

Divergent Rabies Virus Variant of Probable Bat Origin in 2 Gray Foxes, New Mexico, USA

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In the Western Hemisphere, bat-associated rabies viruses (RABVs) have established independent transmission cycles in multiple mammal hosts, forming genetically distinct lineages. In New Mexico, USA, skunks, bats, and gray foxes are rabies reservoir hosts and represent a public health risk because of encounters with humans. During 2015 and 2019, two previously undescribed RABVs were detected in 2 gray foxes (*Urocyon cinereoargenteus*) in Lincoln County, New Mexico. Phylogenetic analysis of the nucleoprotein gene indicated that the isolates are a novel RABV variant. These 2 cases probably represent repeated spillover events from an unknown bat reservoir to gray foxes. Molecular analysis of rabies cases across New Mexico identified that other cross-species transmission events were the result of viral variants previously known to be enzootic to New Mexico. Despite a robust rabies public health surveillance system in the United States, advances in testing and surveillance techniques continue to identify previously unrecognized zoonotic pathogens.

Rabies is a viral zoonotic disease that infects the central nervous system of mammals and causes a highly lethal acute encephalitis. *Rabies lyssavirus* is the most prevalent of the 17 recognized species of the genus *Lyssavirus* and is genetically grouped within the phylogroup I (1,2). Rabies virus (RABV) is distributed worldwide and has an estimated human rabies death toll of >59,000 annually. Most

human rabies deaths are associated with dog-mediated rabies, predominantly in Asia, Africa, and several countries in the Western Hemisphere (3). Rabies is commonly transmitted through direct contact with the saliva of rabid animals; humans or any susceptible mammal usually become infected through a bite. After potential exposure to RABV, if postexposure prophylaxis (PEP) is not administered before symptom onset, the outcome will nearly always be fatal (4).

In the Western Hemisphere, 2 genetic lineages of RABV have been identified: Cosmopolitan Dog lineage and New World lineage. The Cosmopolitan Dog lineage was introduced during European colonization; dog-to-dog transmission and host switching to other terrestrial mesocarnivores enabled this lineage to spread and establish across the Americas and some Caribbean islands. The New World lineages circulate mainly within bat populations, with several exceptions of lineages that shifted to terrestrial mesocarnivores (5,6).

The United States recognized dog and wildlife rabies as a problem and organized large-scale public health efforts to control the disease as early as 1944 (<https://wwwn.cdc.gov/nndss/conditions/rabies-animal>), the year in which a consensus agreement was reached to consider rabies a reportable disease (7). Interrupting the chain of dog-to-dog transmission through immunization led to the milestone of eliminating rabies circulating in dogs (8). According to the most recent annual surveillance reports, since 2015, bats have become the most commonly reported rabies reservoir species in the continental United States (9,10). RABVs circulating in bat populations are incredibly diverse.

Monoclonal antibodies (mAbs) provide evidence of antigenic differences among RABVs,

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and mAbs patterns form the basis for determining conventional RABV variant nomenclature (11). However, RABV variant identification by using mAbs might not be able to provide appropriate resolution because of genetic variation, particularly when applied to the highly diverse bat RABV. Therefore, a comprehensive genetic analysis is frequently used to understand transmission dynamics and explore genetic differences (12). In the United States, RABV variants are often named on the basis of the presumptive reservoir host (e.g., *Tadarida brasiliensis* bats); ≥ 18 different recognized bat-specific variants have been identified (13,14). Detailed genetic studies have suggested several instances in which RABV circulating in bats has shifted to terrestrial mammals. Enzootic cycles of RABV from bat origin have been established by host shift events separately in raccoons (*Procyon lotor*) and skunks (*Mephitis mephitis*) (15).

Host shift events are rare, and the factors that lead to a successful host shift are poorly understood. Some studies have linked such events to ecologic, viral, or host factors that might contribute to long-term establishment (16–18). Circulation of novel RABV variants in wildlife species can remain unnoticed unless there is an outbreak or an event that leads to an infected animal reported the National Rabies Surveillance System (<https://www.healthypeople.gov>), in which testing and additional virus characterization can detect unexpected virus–host infections (19,20). Laboratory-based surveillance using molecular tools is useful to identify genetic changes and explore relatedness at a more refined level, which can help to identify novel RABV variants (21).

