as porcine epidemic diarrhea virus.

Wencheng shrew virus, belonging to the *Alphacoronavirus*, was discovered in 2017 in China in Asian house shrews. Its pathogenicity to humans and animals is unknown [55].

A previously unnamed shrew coronavirus in the *Alphacoronavirus* was discovered in 2016 in Eurasian common shrews in the United Kingdom. Phylogenetically, it falls within the same branch as the Lu-cheng virus found in Chinese rats. Its pathogenicity to humans and animals is unknown [56].

Common shrew coronavirus Tibet-2014, belonging to the *Alphacoronavirus*, was identified in Eurasian common shrews in Tibet, China, in 2014. Its pathogenicity to humans and animals is unknown [57].

8. Flaviviruses in Shrews

The *Flaviviridae* family comprises several significant viruses that are harmful to humans and animals. Viruses in this family are enveloped and spherical, with a viral particle diameter ranging from 40 to 60 nm [58]. The viral genome is a positive-sense, single-stranded RNA, with a length of 8.9 to 13.0 kb. It consists of a single large open reading frame (ORF) flanked by 3' and 5' untranslated regions (UTRs), and it possesses a 5' cap structure. This single ORF encodes a polyprotein that undergoes processing and cleavage by viral protease NS2B/NS3 and cellular proteases. This cleavage results in the formation of three structural proteins, including the C protein of the viral capsid, the M (membrane) protein, and the E (membrane) protein. Additionally, seven non-structural proteins play essential roles in viral replication. These proteins are NS1, NS2A, NS2B, NS3, NS4A, NS4B, and NS5 [59].

Flaviviridae is currently classified into four genera. The *Orthoflavivirus* genus includes 52 animal viruses, including several significant human pathogens such as Yellow Fever virus, Dengue virus, Zika virus, Japanese Encephalitis virus, West Nile virus, and Tick-Borne Encephalitis virus. It also has pathogenicity for livestock and poultry (turkeys, pigs, horses, and sheep), causing economically important diseases such as encephalitis viruses in various livestock. The *Hepacivirus* genus contains 14 mammalian viruses, with human hepatitis C virus being among those capable of infecting humans. The *Pegivirus* genus comprises 11 mammalian viruses.

Usutu virus, belonging to the *Orthoflavivirus*, was first reported in *Crocidura sp.* in Senegal in 2019. At the time of collection, no pathogenic infection or symptoms were observed in shrews. This virus was initially discovered in 1959 and is associated with Culex mosquitoes as its vectors. Currently, the virus has been isolated from birds, arthropods, and humans in Europe and Africa, and subsequently detected in bats and horses [60].

Powassan virus type 2, classified within the *Orthoflavivirus*, was first discovered in 2021 in *Blarina brevicauda* in the United States. Previously, it had been found primarily in ticks and humans. This virus can lead to encephalitis in humans and is primarily transmitted by arthropod vectors [61].

Tick-borne encephalitis virus, classified within the *Orthoflavivirus*, was first discovered in 1967 in Eurasian common shrews in Slovakia. This virus can infect humans, and when it reaches the central nervous system, neurological symptoms can occur. Infection can manifest as meningitis, encephalitis, or meningoencephalitis. In nature, tick-borne encephalitis virus circulates between ticks and small mammals [62].

Japanese encephalitis virus, classified within the *Orthoflavivirus*, was first discovered to infect Asian house shrews in 1984. This virus can infect humans and various livestock. Infected individuals may exhibit mild symptoms such as fever and headache, or they may be asymptomatic. However, approximately 1 in every 250 infected individuals may develop severe illness. Initial symptoms in children can include abdominal pain and vomiting. Severe illness is characterized by a rapid rise in body temperature, headache, neck stiffness, loss of orientation, coma, seizures, spasmodic paralysis, and may lead to death. The fatality rate for individuals displaying disease symptoms can be as high as 30% [63].

Suncus murinus hepacivirus, belonging to the *Hepacivirus*, was discovered in Asian house shrews in 2016. Currently, its zoonotic potential is unknown [64].

Rat pegivirus, belonging to the *Pegivirus*, was discovered in Chinese Asian house shrews in 2020. This virus primarily targets lymphocytes and causes asymptomatic infections in humans and other animals, presenting as benign [65].

9. Arteriviruses in Shrews

The *Arteriviridae* family comprises several significant veterinary pathogens. The viruses in this family are enveloped and generally spherical, with an estimated diameter ranging from 50 to 74 nm [66]. The viral genome is a linear positive-sense RNA, approximately 12 to 16 kb in length. The infectious genome RNA contains a 5' type I cap structure and a 3' polyadenylate sequence, surrounding multiple and mostly overlapping open reading frames (ORFs). The two largest ORFs closest to the 5' end, known as ORF1a and ORF1b, encode non-structural proteins, while the ORFs at the 3' end encode structural viral proteins.

