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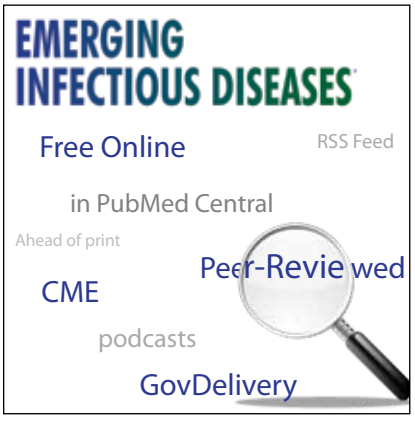

Novel Divergent Rhabdovirus in Feces of Red Fox, Spain

To the Editor: Rhabdoviruses (family *Rhabdoviridae*) are enveloped single-stranded negative-sense RNA viruses belonging to the Mononegavirales order. The International Committee on Taxonomy of Viruses recognizes 11 genera (*Cytorhabdovirus*, *Ephemerovirus*, *Lyssavirus*, *Novirhabdovirus*, *Nucleorhabdovirus*, *Perhabdovirus*, *Sigmavirus*, *Sprivivirus*, *Tibrovirus*, *Tupavirus*, *Vesiculovirus*) (*1*). In addition, many recently described rhabdoviruses remain unassigned. Rhabdoviruses contain 5 major genes, encoding for nucleoprotein (N), phosphoprotein (P), matrix (M), glycoprotein (G), and RNA-dependent RNA polymerase (L). The *Rhabdoviridae* family includes pathogens of various animal species, humans, and plants. Viruses of the genus *Lyssavirus* are the most relevant to public health because they can cause rabies. Bats are the driving force within this genus; foxes and various other species of wild carnivores also can be infected with lyssaviruses and transmit them to humans and dogs (*2*).

During a viral metagenomic survey, conducted as described previously (*3*), of fecal samples collected from 4 red foxes (*Vulpes vulpes*) that were found dead in Álava, Basque Country, Spain, we identified the complete coding sequence and the partial leader and trailer sequence of a novel rhabdovirus, tentatively called red fox fecal rhabdovirus (RFFRV; 15,541 nt, GenBank accession no. KF823814; online Technical Appendix, http://wwwnc.cdc.gov/EID/article/20/12/14-0236-Techapp1.pdf) by mapping 8,287 of the 56,519 sequence reads in the sample of a red fox. A proportion of obtained reads contained sequences that were ≥99% identical to mitochondrial DNA of *V. vulpes*, which confirmed that the sample was collected from a red fox.

The obtained sequence of RFFRV was partially confirmed by specific primers and Sanger sequencing of PCR amplicons. Five major and 3 minor open reading frames (ORFs) were identified that had a genome organization similar to that of other rhabdoviruses (Figure, panel A). No significant hits were obtained by BLAST analysis (http://blast.ncbi.nlm.gov/Blast.cgi) of N, P, M, and G nucleotide and amino acid sequences, which was reported previously for novel divergent rhabdoviruses (*4*).

Predicted N, P, and M genes of RFFRV consist of 1,629, 2,490, and 813 nt, respectively, encoding for 543, 830, and 271 aa (online Technical Appendix Table 1). In addition to the absence of significant hits observed by BLAST analysis, no significant sequence homology was observed with known rhabdovirus proteins in pairwise alignments. Furthermore, no conserved motifs were detected in N, P, and M genes of RFFRV that are commonly observed in rhabdoviruses. However, intergenic regions between all major ORFs contained relatively conserved motifs that could be transcription termination/polyadenylation sequences (A/U) CU_7, similar to other rhabdoviruses (*5*). Adjacent to this termination signal was a stretch of conserved nucleotides that might function as a transcription initiation signal (online Technical Appendix Table 1).

The amino acid sequence of the G protein consisted of 669 aa and contained an N terminal signal peptide (1-MYHLIVLLVMLGQRAVA-17), a noncytoplasmic domain (aa 18–646), a transmembrane domain (647-ITAILMPLLSLAVVVGIIMCC-667), and a cytoplasmic tail of 2 aa, similar to other rhabdovirus G proteins as predicted by using Phobius and TMHMM (http://www.cbs.dtu.dk/services/TMHMM) (*6*,*7*). We predicted 3 potential glycosylation sites in the ectodomain at positions 38–40

(NKT), 554–556 (NAS), and 592–594 (NIS) using NetNGlyc 1.0 (http://www.cbs.dtu.dk/services/NetNGlyc).