New Mexico is known to have ≥ 3 RABV enzootic cycles represented by skunks (south-central skunk variant), gray foxes (Arizona gray fox variant), and numerous variants associated with bats. During 2000–2020, the state surveillance system detected 275 rabies cases in wildlife species and 14 cases in domestic animals (<https://nmhealth.org/about/erd/ideb/zdp/rab>). In 2015, a woman in Lincoln County was attacked by a gray fox and appropriate PEP was given; a sample showed positive results for rabies, but preliminary antigenic and molecular analysis did not align with known RABV variants. In 2019, a second isolate collected from a gray fox that bit a man in the same county, but in a different city, showed a similar genetic pattern. The purpose of this study was to characterize these divergent RABV isolates from gray foxes in Lincoln County and investigate potential reservoir host species.

Materials and Methods

RABV Samples

All samples were collected as part of routine public health surveillance activities, and no animal sampling was performed for this study. Of the 289 samples tested that were positive for RABV in New Mexico during 2000–2020, a total of 90 were available for molecular characterization (Appendix 1 Table 1, <https://wwwnc.cdc.gov/EID/article/28/6/21-1718-App1.xlsx>). Of the 90 samples, 58 were analyzed by the Scientific Laboratory Division Department of Health of New Mexico (SLD-NM) and 32 were submitted for rabies virus characterization to the National Rabies Reference Laboratory (NRRL), Division of Global Migration and Quarantine, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention (CDC) (Appendix 2 Table, <https://wwwnc.cdc.gov/EID/article/28/6/21-1718-App2.pdf>). Five isolates from gray foxes collected by the surveillance system in Arizona and 3 archived isolates from *Lasiurus intermedius* bats from Florida were also included. In addition, from the batch of isolates submitted to CDC, we tested isolates A15-0755 and A19-2238 from gray foxes collected in Lincoln County during 2015 and 2019 by using a panel of RABV nucleoprotein mAbs (22) and obtained the whole genomes.

RNA Extraction and Reverse Transcription PCR Amplification

We extracted total RNA from brain tissue by using either TRIzol (Invitrogen, <https://www.thermofisher.com>) or the Direct-zol RNA MiniPrep Kit (Zymo Research, <https://www.zymoresearch.com>) according to the manufacturer's instructions. We performed traditional reverse transcription PCR to produce partial and full nucleoprotein gene amplicons by using overlapping nucleoprotein gene primers described (19). To obtain the whole RABV genome for isolates A15-0755 and A19-2238, we synthesized cDNA by using specific primer LN34 forward (23) with avian myeloblastosis virus reverse transcriptase (Roche, Sigma-Aldrich, <https://www.sigmaaldrich.com>). PCR amplicons suitable to cover the entire genome were generated by using 6 overlapping pair of primers (Appendix 1 Table 2) and Takara long amplicon Taq polymerase (Takara Bio USA, <https://www.takarabio.com>).

Nucleotide Sequencing and Phylogenetic Analysis

We obtained partial and complete nucleoprotein gene sequences by using overlapping primers with the BigDye Terminator v1.1 Cycle Sequencing Kit

(Thermo Fisher). We sequenced the amplicons in a 3730 DNA Analyzer (Applied Biosystems, (Thermo Fisher) by using standard Sanger sequencing method (19). SADB119 (GenBank accession no. M31046) sequence was used as a reference to assemble the partial and full nucleoprotein gene and the whole genome. Nucleoprotein gene sequences were edited by using Bioedit software (24). We included high-throughput sequencing to obtain whole genome sequences for isolates A15-0755 and A19-2238. We generated amplicons >2 kb by using specific primers (Appendix 1 Table 2) and pooled and fragmented all amplicons for each isolate to 500 bp by using Covaris S220 (<https://www.covaris.com>).

We quantified DNA by using a Qubit instrument (Thermo Fisher), performed library preparation by using the Accel-NGS 2S plus DNA Library Kit (Swift Biosciences, <https://www.idtdna.com>), and obtained sequence reads in a MiSeq Instrument (Illumina, <https://www.illumina.com>). We assembled genomes by using CLC Genomics Workbench version 20 (<https://digitalinsights.qiagen.com>), trimmed reads with a quality limit of 0.05, then mapped to reference JQ685895 to generate a majority draft consensus. We generated final genomes by mapping reads back to draft genomes and extracting consensus sequences with minimum 50× read depth; we inserted ambiguous bases with a noise threshold of 10%. We submitted sequences generated in this study to GenBank (accession nos. OM202982–3049).

