First Case of Lethal Encephalitis in Western Europe Due to European Bat Lyssavirus Type 1

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Keywords

Encephalitis; European bat lyssavirus type 1; Lyssavirus; Metatranscriptomics; Next Generation Sequencing

Running title

EBLV-1a Lyssavirus lethal Encephalitis

Keypoints

European Bat Lyssavirus type 1 is prevalent in bats in Europe. We present the first human case identified in Western Europe. Unless vaccinated against rabies, the public should avoid direct interactions with bats.

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conceptualisation and methodology: BE, AJ, ML, PP, ME, DS

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49

Abstract

Background

Inaccurate diagnosis of encephalitis is a major issue as immunosuppressive treatments can be deleterious in case of viral infection. The European bat lyssavirus type 1, a virus related to rabies virus, is endemic in European bats. No human case has yet been reported in Western Europe. A 59 year-old patient without specific past medical history died from encephalitis. A colony of bats lived in an outbuilding of his house. No diagnosis was made using standard procedures.

Methods.

We used a Next Generation Sequencing (NGS) based transcriptomic protocol to search for pathogens in autopsy samples (meninges and brain frontal lobe). Results were confirmed by PCR and by antibody testing in serum. Immunochemistry was used to characterize inflammatory cells and viral antigens in brain lesions. Cells and mice were inoculated with brain extracts for virus isolation.

Results

The patient's brain lesions were severe and diffuse in white and gray matter. Perivascular inflammatory infiltrates were abundant and rich in plasma cells. NGS identified European bat lyssavirus type 1a in brain, which was confirmed by PCR. A high titer of neutralizing antibodies was found in serum. No viral antigen was detected and the virus could not be isolated by cell culture or by mouse inoculation.

Conclusions

The patient died from European bat lyssavirus type 1a infection. NGS was key to identifying this unexpected viral etiology in an epidemiological context that did not suggest rabies. People exposed to bats should be strongly advised to be vaccinated with rabies vaccines, which are effective against EBLV-1.

Introduction

Encephalitides are defined by inflammation of the brain parenchyma and are mostly of infectious origin, but the underlying pathogen frequently remains unknown[1]. In addition, inflammation may be associated with autoimmunity (e.g. autoantibodies against neurotransmitter receptors[2]), which is, in some cases, due to an infectious trigger[3]. *In vivo*, blood and cerebrospinal fluid (CSF) based assays, although used routinely for diagnostic purpose, are also associated with poor performance. Although difficult to access, cerebral tissue is the most informative sample in encephalitides[4], while CSF and other clinical samples are surrogates, more readily available in clinical practice. Here, using agnostic metatranscriptomics procedures, we analyzed the brain tissue from a fatal case of encephalitis with unusual pathological features for which a viral etiology was suspected. We found evidence of infection by the European bat lyssavirus type 1a (EBLV-1a), a rabies-related lyssavirus, which widely circulates in some European bats (mainly the common serotine or *Eptesicus serotinus*). This case demonstrates that the risk of bat lyssavirus transmission to human exists in Europe.

Methods

Case history

A 59-year-old patient without specific past medical history was hospitalized in July 2019 for temporal headache, phono- and photophobia, vomiting, dysarthria and swallowing disorders, which had started 3 days earlier. His family reported that he had had asthenia without weight loss or anorexia for a few months. No travel outside France was noted in the previous two years. The patient lived in central France in a rural wooded area. After the cause of the death was established, the family reported that in an outbuilding of his house lived a colony of bats. At admission, physical examination showed mild fever (38.5°C), paralysis of the oculomotor (III), left abducens (VI) and facial (VII) nerves, salivary stasis and dysphonia. No other sensory or motor deficit was noticed. The main clinical and non-clinical

findings are described in Table 1. A few hours after admission, the patient developed an acute coma for which mechanical ventilation was introduced. Suspecting meningoencephalitis, a treatment with acyclovir (800 mg/8h) and amoxicillin (12g/24h) was started. In the two following days, a complete paralysis of all cranial nerves was evidenced associated with the progression to a non-reactive coma and clinical seizures. The electroencephalogram (EEG) showed no status epilepticus under leviteracetam but a poor cerebral activity. Because immune encephalitis was suspected, treatment with intravenous immunoglobulins (32 g/day for 5 days) and steroids (methylprednisolone 1 g/day for 3 days, followed by 2 mg/kg/day) were started. Serial EEG monitoring showed a severe worsening of electrical activity over a few weeks with diffuse theta frequency and delta frequency organization, potentially compatible with necrotizing encephalitis. MRI findings at day 5 and 23 post-admission in the ICU are described in Fig. 1. ICU evolution was characterized by a non-reactive coma without any improvement despite absence of any status epilepticus. Fifty-one days after admission, in the face of persistent coma, the patient died following withdrawal of life-sustaining therapy and an autopsy was performed in accordance with current French regulation, after obtaining informed consent from the patient's family and query of the National Refusal Register (Agence de la Biomedecine).

A full description of pathological findings is presented as Supplementary data. In brief, the brain was edematous. At microscopic examination, the lesions were diffuse, observed in both white and grey matter, and in all of the samples. They were characterized by abundant inflammatory perivascular infiltrates, astrocytic gliosis and microglial activation, in contrast with limited necrosis [Fig. 2]. The perivascular infiltrates were rich in plasma cells [Fig. 2]. The cerebellum was severely damaged with loss of Purkinje cells. The roots of the cranial pairs were atrophic.

Despite the absence of a cytopathogenic effect, including Negri's bodies, the lesions were not evocative of autoimmune encephalitis, but rather suggested a viral origin due to the involvement of both white and grey matter and the spread of plasma cell infiltrates. For this reason, frozen samples were sent to the collaborative diagnostic platform of the Institut Pasteur and Necker Hospital for further analysis aimed at identifying a pathogenic agent.

Post Autopsy Diagnostic Methods We used Next Generation Sequencing (NGS)-based transcriptomic analysis to search for viral transcripts in meninges and brain frontal lobe. This technique is agnostic and provides sequences of both the human transcriptome and pathogen, the latter of which that may be identified by similarity with known microbes. RNA from meninges and brain frontal lobe samples were extracted and used to construct a cDNA library and sequenced using the Illumina technology. Sequences were aligned after translation against a comprehensive viral protein reference database (details in supplementary data). We completed the viral genome gaps by applying standard molecular biology methods (supplementary data). Once the pathogen identified, we used previously described PCRs (Supplementary data and [5–7]) to confirm the presence of virus from necropsy samples and CSF.

Classical reference methods for the *post-mortem* diagnosis of rabies were performed on non-fixed meninges and brain samples. They included antigen detection by the direct fluorescent antibody test (FAT)[8]) and virus isolation with the rapid tissue culture infection test (RTCIT)[9] and the mouse inoculation test (MIT)[10]. Electronic microscopy was conducted as described in Supplementary data.

Detection of neutralizing antibody against rabies virus (RABV, CVS strain) and against rabies-related EBLV-1 lyssavirus (EBLV-1b, strain 8918FRA) was performed by a modified rapid fluorescent focus inhibition test (RFFIT)[11] on serum and CSF samples.

Results

We found sequences in meninges and brain frontal lobe samples covering the quasi-full length of a genome related to EBLV-1a lyssavirus (Genbank accession number MW551946). Based on phylogenetic analysis (Fig. 3), the closest relatives were other EBLV-1a strains from bats identified in France[12]. Based on PCR results, the viral load was around 500-fold higher in the frontal lobe than in meninges. In contrast, no viral RNA was detected in CSF sampled on the day of hospitalization and 34 days later. Immunochemical analyses of multiple paraffin-embedded brain samples using a polyclonal antiserum detecting EBLV-1a was negative, but electronic microscopy suggested the presence of rhabdovirus particles (Supplementary data). Infectious virus was not detected from these samples. A

high titer (1/1200) of antibodies neutralizing EBLV-1 virus was detected in the serum sampled the day of hospitalization, but not detected in the CSF samples collected the same day and 34 days later. These serum antibodies were unable to neutralize RABV.