Arteriviridae is currently classified into 13 genera. The *Muarterivirus* genus contains only one shrew arterivirus, Olivier's shrew virus 1, which was discovered in 2018 in Olivier's shrews (*Crocidura olivieri guineensis*) in Guinea. Both phylogenetic analysis and pairwise sequence comparison indicate that this virus is distinctly different from the established arterivirus genera and belongs to a new genus [67].

10. Other Viruses in Shrews

Shrews serve as the hosts for multiple other viruses, such as adenovirus, hepatitis B virus, herpesvirus, Ebola virus, pegivirus, and astrovirus, as listed in Table 2.

Table 2. The taxonomy and zoonotic potential of the viruses having been identified in shrews.

Family	**Genus**	**Virus**	**Zoonotic Potential**	**Year / Country / Host Species**
Paramyxoviridae	*Henipavirus*	Langya virus	Infects humans and some other mammals	2022 / China / *Crocidura lasiura, Crocidura shantungensis* [10]
Paramyxoviridae	*Henipavirus*	Gamak virus	Unknown	2021 / China / *Crocidura lasiura, Crocidura shantungensis* [11]
Paramyxoviridae	*Henipavirus*	Daeryong virus	Unknown	2021 / China / *Crocidura lasiura, Crocidura shantungensis* [11]
Paramyxoviridae	*Henipavirus*	Melian virus	Unknown	2022 / Guinea / *Crocidura grandiceps* [12]
Paramyxoviridae	*Henipavirus*	Denwin virus	Unknown	2022 / Belgium / *Crocidura russula* [12]
Paramyxoviridae	*Henipavirus*	Ninorex virus	Unknown	2023 / Belgian / *Sorex minutus* [13]
Paramyxoviridae	*Jeilongvirus*	Beilong virus	Unknown	2019 / China / *Crocidura shantungensis, Suncus murinus* [14]
Hantaviridae	*Mobatvirus*	Lena mobatvirus	Unknown	2021 / Siberian and Russia / *Sorex caecutiens, Sorex roboratus* [17]
Hantaviridae	*Orthohantavirus*	Asikkala virus	Unknown	2010 / Finland / *Sorex minutus* [18]
Hantaviridae	*Orthohantavirus*	Bowé virus	Unknown	2012 / Guinea / *Crocidura douceti* [19]
Hantaviridae	*Orthohantavirus*	Cao Bang virus	Unknown	2006 / China / *Anourosorex squamipes* [20]
Hantaviridae	*Orthohantavirus*	Imjin virus	Unknown	2009 / South Korea / *Crocidura lasiura* [21]
Hantaviridae	*Orthohantavirus*	Jeju virus	Unknown	2012 / South Korea / *Crocidura lasiura* [22]
Hantaviridae	*Orthohantavirus*	Kenkeme virus	Unknown	2010 / Sakha Republic, Siberia / *Sorex roboratus* [23]
Hantaviridae	*Orthohantavirus*	Seewis virus	Unknown	2006 / Switzerland / *Sorex araneus* [24]
Hantaviridae	*Orthohantavirus*	Yakeshi virus	Unknown	2013 / China / *Sorex unguiculatus* [25]
Hantaviridae	*Orthohantavirus*	Lianghe virus	Unknown	2013 / China / *Anourosorex squamipes* [25]
Hantaviridae	*Orthohantavirus*	Seoul virus	Infects humans	2014 / China / *Crocidura lasiura* [26]
Hantaviridae	*Orthohantavirus*	Altai virus	Unknown	2007 / Altai Republic / *Sorex araneus* [27]
Hantaviridae	*Orthohantavirus*	Artybash virus	Unknown	2006 / Altai Republic / *Sorex caecutiens* [28]
Hantaviridae	*Orthohantavirus*	Xinyi virus	Unknown	2016 / Chian / *Anourosorex yamashinai* [29]
Hantaviridae	*Orthohantavirus*	Ash River virus	Unknown	2008 / United States / *Sorex cinereus, Sorex monticolus* [30]
Hantaviridae	*Orthohantavirus*	Camp Ripley virus	Unknown	2007 / United States / *Blarina brevicauda* [31]
Hantaviridae	*Orthohantavirus*	Boginia virus	Unknown	2013 / Poland / *Neomys fodiens* [32]
Hantaviridae	*Orthohantavirus*	Azagny virus	Unknown	2011 / Côte d'Ivoire / *Crocidura obscurior* [33]
Hantaviridae	*Orthohantavirus*	Puumala virus	Unknown	2014 / Finland / *Sorex araneus* [34]
Hantaviridae	*Orthohantavirus*	Kilimanjaro virus	Unknown	2014 / West Africa / *Myosorex geata* [35]