We aligned sequences generated in this study by using ClustalW in Geneious 10.2.2 (<https://www.geneious.com>). We conducted phylogenetic analysis by using a Bayesian approach in the BEAST v1.10.4 package (25). To estimate the time since the most recent common ancestor of fox-associated viruses and other bat and carnivore-associated RABVs, we analyzed 141 nucleoprotein gene sequences (Appendix 1 Table 2). Preliminary analyses used iqTree to compare substitution models and obtain a maximum-likelihood topology without a molecular clock assumption (26).

We used the most likely substitution model according to the corrected Akaike Information (generalized time reversible plus finite sites plus invariant sites plus gamma 4) in subsequent analyses. We checked for temporal signal in our sequence data by correlating sampling time with root-to-tip divergence by applying TempEst (27) to the maximum-likelihood tree estimated in iqTree (28). We subsequently performed Bayesian phylogenetic analyses in duplicate by using the relaxed lognormal molecular clock and the Bayesian skyline demographic model with BEAST (25,29). We partitioned codon positions 1 and

2 separately from codon position 3 and applied the generalized time reversible plus invariant sites plus gamma substitution model to both partitions. We modeled 1 year of uncertainty around each sampling date. We performed each analysis for 100 million generations, sampling trees, and parameters every 5,000 steps and checked chains for convergence within and between runs in Tracer (<https://beast.community/trac>). We combined trees and log files in LogCombiner (<https://beast.community/logcombiner>) after removing 10 million generations as burn-in; we further thinned tree files to be sampled every 10,000 steps. This strategy led to effective sample size values >200 for all parameters. We visualized all the phylogenetic trees by using Fig Tree v1.4.0 (30).

We calculated genetic distance in Geneious and visualized rabies distribution across New Mexico by exporting partial nucleoprotein gene Bayesian tree into ArcGIS desktop v10.7.1 (<https://www.esri.com>). We sourced administrative boundaries (Figure 1) from GADM version 4 (Database of Global Administrative Areas; www.gadm.org) and specific imagery from Maxar Technologies Inc. (<https://www.maxar.com>) accessed from ESRI World Imagery.

Results

During 2015 and 2019, two persons in Lincoln County were bitten by rabid gray foxes. Initially, we compared the full nucleoprotein gene sequence of the 2015 isolate, A15-0755, with sequences available in GenBank. The most similar sequence was the RABV isolate collected in Canada from a *Myotis lucifugus* bat (GenBank accession no. AF351837) and characterized as silver-haired bat RABV variant (*Lasionycteris noctivagans* bats) with a sequence identity of 93.25%. A15-0755 showed an atypical reaction pattern with mAbs 2 and 11; a similar reaction pattern was observed in a historic isolate from a northern yellow bat (*Lasiurus intermedius*) collected in Florida and archived at CDC. During 2019, a second isolate, A19-2238, from a second rabid gray fox from the same county was identified in SLD-NM and was further characterized at CDC. A full nucleoprotein gene sequence showed a single nucleotide mismatch with the 2015 isolate. A19-2238 produced a Mab reaction pattern similar to a RABV variant circulating in hoary bats (*Lasiurus cinereus*).

Phylogenetic Analysis

Bayesian phylogenetic inference of partial and complete nucleoprotein genes in BEAST showed consistent tree topologies, grouping the New Mexico isolates into 3 major clades. The first clade of bat RABV variants included isolates from bats and