Discussion

Members of the *Lyssavirus* genus, *Rhabdoviridae* family, are the causative agents of rabies, a progressive viral encephalitis transmitted from infected animals by bites and scratches, or licking of mucous or wounds. Rabies virus (RABV) transmitted by non-flying terrestrial mammals has now disappeared from Western and central Europe following efficient control measures. Various other lyssaviruses, however, still circulate in bats. To date, five different lyssaviruses have been identified in Western Europe: (EBLV-1) hosted by the common serotine *(Eptesicus serotinus)*, European bat lyssavirus type 2 (EBLV-2) in Daubenton's (*Myotis daubentonii*) and pond (*Myotis dasycneme*) bats, the Bokeloh bat lyssavirus (BBLV) in Natterer's bat (*Myotis nattereri*)[13], the Lleida bat lyssavirus (LLEBV) in bent-winged bats (*Miniopterus* schreibersii) (review in[14]) and the Kotalahti bat lyssavirus (KBLV) in Brandt's bat (*Myotis brandtii*) in Finland [15]. EBLV-1 is widely spread in European and North African bat colonies[12,16,17]. Its importance in public health has been raised, as spillovers of EBLV-1 to terrestrial mammals have been described in sheep in Denmark[18], in two cats in France[19], in a stone marten (*Martes foina*) in Germany[20] and in Egyptian fruit bats (*Roussetus aegyptiacus*)[21]. To date, however, only a single human EBLV-1 case (Yuli strain, EBLV-1a lineage[22], occurring in Belgorod, Russia in 1985, has been described, though an earlier one was suspected but not characterized in Voroshilovgrad, Ukraine in 1977[23]. Therefore, the patient described in the present study represents the first identified in Western Europe, more than 35 years after the previous one(s) in Eastern Europe. We provide the first neuropathological description of the panencephalitis caused by the virus, characterized by dense plasmocytic infiltrates.

The lack of detectable viral antigen in brain sections and the failure to isolate live virus are puzzling. Indeed, upon inoculation of mice with the Yuli strain (the only known EBLV-1a human strain), viral

antigens were observed to accumulate in the brain, as is the case for other EBLV-1 strains [24]. Viral detection in natural cases, however, seems to be more challenging. Indeed, fatal encephalitis in cats after natural exposure to EBLV-1 has proven difficult to diagnose, as little if any antigen has been detected by immunofluorescence. Moreover, virus isolation was inefficient or even impossible in cell culture or in mice [19]. Similarly, identification of EBLV-1 antigens and virus isolation from naturally infected sheep and stone martens have also been difficult[18,20]. The absence of virus isolation in our study could have various causes, possibly in relation to the type (meninge and cortex), size or conservation of brain samples, or to sample processing to dilute inhibitors. Likewise, isolation of KBLV has been unsuccessful in cell culture using standard procedures[25]. According to his family, the patient had been suffering from asthenia for several months prior to hospitalization. It is therefore possible that brain neuroinvasion preceded the acute symptoms by several months. The viral load may have become undetectable despite the persistence of viral genomes, considering the additional delay of about two months, due to management in an intensive care unit, between the onset of major symptoms and death. EBLV-1 replication was nevertheless evidenced in the present study by the presence of antibodies neutralizing the virus in serum collected at the onset of symptoms. Antibodies elicited by EBLV-1 infection have little or no capacity to cross-neutralize RABV, as shown both in our study and previously in sheep[18]. Antibodies neutralizing lyssaviruses (RABV) have already been identified in asymptomatic humans exposed to vampire bat bites, which shows that antibody responses can be elicited in case of prolonged incubation times or clearance of the virus[26].

Serotine bats were the most likely hosts responsible in France for human exposure to EBLV-1[27]. Transversal surveys and longitudinal capture-recapture studies have shown that infected bats may remain healthy[28,29] in contrast to earlier findings[30]. Transmission between bats seems to occur mainly by biting and is inefficient per intranasal route[30]. It is reasonable to speculate that the same applies in spillover conditions including transmission to humans. According to his family, the patient had handled a dead or sick bat from the colony living near his house at least on one occasion. The family was unaware of any cases of biting, but this type of event would probably not have been

reported to the family given their unease regarding the accommodation of the bat colony. The entrance to the colony was condemned after the patient's death and any investigation regarding bat species and virological status unfortunately proved impossible.

Inaccurate diagnosis of encephalitis is a major issue as immunosuppressive treatments can be deleterious in case of viral infection. Metranscriptomics NGS was key in identifying this unexpected viral etiology in an epidemiological context that did not suggest rabies, which is an additional demonstration of the efficacy of such techniques when applied to brain tissues in encephalitis cases[31]. The patient had no known comorbidities and in particular was not immunocompromised. Our results suggest that the risk of EBLV-1 transmission to human, even if low, persists and could be higher than previously perceived. Most EBLV-1 cases in bats are probably not detected (69 cases only detected in Western Europe in 2019-2020, eurl-rabies.anses.fr), but surveys indicate that the virus circulates in bat colonies[32–34] and sometimes lead to high mortality[35]. The public should be reminded to avoid direct interactions with bats. In a context where the disappearance of rabies from terrestrial mammals in Western Europe is reducing the frequency of vaccination among professionals exposed to wildlife, people exposed to bats should be strongly incited to be vaccinated with rabies vaccines, which are effective against EBLV-1[36], and their antibody titer regulatory monitored [27] according to national recommendations[37].

Notes

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References

1. Abdullahi AM, Sarmast ST, Singh R. Molecular Biology and Epidemiology of Neurotropic Viruses. Cureus **2020**; 12. Available at: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7485989/. Accessed 22 January 2021.

2. Fukata M, Yokoi N, Fukata Y. Neurobiology of autoimmune encephalitis. Curr Opin Neurobiol **2017**; 48:1–8.

3. Armangue T, Leypoldt F, Málaga I, et al. Herpes simplex virus encephalitis is a trigger of brain autoimmunity. Ann Neurol **2014**; 75:317–323.

4. Brown JR, Bharucha T, Breuer J. Encephalitis diagnosis using metagenomics: application of next generation sequencing for undiagnosed cases. J Infect **2018**; 76:225–240.

5. Dacheux L, Larrous F, Lavenir R, et al. Dual Combined Real-Time Reverse Transcription Polymerase Chain Reaction Assay for the Diagnosis of Lyssavirus Infection. PLoS Negl Trop Dis **2016**; 10:e0004812.

6. Rupprecht CE, Fooks AR, abel-Ridder B. Rabies real-time reverse transcriptase polymerase chain reaction. In: Laboratory techniques in rabies. geneva: : 17–34.

7. Dacheux L, Reynes J-M, Buchy P, et al. A reliable diagnosis of human rabies based on analysis of skin biopsy specimens. Clin Infect Dis Off Publ Infect Dis Soc Am **2008**; 47:1410–1417.

8. Rupprecht CE, Fooks AR. WHO. The direct fluorescent antibody test. 2018: 108–129.

9. Dacheux L, Bourhy H. Virus isolation in cell culture, the rapid tissue culture inoculation test (RTCIT). In: Current Laboratory Techniques in Rabies Diagnosis, Research, and Prevention. 2015: 25–31.

10. Rupprecht CE, Fooks AR, abel-Ridder B. WHO. Virus isolation in animals: the mouse inoculation test. In: Laboratory techniques in rabies. Geneva: 2018: 74–84.

11. Fooks AR, Abela-Ridder B, Fooks AR. Laboratory techniques in rabies. **2018**; 1:215.

12. Troupin C, Picard-Meyer E, Dellicour S, et al. Host Genetic Variation Does Not Determine Spatio-Temporal Patterns of European Bat 1 Lyssavirus. Genome Biol Evol **2017**; 9:3202–3213.

13. Eggerbauer E, Troupin C, Passior K, et al. The Recently Discovered Bokeloh Bat Lyssavirus: Insights Into Its Genetic Heterogeneity and Spatial Distribution in Europe and the Population Genetics of Its Primary Host. Adv Virus Res **2017**; 99:199–232.

14. Shipley R, Wright E, Selden D, et al. Bats and Viruses: Emergence of Novel Lyssaviruses and Association of Bats with Viral Zoonoses in the EU. Trop Med Infect Dis **2019**; 4.

15. Nokireki T, Tammiranta N, Kokkonen U-M, Kantala T, Gadd T. Tentative novel lyssavirus in a bat in Finland. Transbound Emerg Dis **2018**; 65:593–596.

16. Serra-Cobo J, López-Roig M, Lavenir R, et al. Active sero-survey for European bat lyssavirus type-1 circulation in North African insectivorous bats. Emerg Microbes Infect **2018**; 7:213.

