Centre of Expertise on Animal Disease Outbreaks

Report

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Evaluating further midge disease threats that may cause disease in Scotland

Authors Jack Hearn
Reviewers Davide Pagnossin

Key Message:

Culicoides midges vector a variety of diseases that may cause outbreaks in livestock in Scotland.

Executive Summary

Species of *Culicoides* midges vector many animal diseases in Europe in addition to Bluetongue and Schmallenberg. I have reviewed the literature and identified which diseases may cause outbreaks in Scotland. The key metric for inclusion was prior outbreaks in Europe and/or other temperate region. Many of the diseases will be familiar to policy makers as they are already notifiable to the Scottish Government (see Table 1).

In summer 2026, two strains of Shamonda-like virus (SHAV-EU1 and SHAV-EU2) independently emerged in Europe and quickly spread across the continent. At present SHAV is known to infect cattle, horses, alpaca, sheep and goats. Given the rapid spread of the related Schmallenberg virus (SBV) in Europe 15 years ago, at least one if not both strains of SHAV are likely to reach Scotland soon. There is no vaccine and assessing damage to foetuses in infected animals is not yet possible. Testing of animals with signs of SHAV/SBV is recommended to determine if, when and which SHAV is circulating in Scotland.

Horse diseases are recommended for increased focus alongside those of cattle and sheep. They are infected by SHAV-EU1 and are at risk from African horse sickness (AHS) virus and West Nile virus (WNV). Although WNV is primarily transmitted by mosquitoes, *Culicoides* have occasionally been implicated as potential vectors. A multivalent vaccine shows promise against AHS, but it has not yet been tested in horses. Mitigation of the risk of spread through prevention of midge biting may be more successful in horses than sheep or cattle. Biting mitigation approaches are recommended for inclusion in any response to an outbreak of midge-vectored disease in horses.

Another recent observation of note is the detection of bovine leukaemia virus, which causes enzootic bovine leukosis in cattle, in *Culicoides* in Poland.



Main Report

Culicoides midges are capable of spreading many diseases of veterinary and public health importance. Key vector species in Scotland include members of the *C. obsoletus* complex and *C. pulicaris* group [1]. At present, *C. imicola*, a prolific vector of midge-borne diseases, is restricted to the Mediterranean basin (see Appendix, Figure S1), although its range is likely to expand with climate change. *Culicoides* are responsible for vectoring the current European outbreak of Bluetongue virus 3, which reached Scotland in summer 2026. A changing climate of increasing temperatures and unsettled weather patterns may facilitate more wind-borne incursions of known and novel (see Shamonda-like virus reviewed here) diseases to Scotland. In addition, animal movements remain a threat for seeding undetected or novel diseases in Scotland that can subsequently spread through local midge activity. *Culicoides* species transmit a variety of animal diseases beyond cattle and sheep to horses and humans. One such disease of horses, African horse sickness, has high mortality and has caused outbreaks in Europe previously.

Culicoides can transmit a variety of pathogens including viruses, protozoa and filarial nematodes. Over 50 viruses have been isolated from *Culicoides* species worldwide [2]. They are also capable of causing allergic reactions through biting [3]. In this report, I have reviewed diseases and one case of potential midge-associated biting behaviour that present the most risk to Scotland. I have not included Bluetongue or Schmallenberg viruses which are responsible for ongoing outbreaks of disease in Scotland. The principal criterion for inclusion here was for pathogens to have caused outbreaks of disease in Europe or other temperate regions. Pathogens are presented in alphabetical order except for Shamonda-like virus, which is discussed first given its emergence in Europe in summer 2026 and ongoing rapid spread.

1. Shamonda-like Virus

In summer 2026 an Orthobunyavirus of the Simbu subgroup causing disease in cattle, horses and Alpaca was identified in Austria, Belgium, France, Germany, the Netherlands and Switzerland [4,5]. It has been named Shamonda-like virus (SHAV), and its emergence shares similarities with the rapid spread across Europe of Schmallenberg virus (SBV) in 2011. Signs in cattle last for 2-3 weeks and include a fever, drop in milk yield, loss of appetite and diarrhoea. Abortions of bovine foetuses from different herds were reported in France, hence transplacental transmission is suspected [4]. SHAV circulating in the Netherlands and northwestern Germany is genetically distinct from SHAV in southern Germany, Switzerland, Italy [6], and France but causes the same clinical signs in affected animals ([7] and https://www.gddiergezondheid.nl/Actueel/Nieuws/2026/08/Recente-bevindingen-Shamonda-like-virus). As of September 2026, it has not been confirmed if SHAV circulating in the Netherlands and northwestern Germany are the same or distinct strains.