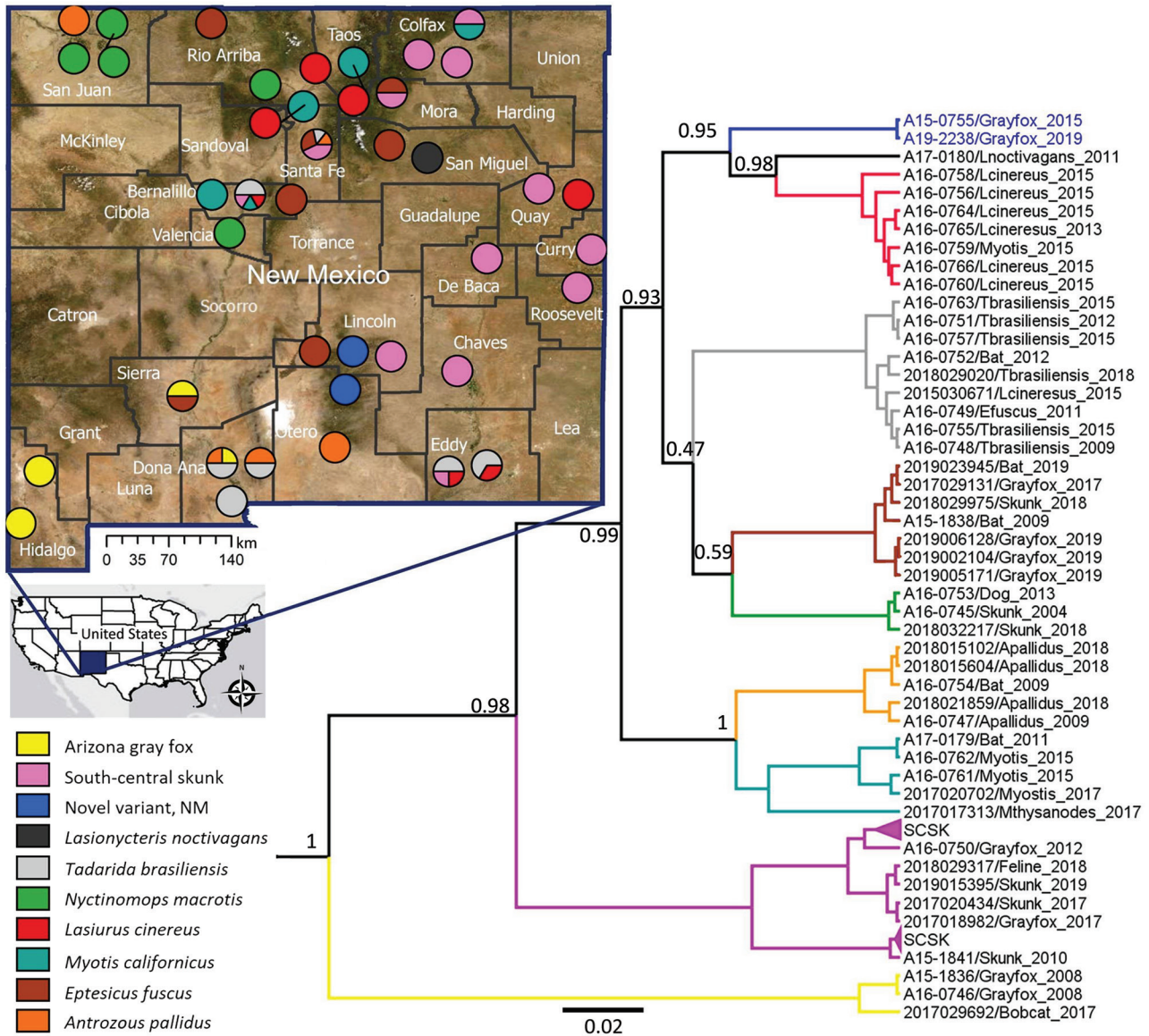


Figure 1. Phylogenetic tree based on partial nucleoprotein gene (348 bp) sequences and geographic distribution of rabies virus (RABV) variants, New Mexico, USA. The tree was constructed by using representative isolates and only posterior values leading to the RABV variants are included on the tree nodes. Three major clades were identified in New Mexico. The RABV variants are displayed in distinct colors in the tree and map according to the legend included in the figure. Blue indicates novel RABV isolates collected from gray fox in Lincoln County. Accuracy of the location in the map is at city level; for samples that did not have city information, the location was randomly assigned within the county. Numbers along branches are bootstrap values. Scale bar indicates nucleotide substitutions per site.

terrestrial carnivores that were presumed to be the result of cross-species transmission (Figure 1). Within this clade, 7 previously known RABV genetic variants were identified. Isolates A15-0755 and A19-2238 formed an independent branch. Phylogenetic analysis did not identify a close relationship with any RABV sequences available in GenBank. Both isolates were most closely related to, but still highly divergent from (mean \pm SD identity 95.85%

\pm 2.21%), the branches containing RABVs detected in *Lasiurus cinereus* bats and *L. noctivagans* bats. The third RABV isolate from a gray fox in Lincoln County (A15-1838) clustered within a branch that contained isolates from *Eptesicus fuscus* bats, which indicated a spillover event of a bat RABV variant to a terrestrial mammal.