17. Leopardi S, Priori P, Zecchin B, et al. Active and passive surveillance for bat lyssaviruses in Italy revealed serological evidence for their circulation in three bat species. Epidemiol Infect **2018**; :1–6.

18. Tjørnehøj K, Fooks AR, Agerholm JS, Rønsholt L. Natural and experimental infection of sheep with European bat lyssavirus type-1 of Danish bat origin. J Comp Pathol **2006**; 134:190–201.

19. Dacheux L, Larrous F, Mailles A, et al. European bat Lyssavirus transmission among cats, Europe. Emerg Infect Dis **2009**; 15:280–284.

20. Müller T, Cox J, Peter W, et al. Spill-over of European bat lyssavirus type 1 into a stone marten (Martes foina) in Germany. J Vet Med B Infect Dis Vet Public Health **2004**; 51:49–54.

21. Wellenberg GJ, Audry L, Rønsholt L, van der Poel WHM, Bruschke CJM, Bourhy H. Presence of European bat lyssavirus RNas in apparently healthy Rousettus aegyptiacus bats. Arch Virol **2002**; 147:349–361.

22. Amengual B, Whitby JE, King A, Cobo JS, Bourhy H. Evolution of European bat lyssaviruses. J Gen Virol **1997**; 78 (Pt 9):2319–2328.

23. Kuzmin IV, Botvinkin AD, Poleschuk EM, Orciari LA, Rupprecht CE. Bat rabies surveillance in the former Soviet Union. Dev Biol **2006**; 125:273–282.

24. Eggerbauer E, Pfaff F, Finke S, et al. Comparative analysis of European bat lyssavirus 1 pathogenicity in the mouse model. PLoS Negl Trop Dis **2017**; 11:e0005668.

25. Calvelage S, Tammiranta N, Nokireki T, et al. Genetic and Antigenetic Characterization of the Novel Kotalahti Bat Lyssavirus (KBLV). Viruses **2021**; 13.

26. Gilbert AT, Petersen BW, Recuenco S, et al. Evidence of Rabies Virus Exposure among Humans in the Peruvian Amazon. Am J Trop Med Hyg **2012**; 87:206–215.

27. Parize P, Travecedo Robledo IC, Cervantes-Gonzalez M, et al. Circumstances of Human-Bat interactions and risk of lyssavirus transmission in metropolitan France. Zoonoses Public Health **2020**; 67:774–784.

28. Robardet E, Borel C, Moinet M, et al. Longitudinal survey of two serotine bat (Eptesicus serotinus) maternity colonies exposed to EBLV-1 (European Bat Lyssavirus type 1): Assessment of survival and serological status variations using capture-recapture models. PLoS Negl Trop Dis **2017**; 11:e0006048.

29. Vázquez-Morón S, Juste J, Ibáñez C, et al. Endemic circulation of European bat lyssavirus type 1 in serotine bats, Spain. Emerg Infect Dis **2008**; 14:1263–1266.

30. Freuling C, Vos A, Johnson N, et al. Experimental infection of serotine bats (Eptesicus serotinus) with European bat lyssavirus type 1a. J Gen Virol **2009**; 90:2493–2502.

31. Seilhean D. Infections of the central nervous system: Neuropathology. Rev Neurol (Paris) **2019**; 175:431–435.

32. Schatz J, Ohlendorf B, Busse P, et al. Twenty years of active bat rabies surveillance in Germany: a detailed analysis and future perspectives. Epidemiol Infect **2014**; 142:1155–1166.

297 33. Serra-Cobo J, López-Roig M, Seguí M, et al. Ecological Factors Associated with European Bat
298 Lyssavirus Seroprevalence in Spanish Bats. PLOS ONE **2013**; 8:e64467.

299 34. López-Roig M, Bourhy H, Lavenir R, Serra-Cobo J. Seroprevalence dynamics of European bat
300 lyssavirus type 1 in a multispecies bat colony. Viruses **2014**; 6:3386–3399.

301 35. Picard-Meyer E, Servat A, Wasniewski M, Gaillard M, Borel C, Cliquet F. Bat rabies surveillance
302 in France: first report of unusual mortality among serotine bats. BMC Vet Res **2017**; 13:387.

303 36. Brookes SM, Parsons G, Johnson N, McElhinney LM, Fooks AR. Rabies human diploid cell
304 vaccine elicits cross-neutralising and cross-protecting immune responses against European and
305 Australian bat lyssaviruses. Vaccine **2005**; 23:4101–4109.

306 37. HCSP. Vaccinations contre la rage et prophylaxie post-exposition. Recommandations. Paris:
307 Haut Conseil de la Santé Publique, 2013. Available at:
308 https://www.hcsp.fr/explore.cgi/avisrapportsdomaine?clefr=316. Accessed 29 January 2021.

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Figure legends

Figure 1: Representative images of MRI scans at 5 and 23 days of ICU admission

At day 5, Fluid Attenuated Inversion Recovery (FLAIR) transverse images showed an apparently normal cerebellum (A) whereas a well demarcated zone of high intensity was visible at the bottom of the pons (B). At that stage, the thalamus and caudate nucleus were slightly hyperintense bilaterally (C) and the other part of the brain seemed normal (D). At day 23, there was an obvious edema of the cerebellum (E) and the high intensity signal of the pons had diffused to the dentate nucleus of cerebellum bilaterally (F). The brain was overtly swollen with an increased high intensity signal of the lenticular nuclei and insula (G). This high intensity signal seemed to have diffused to the whole brain (H).

Figure 2: Histopathology of necropsy samples

Abundant inflammatory perivascular infiltrate in the caudate nucleus (a: hematoxylin eosin staining, x10), composed of T CD3+ and B CD20 + lymphocytes, among which a high number of large plasma cells (b: hematoxylin eosin staining, x400). Astrocytic gliosis, microglial activation, and neuronal loss in the caudate nucleus (c: hematoxylin eosin staining, x400). Atrophy of a nerve root in the medulla oblongata (d: hematoxylin eosin staining x100). Immunohistochemistry against rabies was negative (e: caudate nucleus, x200) whereas the cerebral cortex of a rabid patient was positive (f: cerebral cortex x200).

Figure 3: Phylogenetic analysis

Phylogenetic tree based on full-genome sequences of representatives of the lyssavirus species belonging to the Phylogroup I. Clades are collapsed into triangles representative of species diversity. The sequence of Hum1_FRA clusters into the clade EBLV1-a.

Table 1: Main clinical and non-clinical findings

Physical examination	**Imaging**	**Biology**
Paralysis of the oculomotor (III), left abducens (VI) and facial (VII) nerves Salivary stasis Dysphonia	CT scan: normal MRI: hyperintensity at the posterior part of the pons on the axial Fluid Attenuated Inversion Recovery (FLAIR) sequence	CSF: turbid liquid with 26 WBC/mm^3 (84% lymphocytes), high protein (1.43 g/l) and normal glucose level Gram stain and multiplex PCR (Meningitidis/encephalitis panel, FilmArray Biomérieux, Marcy l'Etoile) negative. Immune encephalitis screening negative (anti-aquaporin-4 antibody, anti-MOG and antineuronal antibodies)