Epidemiological and phylogenetic evidence indicates SHAV-EU1, predominantly circulating in southern Europe, and SHAV-EU2, more common in northern Europe, represent two independent introductions into Europe [7] (Figure S2). After initial discovery in cattle, on 25th August 2026 Swiss authorities reported SHAV-EU1 in the brain tissue of two dead horses. This followed an increase in reports of central nervous system disorders including ataxia, muscle tremors, drowsiness, head tilt and strabismus, in horses since late July 2026. By 28th August, Schmallenberg and SHAV cross-reactive antibodies had been detected in several horses and two alpacas (see https://beaconbio.org/en/report/?reportid=42999059-6aa4-459e-8264-0f7652687775). As of September 2026, SHAV-EU2 has been identified only in cattle [7]. Very high summer temperatures in continental Europe and the introduction of infected midges by air travel to airports in close proximity to livestock are speculated to have helped the establishment

and rapid spread of SHAV strains [8].

A SHAV surveillance gap

As of September 2026, no cases of SHAV have been reported in Great Britain (GB), however APHA reported the detection of SHAV in cattle on Jersey in the Channel Islands in August 2026 (https://www.gov.uk/government/news/emerging-shamonda-virus-detected-in-jersey). APHA did not state which strain of SHAV was detected but it is likely SHAV-EU2 which emerged nearby in continental northern Europe. Due to its very recent emergence, there is no mandatory reporting of detect SHAV cases in Europe, GB or Scotland. At present, detection systems are not harmonized across European countries, which is limiting assessment of the extent of the outbreak.

The overlap of clinical signs with SBV may delay early detection of SHAV in Scotland. SBV is not a notifiable disease, but testing is recommended to confirm the presence of SBV versus SHAV. Reports of equine central nervous disorders should also be investigated further, especially if a similar increase in frequency of reports as occurred in Switzerland is reported in Scotland. Developing molecular and serology testing capability that differentiates SBV and the strains of SHAV in Scotland is a further consideration. Syndromic surveillance of milk production will also help detect SHAV as observed in France [4]. The massive and ongoing spread of SHAV-EU1 and SHAV-EU2 across Europe is a developing situation which requires ongoing monitoring to assess the risk to Scotland.

Given the fast-moving situation this summary of SHAV in Europe, this report will rapidly become obsolete. EPIC is on hand to continue monitoring the spread of SHAV strains if requested.

2. Additional orthobunyaviruses

Orthobunyaviruses like SHAV are primarily vectored by midges and mosquitos but ticks [9] and bat bugs, a close relation of human bed bugs [10], can also vector viruses of this genus. They represent a specific One Health threat as different viruses cause disease in humans and animals. Indeed, there were initial fears in Europe that SBV may infect humans given that other orthobunyaviruses do so [11]. Orthobunyaviruses are capable of rapid spread, as observed following the emergence of SBV in Europe and, more recently, with SHAV. Orthobunyaviruses have segmented negative-sense RNA genomes that can readily reassort to create novel strains with altered virulence and host ranges [12]. The genome consists of three segments, named the "L", "M" and "S" segment respectively. Reassortment events can occur during co-infection of two distinct viruses which exchange segments. Ngari virus is an example of this, as its "L" and "S" segments are related to Bunyamwera virus and its "M" segment is related to Batai virus [12]. In the case of SHAV-EU1 and SHAV-EU2, the "M" segments share less than 40% sequence identity between the two strains [7] (Figure S2). It is feasible that SHAV-EU1, SHAV-EU2 and SBV may re-assort in Europe where they co-circulate [13]. Further examples of re-assortment among orthobunyaviruses have been identified [12]. To avoid missing re-assortment events, sequencing of all genome segments is recommended when undertaking molecular surveillance [12]. This re-assortment behaviour is of concern for the emergence of future diseases of animals and humans. This is particularly important given that many orthobunyaviruses are poorly characterised. Hence, silent circulation and re-assortment events may only be detected following poorly characterised. Hence, silent circulation and re-assortment events may only be detected following the emergence of a novel virus, such as SHAV in Europe in 2026.