We also identified other spillover events from bats to terrestrial mammals (Appendix 2 Table). The

variant commonly circulating among *E. fuscus* bats was detected in gray foxes and skunks, and a RABV variant circulating in *Nyctinomops macrotis* bats was found in a skunk isolate (A16-0745) from San Juan County and a dog isolate (A16-0753) from Valencia County. The second clade containing isolates identified as south-central skunk RABV variant included isolates collected from gray foxes, coyotes, and domestic cats. The third clade identified as Arizona gray fox contained 2 isolates from gray foxes and 2 from bobcats. Circulation of variants A16-0745 and A16-0753 in terrestrial mammals was consistent with previous reports (Figure 1) (31,32). Bat virus variants

were found throughout the state but showed no notable epidemiologic pattern.

Phylogenetic inferences including all 32 nucleoprotein gene sequences from New Mexico generated at CDC and representative sequences retrieved from GenBank produced a phylogenetic tree with similar topologies to the partial nucleoprotein gene (Figure 1). Gray fox isolates A15-0755 and A19-2238 formed a unique branch high posterior support (1); the most similar isolate available on GenBank (accession no. AF351837) clustered separately within the *Perimyotis subflavus* and *Lasionycteris noctivagans* bat RABV variants (Figure 2).

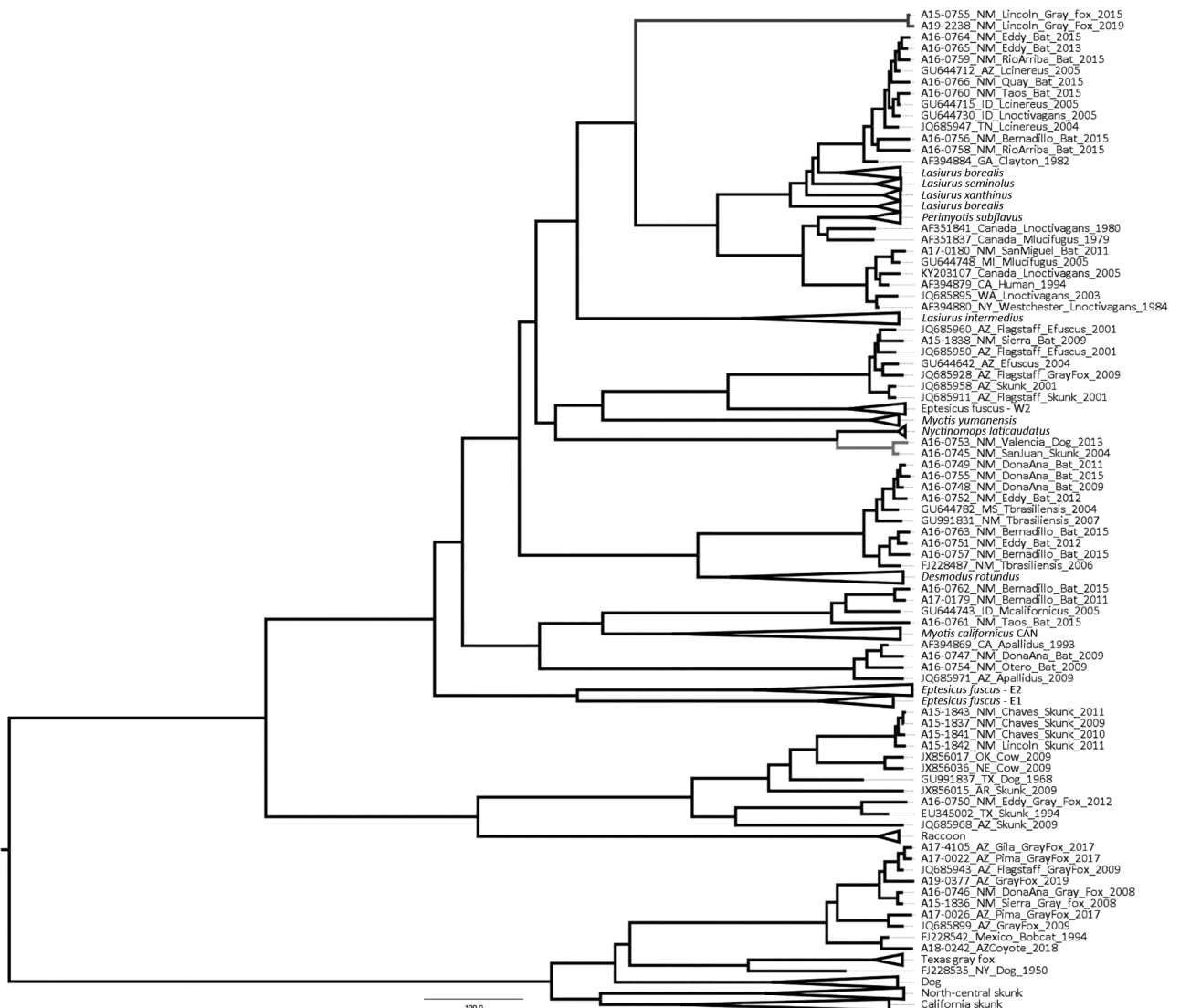


Figure 2. Maximum clade credibility tree using full nucleoprotein gene sequences of RABV variants identified in New Mexico, USA, and representative sequences from RABV variants in the Western Hemisphere. Values in the nodes indicate estimates for the posterior clade probability for each RABV variants. Branch in blue indicates novel RABV variant that includes the 2 isolates from Lincoln County, and branch in green indicates RABV associated with *Nyctinomops macrotis* bats. Scale bar indicates nucleotide substitutions per site. RABV, rabies virus.

Novel Gray Fox Isolates