Figure 1

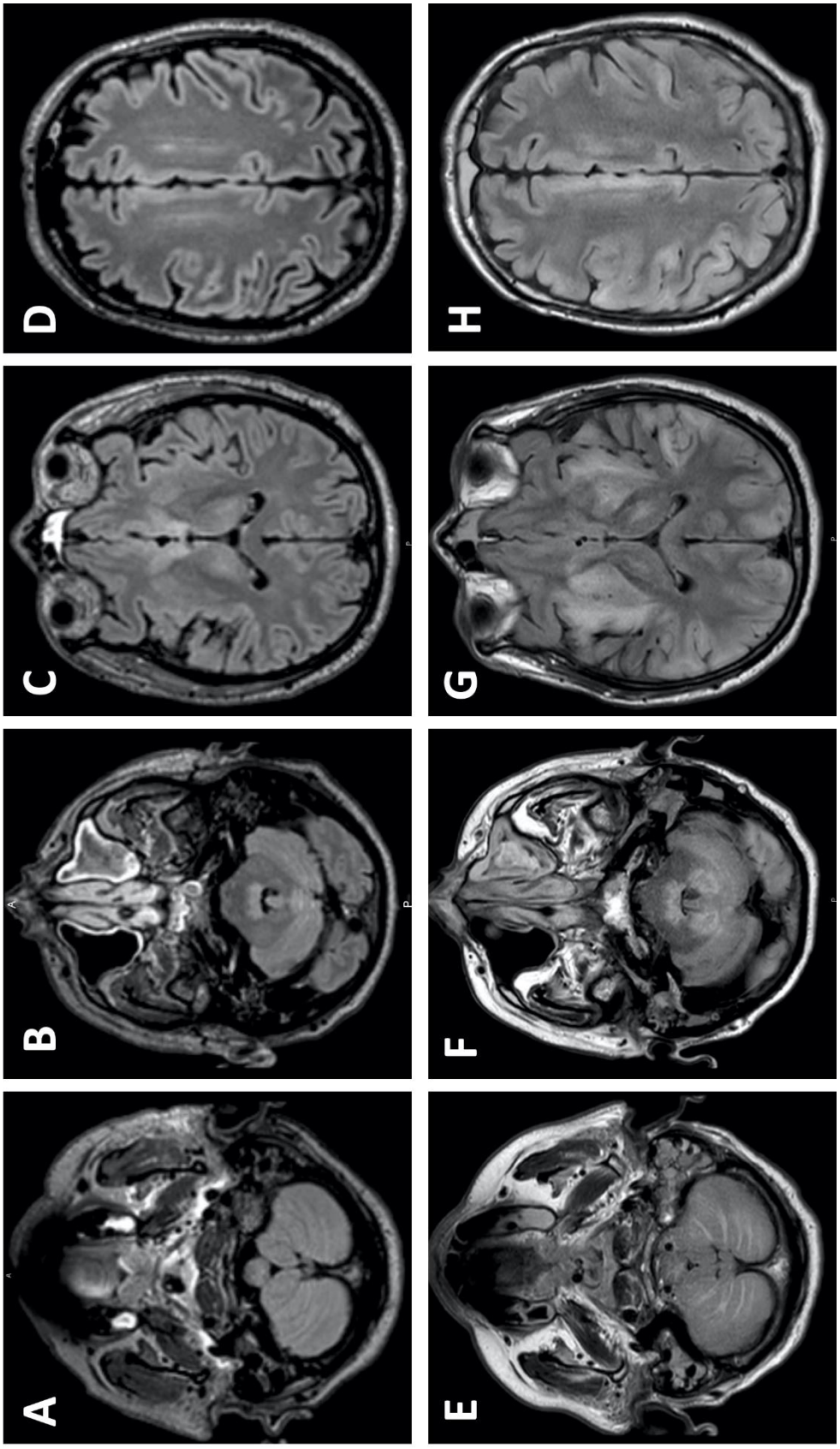


Figure 2

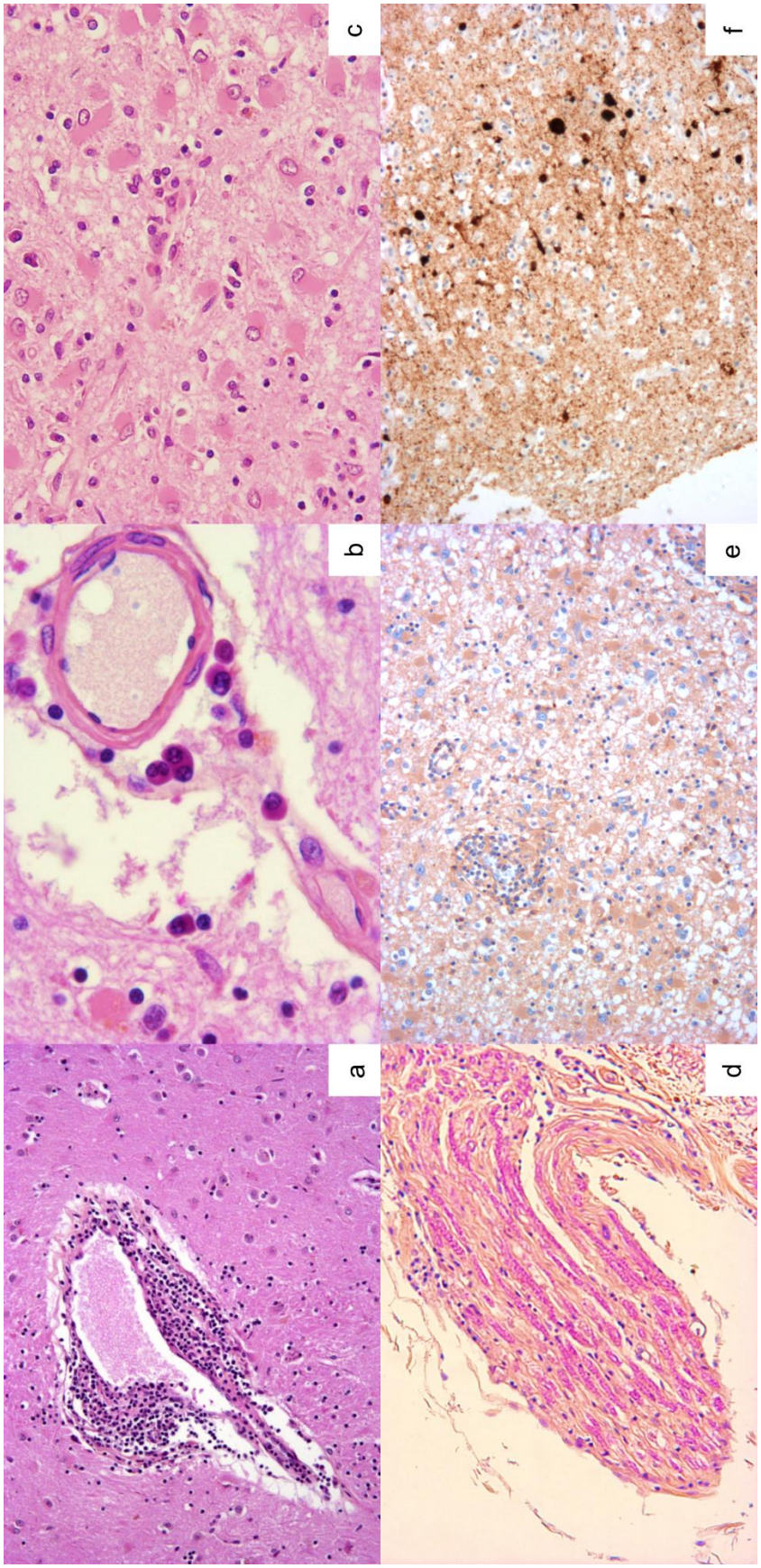
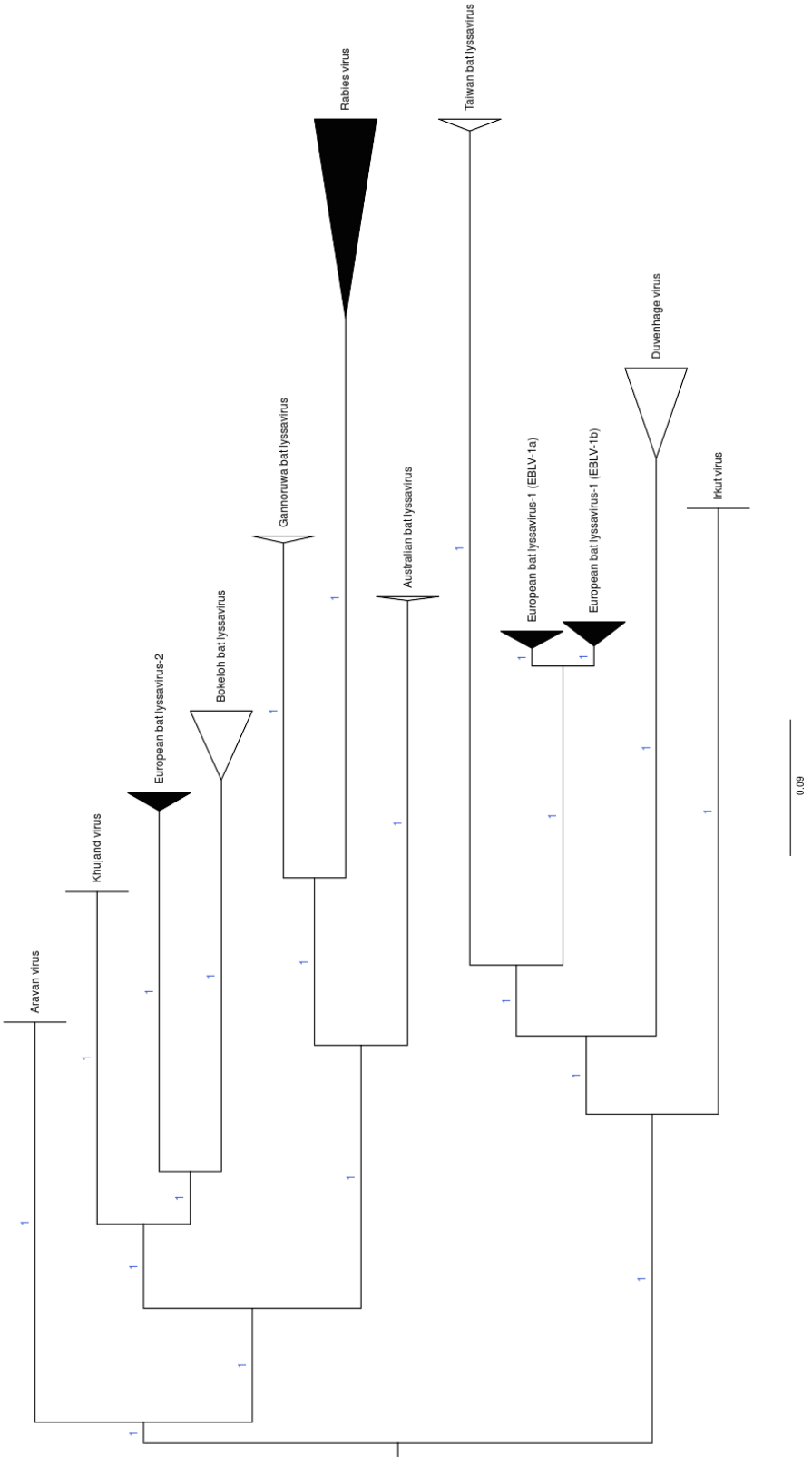