3. African horse sickness

African horse sickness is transmitted by *Culicoides* species and is caused by the African horse sickness virus (AHSV) of the Orbivirus genus. It is a notifiable disease in Scotland (Table 1). There are 9 distinct serotypes currently recognised [14] which are endemic to sub-Saharan Africa. There are four forms of the disease, three of which cause severe clinical signs in naïve horses and other equids. AHSV affects the respiratory and circulatory systems, causing effusions and haemorrhage. In an outbreak, all forms of the disease can occur and combined rates of fatality may reach 80-90% [15]. Seroconversion for AHSV has been reported in other animals which may help propagate horse infections. An outbreak of AHSV serotype 1 in Thailand in 2020 affected ~2700 horses and was likely imported in sub-clinically infected animals like Zebras [16]. Other outbreaks have occurred in Morocco [17] and Spain [18]. A systematic review of AHS epidemiology identified that donkeys often have high seroprevalence coupled with a propensity for subclinical infection which may help silently maintain outbreaks if overlooked [19,20]. Not surprisingly for a *Culicoides* vectored virus, vector distribution and seasonal peaks are key determinants of outbreaks [19]. More notably, habitat connectivity is also important [19].

Vaccination with live attenuated vaccines (LAV) has been used to control outbreaks in sub-Saharan Africa, including a polyvalent vaccine in Senegal [15]. Such vaccines are not without drawbacks as there is a risk of reversion to virulence, transmission of the live attenuated virus by vectors, and reassortment between vaccine and wild strains [15]. A Differentiated Infected from Vaccinated Animals (DIVA) vaccine is not currently available. A multi-valent candidate DIVA vaccine under development is broadly protective against AHSV serotypes in an established mouse model (IFNAR -/-) for AHS [21]. This vaccine is an example of the Disabled Infectious Single Animal (DISA) platform developed originally as a platform for BTV vaccines [22]. The candidate vaccine caused no clinical signs of AHS, viraemia or other detected side effects in mice but has not yet been tested in horses [21]. Further control measures effective against AHS alongside LAV vaccination include stabling animals during peak-biting hours, vector-proofing housing, insecticide treatments and reducing midge breeding sites [19].

4. Avian blood parasites

A variety of avian bloodborne parasites are vectored by *Culicoides*, some of which may cause disease in poultry and game birds (Galliformes) in addition to wild birds. These parasites are widespread and are present in Scotland [23–25]. Specifically, many species of *Haemoproteus* have been identified in *Culicoides* in Europe (reviewed by [26]) as have species of *Plasmodium, Leucocytozoon* and *Trypanosoma*. Of note for Scotland, the highland midge, *C. impunctatus*, is a vector of multiple *Haemoproteus* species [27]. Midge control measures should be considered as part of any response in the event of an outbreak of an avian bloodborne parasite in poultry.

5. Bovine ephemeral fever (BEF)

Bovine ephemeral fever virus is a member of the Rhabdoviridae family. It is spread by *Culicoides* and causes seasonal illness of high morbidity and low mortality in cattle [14]. Several potential vector species of BEF are present in Scotland including *C. chiopterus, C. dewulfi* and species of the *C. obsoletus* complex [28]. Signs of BEF include fever, lameness, stiffness and reduced milk production [14]. At present, Turkey is the closest country to Scotland that has reported cases of BEF, with BEF present in the Middle East, Africa, Asia and Australia [29]. Risk is therefore low to Scotland, and BEF virus should be considered if overlapping signs of

unknown illness are traced to animals imported from affected regions [14]. A vaccine exists but effectiveness varies by dose and formulation from negligible to 50-60% and immunity may wane quickly (reviewed in [30]).