The substitution rate along the branch leading to the 2 gray fox isolates identified as a novel RABV variant was 1.6×10^{-4} substitutions/site/year (95% highest posterior density 9.2×10^{-5} – 2.4×10^{-4} substitutions/site/year). The substitution rate across the entire tree was 1.7×10^{-4} substitutions/site/year (95% highest posterior density 1.2×10^{-4} – 2.2×10^{-4} substitutions/site/year), indicating a similar rate of evolution. The nucleoprotein gene genetic distance between RABV variants examined showed that the highest identity to isolate A15-0755 was 93.19% for isolate AF351837 (silver-haired bat variant), and the identity for isolate A19-2238 was 93.11% (Appendix 1 Table 3). We conducted a BLAST (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) search of the glycoprotein gene from the 2 novel RABV variant isolates in GenBank; isolate KJ174682 from an *E. fuscus* bat and described as EF-W3 had the closest glycoprotein gene identity (90.42% nt). Nucleotide comparison across the entire genome of isolates A15-0755 and A19-2238 showed 99.78% identity.

The nucleoprotein gene, which is highly conserved and a target for laboratory diagnosis, showed a single synonymous substitution at nt position 333. The glycoprotein gene, which induces production of virus-neutralizing antibodies that provide immunologic protection, showed a nonsynonymous substitution at nt position 554, resulting in a substitution of the amino acid tyrosine at position 184 by serine (Y184S). Phylogenetic analysis using a reduced set of glycoprotein gene sequences placed isolates A15-0755 and A19-2238 in an independent branch, closely related to *L. noctivagans* and *P. subflavus* bats, that has well-supported posterior values (Appendix 2 Figure).

Other Isolates

Two other isolates A16-0745 (skunk 2004) and A16-0753 (dog 2013) were compared with available sequences in GenBank. The partial nucleoprotein (244 bp) of a skunk isolate (A16-0745) showed 100% identity with RABV isolate AY960093 from GenBank, previously detected in an *N. macrotis* bat in Colorado, and 99.5% to isolate AY170304 from GenBank, detected in Arizona. The full nucleoprotein gene showed 98.0% (A16-0745) and 97.8% (A16-0753) identities with a RABV (GenBank accession no. KM594034) found in *N. laticaudatus* bats from Brazil. In the phylogenetic analysis using the full nucleoprotein gene, we found that both isolates branched independently and contained only these 2 terrestrial mammals (Figure 2).