Figure 3


Rabies virus
Taiwan bat lyssavirus
Duvenhage virus
Gannoruwa bat lyssavirus
Australian bat lyssavirus
European bat lyssavirus-1 (EBLV-1a)
European bat lyssavirus-1 (EBLV-1b)
Irkut virus
Bokeloh bat lyssavirus
European bat lyssavirus-2
Khujand virus
Aravan virus
0.09

Supplementary material

METHODS

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METHODS

Metatranscriptomics

Nucleic acids from meninges and brain frontal lobe samples were extracted after a bead-beating step with the MagNA Lyser using the MagNA Pure Compact RNA Isolation kit (Roche Molecular Systems, Inc.) including a DNase treatment. Total RNA was used to construct a cDNA library with the SMARTer Stranded Total RNA-Seq Kit - Pico Input Mammalian (Takara Bio, kit v.2).

A total of 49 and 94 raw million reads of 150 bp for meninges and frontal lobe sample respectively were processed with an agnostic in-house bioinformatics pipeline as described[1]. Sequences were aligned after translation against a viral protein reference comprehensive database (RVDB-prot.V20.0)[2]. Ninety percent coverage of the genome was obtained by NGS from the frontal lobe sample.

Reverse-transcription

Reverse-transcription was carried out using the SuperScript IV First-Strand Synthesis System kit (Invitrogen) according to the manufacturer's instructions with random primers, 440 ng RNA input for the brain frontal lobe sample and 316 ng RNA input for the meninges sample.

Extraction of nucleic acids from CSFs

Each CSF (July, August) was mixed with ATL buffer and DX reagent into a Pathogen Lysis Tube L (QIAGEN). Bead beating was carried out twice 60 sec at full speed with 1 min resting time on ice on Minilys (Bertin). Linear acrylamide (Ambion), Proteinase K and VXL buffer (INDICAL Bioscience) were added to CSF after the bead beating step, and incubated at room temperature for 15 min. Lysate was transferred into a QIAamp mini column (INDICAL Bioscience) and purified according to the manufacturer's instructions, with a DNase treatment on the column after the binding step. Purified RNA was eluted into 50 µL of elution buffer.

Quantitative PCR

qPCR was performed in SybrGreen technology using FastStart Essential DNA Green Master kit (Roche Diagnostic) with 45 cycles of amplification, specific primers at 0.5 µM final concentration and 1 µL of cDNA. Four sets of primers were used to detect viruses [Table S1]. Each reaction was run in duplicate on a LightCycler® 96 instrument (Roche Diagnostic). Results were normalized using the human beta-actin housekeeping gene.

Table S1. List of primers used in quantitative PCR

Primer	Sequence (5' => 3')	Region	Size	Reference
EBLV1-G-F	TGA TAA CAG AGG CAG AGA CC	G	317 pb	this study
EBLV1-G-R	ACA ACA TAT GGC ACT CGG			
EBLV1-N-F	ACC AAT GTG GCA GAT AGA ATG G	N	315 pb	
EBLV1-N-R	TCT TCC TCG AAG TTC TTG TGG			
1671 P_2F	CTG AGG ATA TTA AGA GGC TCA	P	686 pb	3
2357 P_2R	GCC YAR TTT CGC CGA ATT GAC			
4712 GL_2F	ATA TCT GTG CTT GCC CTT CT	G-L	763 pb	
5475 GL_2R	CCA CCG GAT CAT CGT AAA CC			

Genome Finishing

Complete genome was obtained by conventional PCR using Phusion high fidelity DNA polymerase (Thermo Fischer Scientific FINNZYMES). Primers were designed according to our NGS sequences and a 45 cycles of amplification round was performed. The end of 5'UTR anti-genome region was obtained by RACE-PCR using 5'/3' RACE Kit 2nd Generation (Roche). After running into a 2 % agarose gel, amplicons were purified by NucleoSpin Gel & PCR Clean-up kit (Macherey-Nagel) and sequenced by Sanger sequencing.

Nested PCR

For testing CSFs, a nested PCR was performed using Phusion high fidelity enzyme kit (Thermo Fischer Scientific FINNZYMES) and sets primers [Table 2]. Thermal Cycling conditions were as follows : first round PCR at 98°C for 30 s, 45 cycles at 98°C for 15 s, annealing temperature according to the Tm of primers for 30 s and 72°C for 1min, then a final extension at 72°C for 7 min. Second round PCR was performed in the same conditions with *annealing temperature* according to primers' Tm.

Table S2. List of primers used in PCR

Primer	Sequence (5' => 3')	Tm	Tm for PCR	Region	Size	Reference
1617 P_1F	TGG AGG ATA GTC AAG CCC AC	59 °C	52 °C	P	769 bp	3
2386 P_1R	TAT CTG TTK ARA TCA TCTY GC	53 °C				
1671 P_2F	CTG AGG ATA TTA AGA GGC TCA	56 °C	54 °C	P	686 bp	
2357 P_2R	GCC YAR TTT CGC CGA ATT GAC	60 °C				
4633 GL_1F	TCA CCT TCC AGA CAC CCA	56 °C	55 °C	G-L	896 bp	
5502 GL_1R	TCA GGT CTG CTT CTG GCT CA	59 °C				
4712 GL_2F	ATA TCT GTG CTT GCC CTT CT	55 °C	54 °C	G-L	763 bp	
5475 GL_2R	CCA CCG GAT CAT CGT AAA CC	59 °C				

Immunochemistry

The immunostaining was performed by an automate (Ventana BenchMark Stainer, Roche). The biotinylated secondary antibody was included in the detection kit (Ventana Medical Systems Basic DAB Detection Kit 250-001). The streptavidin–biotin-peroxidase complex was revealed by diaminobenzidine. Antibodies used for immunohistochemistry and pretreatments are listed in the table S3.

Table S3: Immunohistochemical methods.