Between the G and L genes, a complex intergenic region was present that contained 3 ORFs of 246 nt (7,413–7,658 aa), 231 nt (7,716–7,946 aa), and 459 nt (7,893–8,355 aa), of which 2 were overlapping frames (U1–3). Additional ORFs between G and L genes were detected previously in other rhabdoviruses (*8*,*9*). We detected transmembrane domains in the amino acid sequences of all 3 additional ORFs, suggesting they might act as viroporin (*8*,*9*).

The L gene of RFFRV contained 6,591 nt (2,197 aa). We detected several conserved domains and motifs, including RNA-dependent RNA polymerase, mRNA-capping region, mRNA capping enzyme, and virus-capping methyltransferase. Alignment of the deduced amino acid sequence of the L gene with the L gene of various other viruses belonging to the Mononegavirales order by using MAFFT version 7 (http://mafft.cbrc.jp/alignment/software/) and subsequent phylogenetic reconstruction by using a maximum-likelihood tree (WAG+F+I+G model with 100 bootstrap replicates in MEGA5 [http://www.megasoftware.net]) suggested that this virus belongs to a novel genus of the *Rhabdoviridiae* family. In addition, pairwise identities of the deduced amino acid sequence of the L gene of RFFRV with that of other rhabdoviruses of the *Rhabdoviridae* family were only ≤35% (online Technical Appendix Table 2).

Because the fox was found dead and no tissue samples were collected, whether RFFRV played a role in the animal's death is unknown. In addition, multiple attempts to isolate this virus on various cell lines of eukaryotes (Vero E6, MDCK, CRFK, N2a, and BHK cells, primary fox kidney cells) failed because of the absence of cytopathic effects and viral replication by quantitative reverse transcription PCR, despite a high number of reads in the original sample. The fox might have acquired the virus through spillover from a small prey, such as a bat, and additional studies are required to elucidate the prevalence, original host, and pathogenic potential of this novel virus.