6. Enzootic bovine leukosis

Bovine leukaemia virus (BLV) causes enzootic bovine leukosis in cattle. Under experimental conditions it can also affect sheep and other non-ruminants. It is a notifiable disease in Scotland (Table 1) and was last detected in Great Britain in 1996 (*https://www.gov.scot/publications/enzootic-bovine-leukosis/*). *Culicoides* species have the potential to mechanically vector BLV [31]. However, successful onward transmission of BLV mediated by *Culicoides* has not yet been demonstrated. Further studies are required to determine the role of *Culicoides* in spreading BLV.

In 2026, BLV was detected in *Culicoides* midges collected from cattle farms in Poland [31]; BLV was also identified in the stable fly *Stomoxys calcitrans*. In this study, *Culicoides* midges were pooled by species and gonotrophic condition of 5-20 individuals and tested for BLV by PCR. Of 126 pools tested 18 (14%) were positive for BLV DNA. The study did not distinguish between BLV present in ingested blood or retained on the mouthparts. The highest number of positive pools were for *C. punctatus, C. achrayi* and *C. obsoletus/C. scoticus* all of which are present in Great Britain. Current BLV control recommendations focus on testing, segregation, culling and prevention of iatrogenic blood transfusion. Control measures may require expansion to reflect potential transmission by *Culicoides* (and *Stomoxys*) [31].

7. Epizootic haemorrhagic disease (EHD)

Epizootic haemorrhagic disease (EHD) was monitored by EPIC following the 2024 outbreak in France (see EPIC_202324_REP_005 prepared by Lucy Gilbert). In France, no outbreaks of EHD have been detected since the 1st of June 2026 (https://agriculture.gouv.fr/mhe-la-maladie-hemorragique-epizootique). In the previous year between 1st of June 2025 and 1st of June 2026 five outbreaks were identified. Although there is currently no evidence of EHD circulation in France, EHD is of continuing concern to Scotland and hence is actively monitored by EPIC.

8. Lumpy skin disease virus (LSDV)

LSDV is mechanically transmitted by several groups of blood feeding insects including *Culicoides* to domestic and wild bovines. It causes fever, nodules on the skin (lumpy skin), mucous membranes and other organs [14]. Disease can be severe and, in rare cases, lead to the death of the affected animal. An LSDV outbreak in Eastern and South-Eastern Europe in 2016-2017 was controlled by a successful mass vaccination campaign, demonstrating the efficacy of vaccination as a disease control measure [32]. Since 2025, France has experienced an outbreak of lumpy skin disease, as a result of which a stage of the Tour de France was re-routed to avoid an affected area (https://www.letour.fr/en/news/2025/change-to-stage-19-albertville-la-plagne/1331722). The outbreak, initially focussed in Eastern and South-Western France, spread to Spain and Italy before being brought under control by early 2026 (reviewed at beacionbio.org: https://tinyurl.com/nrcf8nh3). As Northern France was unaffected, the risk of windborne incursions of midges into Great Britain from these regions was very low. Vaccination is recommended to control an LSD virus outbreak in Scotland if vaccine is available (see EPIC IV, Deliverable 2.5.4, where Tabanid flies were considered as potential LSD vectors).

9. Vesicular stomatitis virus (VSV)

VSV is a single stranded RNA virus of the Rhabdoviridae family. It infects a variety of animals including cattle, sheep, pigs, horses, donkeys and humans and is a notifiable disease in Scotland (Table 1). Since VSV causes blisters around the mouth and feet which resemble signs of foot and mouth disease [14], laboratory testing is required to confirm infection. It is endemic to South America, Central America and Mexico, and causes outbreaks of disease in North America [33]. In the USA, *C. sonorensis* is the key vector of VSV [34]. *Culicoides* are one of four groups of species which are known to act as biological vectors of VSV alongside blackflies, sandflies, and mosquitoes [34]. The extrinsic incubation period (EIP) is sensitive to temperature for VSV infected *C. sonorensis*. The highest infection rate and number of disseminated infections of VSV was found at 25°C and 30°C for *C. sonorensis* held at a range of temperatures from 20 to 35°C. By comparison, rates of infection were reduced at 20°C, the lowest temperature tested in the experiment [35]. However, there is evidence to suggest that VSV remains infectious below 20°C in C. sonorensis and, anecdotally, that *C. sonorensis* is responsible for VSV transmission on cooler days [35]. Hence, VSV has the potential to cause seasonal outbreaks of disease in temperate regions of Europe, including Scotland, if local midge species are competent vectors.