Antigen	Poly/monoclonal	Producer	Immunogen	Clone	Pretreatment	Dilution	Incubation Time (minutes)
CD163	Monoclonal (mouse)	Cell Marque®	Acute phase-regulated transmembrane protein on monocytes	MRQ-26	CC1	1:50	32
CD20	Monoclonal (mouse)	Dako®	Transmembrane protein expressed on B cells	L26	CC1	1:100	32
CD3	Monoclonal (rabbit)	Ventana®	Epsilon chain of the human CD3	2GV6	CC1	prediluted	32
CD4	Monoclonal (mouse)	Dako®	T helper cells	4B12	CC1	1:40	60
CD8	Monoclonal (mouse)	Dako®	Suppressor/cytotoxic T cells	C8/144B	CC1	prediluted	32
GFAP	Monoclonal (mouse)	Dako®	Glial Fibrillary Acidic Protein	6F2	CC1	1:500	28
CMV	Monoclonal (mouse)	Agilent©	Early nuclear protein	CCH2 + DDG9	protease	1:50	32
HSV1	Monoclonal (mouse)	Cell Marque®	Nuclear proteins	10A3	CC1	prediluted	32
VZV	Monoclonal (mouse)	Monosan®		7 clone cocktail (SG1-1, SG1-SG4, NCP-1, IE-62)	CC1	prediluted	32
Measles	Polyclonal (rabbit)	Diagomics ©	Fusion protein		CC1	1:100	60
Rabies	Polyclonal (rabbit)	Biorad	Rabies virus nucleocapsid	3572112	CC2	1:100	92

CC1, a proprietary high pH (=8) buffer; CC2, a proprietary low pH (=6) buffer.

Transmission electron microscopy

Samples from brain stored during several months after autopsy were taken from macroscopically abnormal areas of the white matter. These samples were fixed in 2.5% glutaraldehyde in 0.05 M sodium cacodylate

buffer, post-fixed in 1% osmium tetroxide and embedded in epoxy resin. Ultrathin sections were stained with uranyl acetate and lead citrate and were examined using a JEOL (Flash 1400) electron microscope at 120 KeV.

Phylogenetic analyses

Phylogenetic analyses were performed using NGPhylogeny.fr[4] . The glycoprotein complete CDS of the French EBLV1a sequence (Hum1_FRA) was aligned along with 91 other representative sequences of sublineages *EBLV1a* and *EBLV1b* using MAFFT (Multiple Alignment using Fast Fourier Transform) aligner with default parameters. Tree inferences were constructed with PhyML using approximate Bayes branch supports. The phylogenetic tree was visualised by using FigTree (version 1.4.4).

SUPPLEMENTARY PATHOLOGICAL DATA

The brain was edematous (1575 grams). There was no herniation, atrophy or focal lesion. After formalin fixation, sampling and paraffin embedding, 5 µm thick sections were stained with hematoxylin and eosin. Additional immunohistochemistry analyses were performed (as described in Supplementary methods). At microscopic examination, the lesions were diffuse, observed in both white matter and grey matter, and in all the samples. They were characterized by abundant inflammatory perivascular infiltrates, astrocytic gliosis, microglial activation, contrasting with few necrosis [Fig. 2]. Lymphoid cells in the leptomeningeal space were relatively few in number, contrasting with the abundance of perivascular intra-parenchymal infiltrates. The latter were composed of T and B lymphocytes, among which a high number of large plasma cells [Fig. 2]. There was no noticeable imbalance between the number of CD8 and CD4 T lymphocytes.

The cerebellum was one of the most severely damaged region with white matter pallor, axonal loss and astrocytic gliosis. There was a loss of Purkinje cells associated with hyperplasia of the Bergmann glia. In the brainstem, the perivascular infiltrates were abundant. The roots of the cranial pairs were atrophic. The *substantia nigra* and *locus cœruleus* were relatively spared.

In the supra-tentorial area, the lesions were also diffuse, affecting white and gray matters with a predominance in the cortical and striatal gray matter. The lesions were necrotic in the occipital region. A spongy state was observed in the visual cortex, in temporal region and in the head of the caudate nucleus. Elsewhere, diffuse microglial activation was associated with neuronal loss and astrocytic gliosis. Perivascular inflammatory infiltrates were abundant and rich in plasma cells [Fig. 2]. Examination of the Ammon's horns showed neuronal rarefaction without necrosis. The thalamus and the mammillary body appeared to be spared. Cytopathogenic effect, including Negri's bodies, was not seen. Immunohistochemistry against herpes simplex virus 1, varicella-zoster, cytomegalovirus, measles virus, and rabies virus were negative.

SUPPLEMENTARY TABLES

Table S4. List of Accession numbers, lineage, Date of isolation, Country of isolation

Accession number	Sublineage	Isolate	Country of isolation	City of isolation	Date of isolation	Source	Host
KF155003.1	EBLV-1a	RV20	Denmark	Køge	1986	-	Eptesicus serotinus
MF187802.1	EBLV-1a	02016DEN	Denmark	Janderup	2002	Mouse	Eptesicus serotinus
MF187803.1	EBLV-1a	03002FRA	France	Chemellier	30/01/2003	Original brain	Eptesicus serotinus
MF187809.1	EBLV-1a	08120FRA	France	Fontenay-le-Comte	15/01/2008	Original brain	Eptesicus serotinus
MF187811.1	EBLV-1a	09034FRA	France	Dignac	16/09/2009	Original brain	Eptesicus serotinus
MF187821.1	EBLV-1a	122938	France	Guéret	26/08/2002	Mouse	Eptesicus serotinus
MF187823.1	EBLV-1a	123801	France	Carmaux	22/10/2003	Original brain	Eptesicus serotinus

MF187824.1	EBLV-1a	124193	France	Guéret	29/06/2004	Original brain	Eptesicus serotinus
MF187826.1	EBLV-1a	124489	France	Vaux sur Mer	13/09/2004	Mouse	Eptesicus serotinus
MF187831.1	EBLV-1a	128210	France	Le Haillan	04/09/2008	Original brain	Eptesicus serotinus
MF187840.1	EBLV-1a	129051	France	La Crèche	24/08/2010	Original brain	Eptesicus serotinus
MF187841.1	EBLV-1a	129055	France	Rochefort sur Mer	27/08/2010	Mouse	Eptesicus serotinus
MF187843.1	EBLV-1a	129090	France	Champagne	04/10/2010	Mouse	Eptesicus serotinus
MF187855.1	EBLV-1a	130904	France	Clisson	18/05/2015	Mouse	Eptesicus serotinus
MF187856.1	EBLV-1a	131054	France	Chenommet	06/02/2015	Mouse	Eptesicus serotinus
EU626552.1	EBLV-1a	07240FRA	France	Fontenay-le-Comte	2007	cat	cat
LT839610.1	EBLV-1a	976	Germany	-	1992	-	Pipistrellus nathusii
LT839611.1	EBLV-1a	5782	Germany	-	2001	-	unknown
LT839614.1	EBLV-1a	5776	Germany	-	2001	-	unknown
LT839615.1	EBLV-1a	13454	Germany	-	2000	-	Eptesicus serotinus
MF187865.1	EBLV-1a	9395GER	Germany	Hamburg	1968	Mouse	Eptesicus serotinus
MF187866.1	EBLV-1a	9396GER	Germany	Rostock	1985	Mouse	Eptesicus serotinus
MF187868.1	EBLV-1a	9399GER	Germany	Bremerhaven	1982	Mouse	Eptesicus serotinus
MF187873.1	EBLV-1a	9436GER	Germany	Stade	18/09/1986	Mouse	Eptesicus serotinus
MF187874.1	EBLV-1a	9438GER	Germany	Neumunster	août-88	Mouse	Eptesicus serotinus
MF187875.1	EBLV-1a	9440GER	Germany	Brauschweig	24/07/1989	Mouse	Eptesicus serotinus
MF187877.1	EBLV-1a	9477GER	Germany	Nienburg	28/08/1986	Mouse	Eptesicus serotinus
MF187860.1	EBLV-1a	9366HOL	Netherlands	Goor	17/06/1992	Mouse	Eptesicus serotinus
MF187871.1	EBLV-1a	94116HOL	Netherlands	Jubbega	14/08/1987	Mouse	Eptesicus serotinus
MF187878.1	EBLV-1a	9478HOL	Netherlands	Rolde	27/08/1987	Mouse	Eptesicus serotinus
MF187879.1	EBLV-1a	9480HOL	Netherlands	Bellingwolde	16/07/1987	Mouse	Eptesicus serotinus
MF187858.1	EBLV-1a	8615POL	Poland	Gdansk	1985	Mouse	Eptesicus serotinus
MF187864.1	EBLV-1a	9394POL	Poland	Ketrzyn	1990	Mouse	Eptesicus serotinus
LT839613.1	EBLV-1a	13027	Russia	-	1982	human	-
MF187867.1	EBLV-1a	9397RUS	Russia	Belgorod	1985	Mouse	Eptesicus serotinus
MF187801.1	EBLV-1a	01018SLO	Slovakia	Presov	08/02/2001	Mouse	Eptesicus serotinus
MF187876.1	EBLV-1a	9443UKR	Ukraine	Volyn Region	août-87	Mouse	Eptesicus serotinus
MF187804.1	EBLV-1b	04032FRA	France	Bourges	10/09/2004	Original brain	Eptesicus serotinus
MF187805.1	EBLV-1b	05001FRA	France	Souesmes	17/05/2005	Original brain	Eptesicus serotinus
MF187806.1	EBLV-1b	06001FRA	France	Ourches-sur-Meuse	16/05/2006	Original brain	Eptesicus serotinus
MF187807.1	EBLV-1b	06002FRA	France	Bourges	08/06/2006	Original brain	Eptesicus serotinus
MF187808.1	EBLV-1b	07058FRA	France	Sainte Mélaine	25/05/2007	Original brain	Eptesicus serotinus
MF187810.1	EBLV-1b	08341FRA	France	Aillant-sur-Tholon	25/09/2008	Original brain	Eptesicus serotinus
MF187812.1	EBLV-1b	78983	France	Bainville sur Madon	04/10/1989	Mouse	Eptesicus serotinus
MF187813.1	EBLV-1b	107251	France	Bourges	16/10/1995	Original brain	Eptesicus serotinus
MF187814.1	EBLV-1b	113852	France	Champigneulles	14/03/1997	Original brain	Eptesicus serotinus
MF187815.1	EBLV-1b	116883	France	Morlaix	18/03/1998	Original brain	Eptesicus serotinus
MF187816.1	EBLV-1b	120914	France	Plouneour-Menez	27/03/2000	Original brain	Eptesicus serotinus
MF187817.1	EBLV-1b	121411	France	Fouesnant	25/09/2000	Mouse	Eptesicus serotinus
MF187818.1	EBLV-1b	121633	France	Joinville	13/12/2000	Original brain	Eptesicus serotinus
MF187819.1	EBLV-1b	122154	France	Waville	22/08/2001	Mouse	Eptesicus serotinus
MF187820.1	EBLV-1b	122319	France	Vallon en Sully	28/09/2001	Original brain	Eptesicus serotinus
MF187822.1	EBLV-1b	123008	France	Lurcy Levis	06/09/2002	Mouse	Eptesicus serotinus
MF187825.1	EBLV-1b	124345	France	Guénin	19/08/2004	Original brain	Eptesicus serotinus
MF187827.1	EBLV-1b	126669	France	Arradon	27/10/2005	Mouse	Eptesicus serotinus
MF187828.1	EBLV-1b	127051	France	Crosses	12/07/2006	Mouse	Eptesicus serotinus
MF187829.1	EBLV-1b	127834	France	Bourges	13/11/2007	Original brain	Eptesicus serotinus