Hantaviridae	*Orthohantavirus*	Uluguru virus	Unknown	2014 / West Africa / *Myosorex zinki* [35]
Hantaviridae	*Orthohantavirus*	Qian hu shan virus	Unknown	2014 / China / *Sorex cylindricauda* [36]
Hantaviridae	*Thottimvirus*	Thottapalayam virus	Unknown	1965 / India / *Suncus murinus* [37]
Sedoreoviridae	*Rotavirus*	Rotavirus A	Infects humans	2016 / China / *Suncus murinus* [40]
Sedoreoviridae	*Orbivirus*	Bluetongue virus	Unknown	1994 / Africa / unknown shrew species [41]
Parvoviridae	*Protoparvovirus*	Bufavirus	Infects humans	2015 / Zambia / *Crocidura hirta* [44]
Parvoviridae	*Bocaparvovirus*	porcine bocavirus G4	Infects pigs	2019 / China / *Suncus murinus* [45]
Parvoviridae	*Dependoparvovirus*	adeno-associated virus	Unknown	2020 / China / *Suncus murinus* [46]
Nairoviridae	*Orthonairovirus*	Lamusara virus	Unknown	2022 / Gabon / *Crocidura sp.* [49]
Nairoviridae	*Orthonairovirus*	Lamgora virus	Unknown	2022 / Gabon / *Crocidura sp.* [49]
Nairoviridae	*Orthonairovirus*	Erve virus	Unknown	1989 / France / *Crocidura russula* [50]
Nairoviridae	*Orthonairovirus*	Thiafora virus	Unknown	2015 / Senegal / *Crocidura sp.* [51]
Nairoviridae	*Orthonairovirus*	Cencurut virus	Unknown	2023 / Singapore / *Suncus murinus* [52]
Coronaviridae	*Alphacoronavirus*	Wencheng shrew virus	Unknown	2017 / China / *Suncus murinus* [55]
Coronaviridae	*Alphacoronavirus*	unnamed shrew coronavirus	Unknown	2016 / United Kingdom / *Sorex araneus* [56]
Coronaviridae	*Alphacoronavirus*	common shrew coronavirus Tibet-2014	Unknown	2014 / China / *Sorex araneus* [57]
Flaviviridae	*Orthoflavivirus*	Usutu virus	Infects birds, arthropods, humans, bats, and horses	2019 / Senegal / *Crocidura sp.* [60]
Flaviviridae	*Orthoflavivirus*	Powassan virus type 2	Infects humans and causes encephalitis	2021 / United States / *Blarina brevicauda* [61]
Flaviviridae	*Orthoflavivirus*	tick-borne encephalitis virus	Infects humans and causes encephalitis	1967 / Slovakia / *Sorex araneus* [62]
Flaviviridae	*Orthoflavivirus*	Japanese encephalitis virus	Infects humans and various domestic animals and causes human encephalitis	1984 / Japan / *Suncus murinus* [63]
Flaviviridae	*Hepacivirus*	Suncus murinus hepacivirus	Unknown	2016 / China / *Suncus murinus* [64]
Flaviviridae	*Pegivirus*	rat pegivirus	Infects humans and other animals without symptoms	2020 / China / *Suncus murinus* [65]
Arteriviridae	*Muarterivirus*	Olivier's shrew virus 1	Unknown	2018 / Guinea / *Crocidura olivieri guineensis* [67]
Caliciviridae	*Lagovirus*	Rabbit hemorrhagic disease virus	Infects rabbits	2019 / Spain / *Crocidura russula* [68]
Arenaviridae	*Mammarenavirus*	Wenzhou virus	Infects humans	2015 / China / *Suncus murinus* [69,70]