10. West Nile virus

West Nile virus (WNV) is primarily vectored by mosquitoes. However, WNV has been detected also in *Culicoides* species in the USA [36,37]. Hence, *Culicoides* species may have the potential to bridge WNV from birds to horses even if their role as vectors is likely to be less important than that of mosquitoes.

Number	*Culicoides* vectored pathogen	Notifiable in September 2026 (Yes/No)
1.	Shamonda virus	No
2.	Additional orthobunyavirus	No
3.	African horse sickness	Yes
4.	Avian blood parasites	No
5.	Bovine ephemeral fever virus	No
6.	Bovine leukaemia virus	Yes
7.	Epizootic haemorrhagic disease virus	Yes
8.	Lumpy skin disease virus	Yes
9.	Vesicular stomatitis virus	Yes
10.	West Nile virus	Yes

Table 1. Animal diseases *Culicoides* contribute to, some of which must be notified to the Scottish Government when suspected. See: https://www.gov.scot/collections/animal-diseases-notifiable-and-non-notifiable-diseases/.

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Appendix

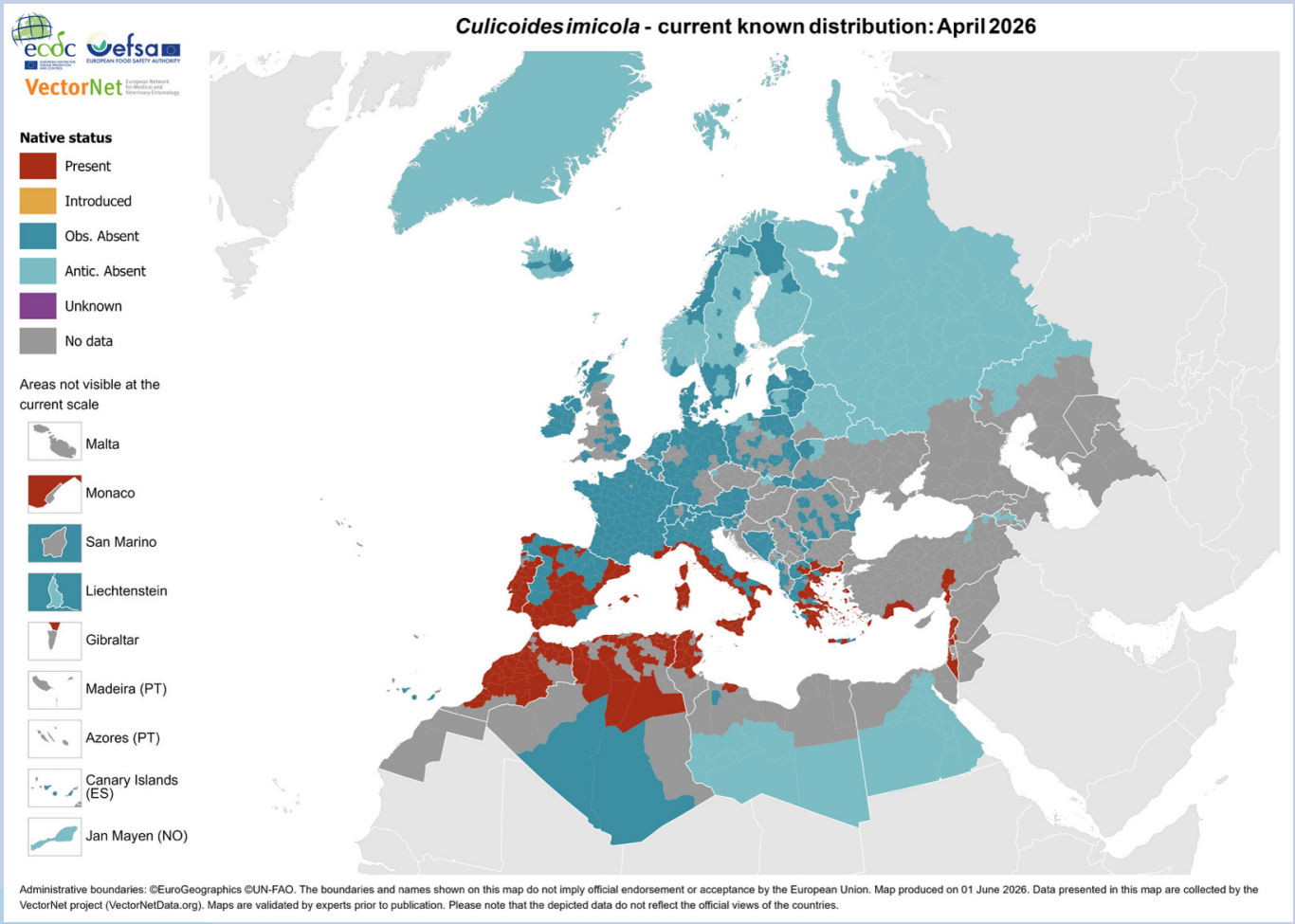

Figure S1. Range of Culicoides imicola in April 2026 (downloaded from: https://www.ecdc.europa.eu/en/publications-data/culicoides-imicola-current-known-distribution-april-2026).

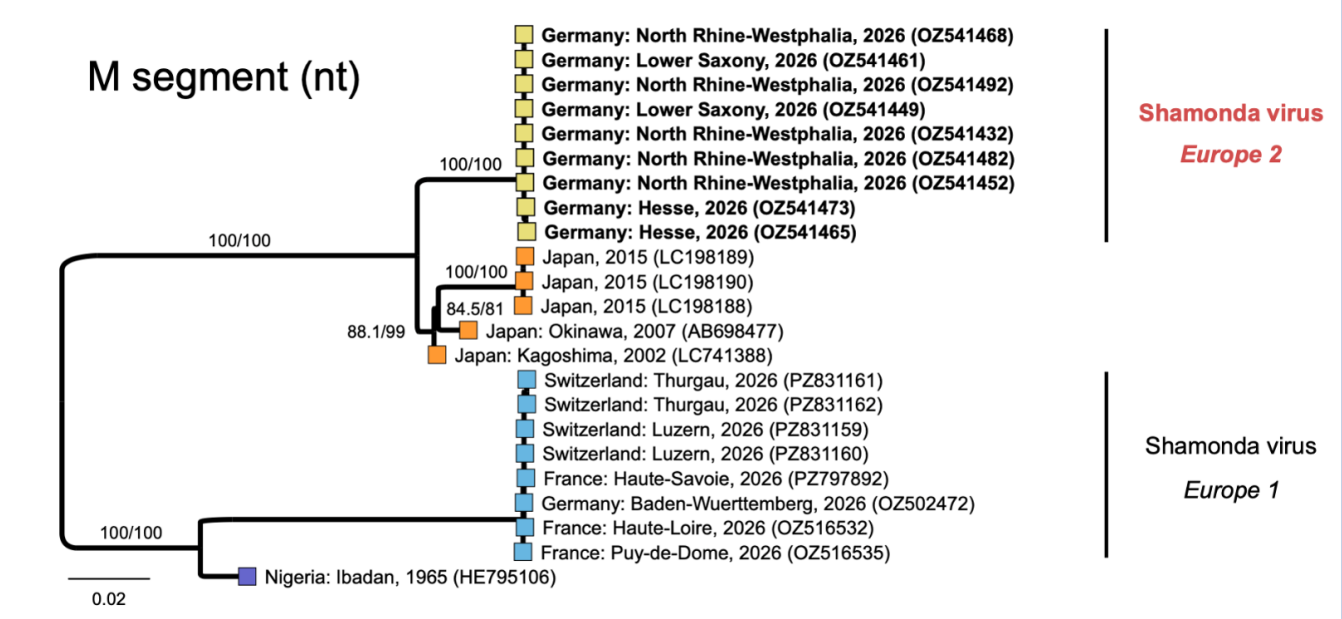

Figure S2. Maximum likelihood phylogeny of the "M" segment of the SHAV genome demonstrating that SHAV-EU1 and SHAV-EU2 are genetically distinct. Adapted from Figure 2B in [7], node numbers reflect 10,000 replicates of Shimodaira-Hasegawa-like approximate likelihood ratio test and ultrafast bootstraps respectively. This phylogeny is corroborated by the "M" segment phylogeny presented in [6].