MF187830.1	EBLV-1b	127835	France	Bourges	13/11/2007	Original brain	Eptesicus serotinus
MF187832.1	EBLV-1b	128633	France	Ancy sur Moselle	30/06/2009	Original brain	Eptesicus serotinus
MF187833.1	EBLV-1b	128635	France	Ancy sur Moselle	30/06/2009	Original brain	Eptesicus serotinus
MF187834.1	EBLV-1b	128637	France	Ancy sur Moselle	30/06/2009	Original brain	Eptesicus serotinus
MF187835.1	EBLV-1b	128665	France	Ancy sur Moselle	07/07/2009	Original brain	Eptesicus serotinus
MF187836.1	EBLV-1b	128681	France	Ancy sur Moselle	13/07/2009	Original brain	Eptesicus serotinus
MF187837.1	EBLV-1b	128683	France	Mars la Tour	17/07/2009	Original brain	Eptesicus serotinus
MF187838.1	EBLV-1b	128708	France	Lure	31/07/2009	Original brain	Eptesicus serotinus
MF187839.1	EBLV-1b	128827	France	Bourges	23/10/2009	Original brain	Eptesicus serotinus
MF187842.1	EBLV-1b	129087	France	Recologne	24/09/2010	Original brain	Eptesicus serotinus
MF187844.1	EBLV-1b	129116	France	Sécheval	08/10/2010	Original brain	Eptesicus serotinus
MF187845.1	EBLV-1b	129123	France	Guingamp	12/10/2010	Original brain	Eptesicus serotinus
MF187846.1	EBLV-1b	129246	France	Monceaux le Comte	29/04/2011	Original brain	Eptesicus serotinus
MF187847.1	EBLV-1b	129290	France	Jouet sur l'Aubois	24/05/2011	Original brain	Eptesicus serotinus
MF187848.1	EBLV-1b	129394	France	Pagny-sur-Moselle	27/07/2011	Mouse	Eptesicus serotinus
MF187849.1	EBLV-1b	129396	France	Billy sous les Côtes	28/07/2011	Mouse	Eptesicus serotinus
MF187850.1	EBLV-1b	129409	France	Pagny-sur-Moselle	09/08/2011	Original brain	Eptesicus serotinus
MF187851.1	EBLV-1b	129428	France	Belleville sur Meuse	12/08/2011	Original brain	Eptesicus serotinus
MF187852.1	EBLV-1b	130544	France	Saint-Martin-d'Auxigny	03/06/2014	Mouse	Eptesicus serotinus
MF187853.1	EBLV-1b	130576	France	Nexon	10/09/2014	Mouse	Eptesicus serotinus
MF187854.1	EBLV-1b	130662	France	Cour-Cheverny	24/06/2014	Mouse	Eptesicus serotinus
MF187857.1	EBLV-1b	15007FRA	France	Gouvieux	04/06/2015	Original brain	Eptesicus serotinus
MF187859.1	EBLV-1b	8918FRA	France	Briey	11/09/1989	Original brain	Eptesicus serotinus
MF187861.1	EBLV-1b	9367HOL	Netherlands	Wassenaar	10/07/1992	Mouse	Eptesicus serotinus
MF187862.1	EBLV-1b	9376HOL	Netherlands	Moerkapelle	08/06/1993	Mouse	Eptesicus serotinus
MF187863.1	EBLV-1b	9377HOL	Netherlands	Apeldoorn	08/06/1993	Mouse	Eptesicus serotinus
MF187869.1	EBLV-1b	94113HOL	Netherlands	Schagen	20/07/1989	Mouse	Eptesicus serotinus
MF187870.1	EBLV-1b	94115HOL	Netherlands	Bovenkarspel	17/08/1989	Mouse	Eptesicus serotinus
KP241939.1	EBLV-1b	RV2416	Spain	Granada	2007	Mouse	Eptesicus isabellinus
MF187872.1	EBLV-1b	94285SPA	Spain	Granada	sept-94	Mouse	Eptesicus serotinus
MF187880.1	EBLV-1b	9483SPA	Spain	Granada	1987	Mouse	Eptesicus serotinus
LT839609.1	EBLV-1b	20174	Germany	-	2008	-	Eptesicus serotinus
LT839612.1	EBLV-1b	5006	Germany	Wadgassen	2000	-	Eptesicus serotinus
LT839608.1	EBLV-1c	13424	Spain	-	1989	-	unknown

SUPPLEMENTARY FIGURES

Figure S1: Transmission electron micrograph

Micrograph of a lesion located behind the right putamen showing cytoplasmic viral particles that look like rods (white "r") (diameter (50–100 nm) and length (100–300 nm); some are bullet-shaped (b) with limiting trilaminar membranes (white arrows). Most have variable shapes, more or less long or oval, as they are arranged in all planes of space (scale bar: 200 nm). A high resolution image is available as a separate file.