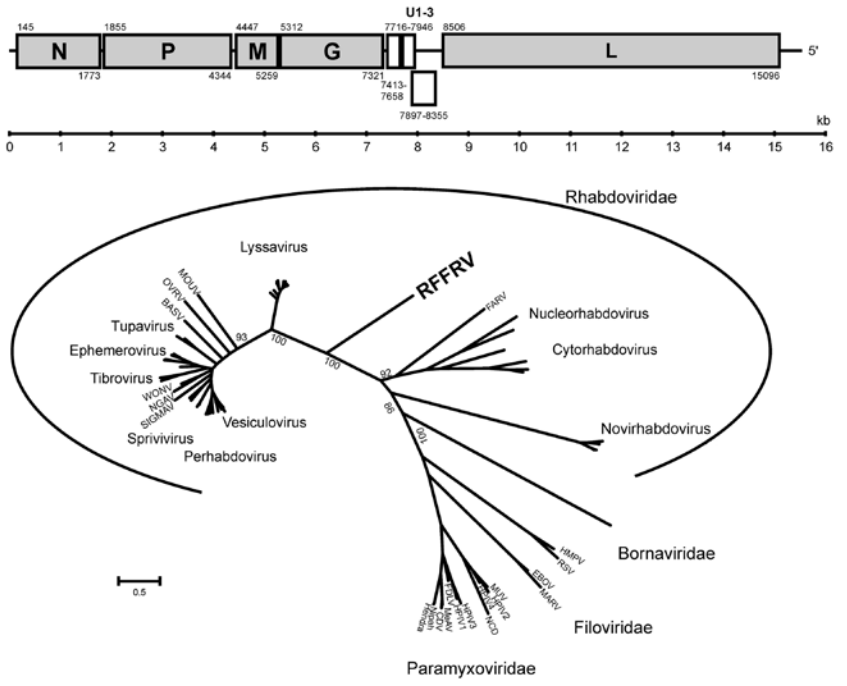

Figure. Genome organization and phylogenetic analysis of RFFRV. A) Genome organization of RFFRV. Indicated are the locations of the major ORFs (including the positions of the first and last nucleotide) and 3 theoretical minor ORFs between the G and L genes. B) Phylogenetic maximum-likelihood tree using the WAG+F+I+G model and 100 bootstrap replicates in MEGA5 (http://www.megasoftware.net) of the deduced amino acid sequence of the L genes of various viruses of the order Mononegavirales. G, glycoprotein; L, RNA-dependent RNA polymerase; M, matrix; N, nucleoprotein; ORF, open reading frame; P, phosphoprotein; RFFRV, RFFRV, red fox fecal rhabdovirus. Only bootstrap values in the close proximity of the branch of the RFFRV are indicated. Scale bar indicates nucleotide substitutions per site. Viruses and GenBank accession numbers are shown in the expanded figure legend online (http://wwwnc.cdc.gov/EID/article/20/12/14-0236-F1.htm).

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Ngari Virus in Goats during Rift Valley Fever Outbreak, Mauritania, 2010

To the Editor: Ngari virus (NRIV) is a single-stranded RNA virus belonging to the family *Bunyaviridae*, genus *Orthobunyavirus*. The genome comprises 3 segments, the small (S), medium (M), and large (L) segments, which encode the nucleocapsid (N) protein, the 2 glycoproteins Gn and Gc, and the RNA-dependent RNA-polymerase, respectively. Sequence analysis showed that NRIV is a reassortant between Bunyamwera virus (BUNV) and Batai virus (BATV), both from the genus *Orthobunyavirus*. S and L segments derived from BUNV, and the M segment derived from BATV (*1*,*2*). NRIV is more virulent than BUNV and BATV and is associated with hemorrhagic fever. NRIV was first isolated from *Aedes simpsoni* mosquitoes in 1979 and from humans in 1993, both in Senegal (*3*). During 1997 and 1998, humans were affected with hemorrhagic fever diseases in Kenya and Somalia that were caused by Rift Valley fever virus (RVFV) and by NRIV (*2*,*4*).

In 2010, during an ongoing RVFV outbreak in Mauritania, we collected 163 serum samples (62 from camels, 8 from cattle, and 93 from small ruminants) (*5*). RVFV RNA was isolated from serum samples as described previously (*5*). Further molecular testing of the samples was conducted by a SYBRGreen–based real-time reverse transcription PCR (RT-PCR) adapted from a conventional RT-PCR and based on generic primers (bun_group_forw 5′-CTGCTAACACCAGCAGTACTTTTGAC-3′ and bun_group_rev 5′-TGGAGGGTAAGACCATCGTCAGGAACTG-3′) that target a 250-nt sequence of the S segment of Bunyamwera serogroup members (*6*). Real-time RT-PCR was performed in a CFX 96 real-time PCR system (Bio-Rad, Hercules, CA, USA) by using 5 μL RNA with a QuantiTect SYBR Green RT-PCR Kit (QIAGEN, Hilden Germany) in a final volume of 25 μL. Cycling conditions included RT at 50°C for 30 min and 95°C for 15 min, followed by amplification with 44 cycles of 95°C for 15 s, 55°C for 25 s, 72°C for 30 s, and 77°C for 5 s. A melting curve analysis was then performed starting with 95°C for 60 s, and a temperature gradient was conducted from 68°C to 94°C in increments of 0.2°C.

Of the 163 serum samples tested, 2 samples from goats resulted in a positive signal with cycle thresholds of 23 (sample 51) and 28 (sample 65), respectively. Both samples showed similar melting peaks at ≈78.2°C and shared the identical partial nucleotide sequence of the S segment. The sequence belongs to the Bunyamwera serogroup, but the short partial sequence was not sufficient for accurate virus determination and identification. For this reason, both serum samples were used to inoculate cell monolayers of Vero E6 cells that were assayed for virus replication. Only sample 51 displayed a cytopathic effect after 72 h and was further analyzed. We isolated the viral RNA from cell culture with TRIzol reagent