Arenaviridae	*Mammarenavirus*	lymphocytic choriomeningitis virus	Infects humans and various animals and dangerous to pregnant women and infants	2021 / Gabon / *Crocidura goliath* [71]
Bornaviridae	*Orthobornavirus*	Borna disease virus	Infects humans, horses, sheep, and various other mammals and causes encephalitis	2006 / Switzerland / *Crocidura leucodon* [72]
Circoviridae	*Anellovirus*	torque teno virus	Infects humans and causes various symptoms	2018 / China / *Suncus murinus* [73]
Picornaviridae	*Parechovirus*	Ljungan Virus	Infects humans and causes various symptoms	2020 / Italy / *Crocidura leucodon, Sorex antinorii* [74]
Picornaviridae	*Hepatovirus*	Hepatitis A virus	Unknown	2015 / Germany / *sorex araneus* [75]
Polyomaviridae	*Betapolyomavirus*	human polyomavirus 12	Infects humans	2017 / Germany, Norway / *sorex Araneus, sorex coronatus, sorex minutus* [76]
Poxviridae	*Orthopoxvirus*	monkeypox virus	Infects humans and other primates	2015 / Zambia, Congo / *Crocidura spp.* [77]
Poxviridae	*Orthopoxvirus*	shrew cowpox virus	Unknown	1998 / Norway / *Sorex araneus* [78]
Astroviridae	*Mamastrovirus*	shrew astrovirus	Unknown	2014 / China / *Suncus murinus* [79]
Filoviridae	*Ebolavirus*	Ebola virus	Infects humans with a high case fatality rate	1999 / Central Africa / *Sylvisorex ollula* [80]
Phenuiviridae	*Phlebovirus*	severe fever with thrombocytopenia syndrome virus	Infects humans with a high case fatality rate	2014 / China / *Suncus murinus* [81]
Herpesviridae	Unknown	shrew herpesvirus	Unknown	2018 / Central Africa / *Crocidura spp.* [55]
Rhabdoviridae	*Lyssavirus*	Mokola virus	Unknown	1968 / Nigeria / *Crocidura spp.* [82]
Hepeviridae	*Paslahepevirus*	shrew hepatitis E virus	Unknown	2013 / China / *Suncus murinus* [83]
Hepadnaviridae	*Orthohepadnavirus*	shrew hepatitis B virus	Unknown	2019 / China / *Suncus murinus* [84]
Adenoviridae	*Atadenovirus*	Asian house shrew adenovirus	Unknown	2016 / China / *Suncus murinus* [85]
Adenoviridae	*Atadenovirus*	shrew adenovirus	Unknown	2019 / Cameroon / *Sylvisorex sp.* [86]
Spinareoviridae	*Orthoreovirus*	shrew orthoreovirus	Unknown	2019 / Zambia / *Crocidura hirta* [87]

11. Discussion

Shrews share overlapping habitats with humans and livestock, highlighting the importance of shrew virus research for public health and animal welfare. This review shows that shrew populations host at least 24 families of viruses, and 23 species of hantaviruses, seven species of paramyxoviruses, six species of flaviviruses, and five species of nairoviruses in shrews have been identified. 17 species of viruses in 14 families in Asian house shrews (*Suncus murinus*) have been identified. Eight species of viruses in six families in Eurasian common shrews (*Sorex araneus*) have been identified. Six species of viruses in two zoonotic families in Ussuri white-toothed shrews (*Crocidura lasiura*) have been identified. These three species of shrews could host more species of zoonotic viruses than other shrew species.

Future research should assess the transmission risks of shrew viruses from shrews to humans and domestic animals. Future research should conduct broader surveys to delve into the diversity, evolution, potential pathogenicity, and effective measures of these viruses. This will enhance our capacity to respond swiftly to the potential outbreaks of shrew viruses in humans or domestic animals.

Shrews' small size and ease of husbandry make them ideal for studying viruses of shrews and other animals including humans. Their biological traits, like reproductive cycles, lifespan, and immune systems, are valuable for investigating the transmission, pathogenicity, and potential therapies of viral diseases.

Author Contributions: H.-Y.G., R.-X.C., S.-M.T., and X.W. wrote the first version of this manuscript under the direction of J.-M.C., Y.-L.Z., M.L. and H.-Y.G. drew the tables and figures. J.-M.C., Y.-L.Z., and M.L. conceived, designed, and financially supported this study and revised this manuscript. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by by the High-Level Talent Fund of Foshan University [No. 20210036] and the Open Competition Program of Top Ten Critical Priorities of Agricultural Science and Technology Innovation for the 14th Five-Year Plan of Guangdong Province [2022SDZG02]. The APC was funded by the second funder.

Data Availability Statement: The data that support the findings of this study are available from the corresponding author Ji-Ming Chen upon reasonable request.

Acknowledgments: This study was supported by the High-Level Talent Fund of Foshan University (No. 20210036) and the Open Competition Program of Top Ten Critical Priorities of Agricultural Science and Technology Innovation for the 14th Five-Year Plan of Guangdong Province (2023SDZG02).

Conflicts of Interest: The authors declare no conflicts of interest.

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