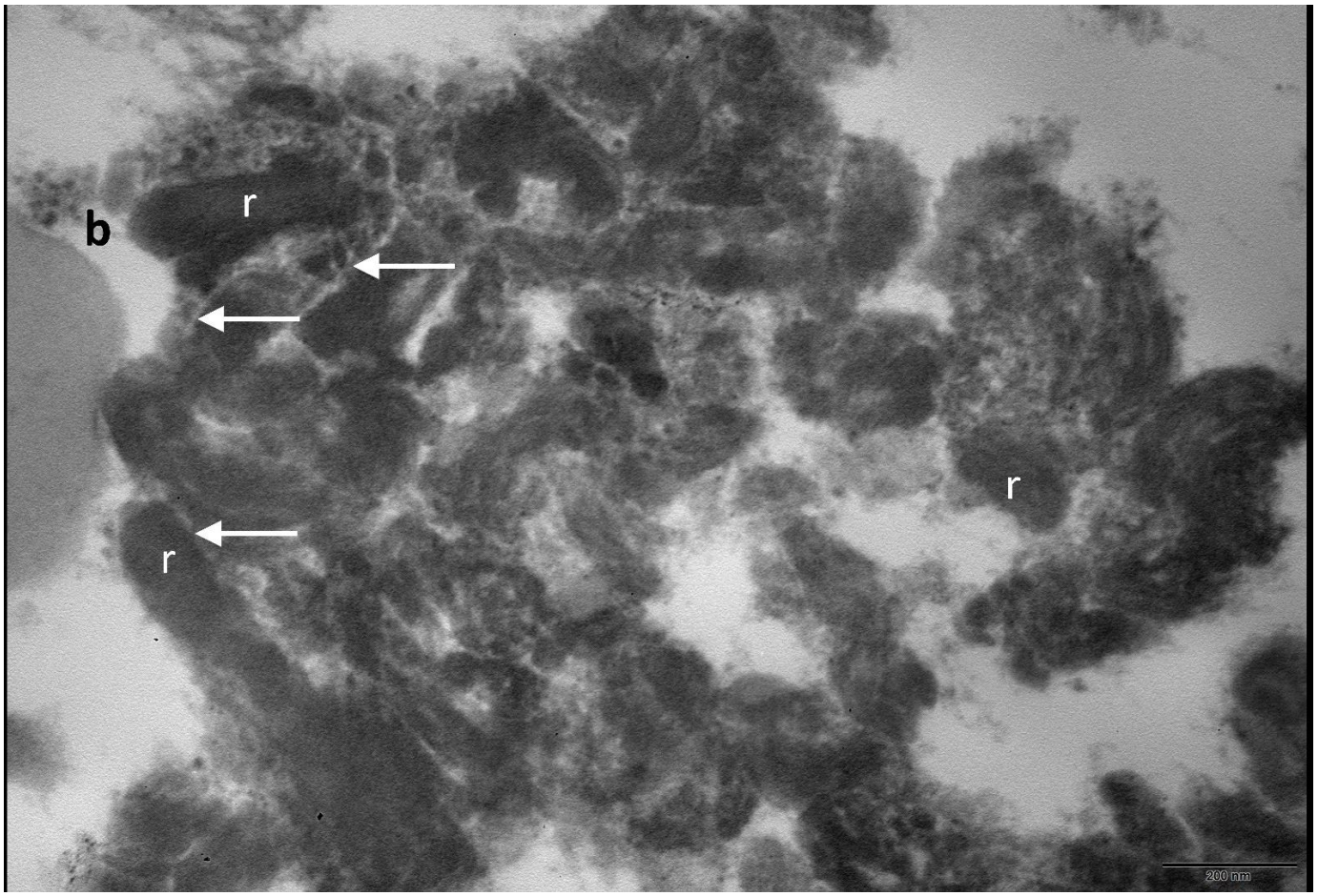
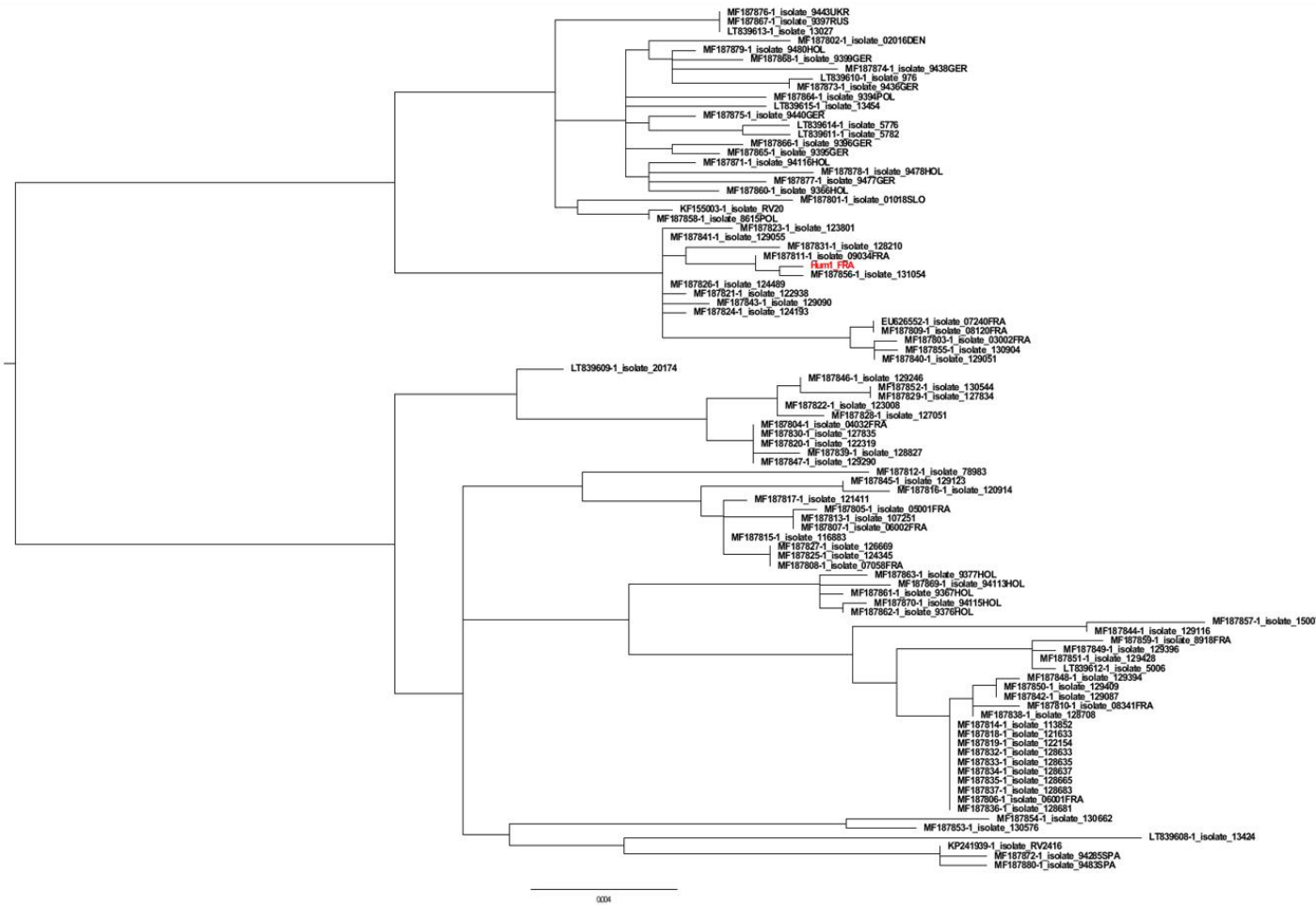


Figure S2: Phylogenetic analysis



The whole genome of the French EBLV-1a sequence (Hum1_FRA) was aligned along with 91 other representative sequences of EBLV1a and EBLV1b listed in table S4.

REFERENCES

1 Pérot P, Bielle F, Bigot T, *et al.* Identification of Umbre Orthobunyavirus as a Novel Zoonotic Virus Responsible for Lethal Encephalitis in 2 French Patients with Hypogammaglobulinemia. *Clin Infect Dis Off Publ Infect Dis Soc Am* 2020; published online June 9. DOI:10.1093/cid/ciaa308.

2 Bigot T, Temmam S, Pérot P, Eloit M. RVDB-prot, a reference viral protein database and its HMM profiles. *F1000Research* 2019; **8**: 530.

3 Mingo-Casas P, Sandonís V, Obón E, *et al.* First cases of European bat lyssavirus type 1 in Iberian serotine bats: Implications for the molecular epidemiology of bat rabies in Europe. *PLoS Negl Trop Dis* 2018; **12**: e0006290.

4 Lemoine F, Correia D, Lefort V, *et al.* NGPhylogeny.fr: new generation phylogenetic services for non-specialists. *Nucleic Acids Res* 2019; **47**: W260–5.