Cross-Species Transmission

Of the 49 bat clade samples that had sequencing results, 11 (22.4%) instances of bat-to-terrestrial cross species transmission were detected. Of 37 isolates with the south-central skunk RABV variant, 9 (24.3%) were cross-species transmissions to nonskunk species, and 2 (50%) of the 4 gray fox RABV variant isolates were cross-species transmissions. There were no instances of a terrestrial RABV variant found in a bat.

Discussion

In the United States, 7 unique RABV variants are defined on the basis of unique mAbs patterns, each associated with a specific terrestrial host species in terrestrial mammals (arctic fox, gray fox, striped skunk, raccoon, and mongoose) (13). Based on patterns of the specific mAbs used, the standard panel can differentiate ≥ 15 RABV variants (33). Robust rabies surveillance systems and regular virus characterization are used to not only define the geographic distribution of variants but also detect RABV spillover into nonreservoir wildlife or domestic species that might reflect changes in rabies epidemiology and affect human or animal health. This study was conducted after the New Mexico Department of Health confirmed human RABV exposures to confirmed rabid foxes and pursued additional laboratory-based methods to determine if these cases represented a shift in the epidemiology of rabies in the state. As a result of this investigation, a novel RABV variant was identified. Detection of this novel variant in 2 gray foxes, separated by 5 years, probably represents independent cross-species transmission events from a cryptic transmission cycle among a species of bats.

Available data for the United States show that the distribution of terrestrial RABV variants is geographically delimited; in contrast, the distribution of bat RABV variants is broader, and these variants show an abundant diversity, each variant associated with specific species (9,14). For example, according to the National Rabies Surveillance System, during 2008–2018, at least 17,700 rabid bats were detected in 39 different bat species, but 54.9% of rabid bats were not identified to species, and 63% did not undergo variant typing (antigenic or molecular) (34,35). Given these apparent gaps in characterizing rabid bats in the United States, it should be no surprise that novel RABV variants are still being discovered. As characterization methods and bat identification guides (36) become more accessible, it is expected that a wider diversity of bat RABV variants will be detected. Furthermore, public health surveillance is biased toward animals with human or domestic

animal exposures, potentially masking detection of RABV variants in species not commonly found near inhabited areas.

RABV isolates from New Mexico included in this study were derived from bats and terrestrial mammals collected in different locations spanning over 20 years. The phylogenetic inferences (Figure 1) clearly show 3 major clades supported that have high posterior values. All isolates were closely associated with RABV variants already described in New Mexico (14,37), except for the 2 isolates from gray foxes collected during 2015 and 2019 in Lincoln County. An extensive analysis of full nucleoprotein and glycoprotein genes supported the uniqueness of the isolates as an unrecognized RABV variant. Nucleotide analysis of the glycoprotein gene of the novel RABV variant had a specific glycoprotein gene mutation that is located in the antigenic site II, which is involved in stimulating the antibody response (38). Although the current rabies vaccine is effective in protecting against all lyssaviruses from phylogroup I, monitoring the nucleotide mutation across the glycoprotein gene on emergent RABVs in domestic and wild animals might help to predict if the vaccine will still be effective against these new viruses (39). This single mutation is not believed to lead to an escape from current RABV biologics, as shown by the lack of development of rabies in the 2 persons exposed to this virus after they received PEP.

On the basis of phylogenetic analysis, we reason that the reservoir of this novel RABV variant is most likely a bat from the group commonly referred to as migratory tree bats, including the genera *Lasiurus* and *Lasionycteris*. The isolates identified probably represent repeated spillover events from a bat reservoir into gray foxes in Lincoln County. This hypothesis is supported by the low frequency of detection of the variant (2 cases in 5 years), which might be expected because bats and wild terrestrial mammals have limited contact with humans and other terrestrial mammals unless they are sick or injured (40). On the basis of available data and analysis, we cannot provide enough evidence to prove that this variant represents a host shift from bat RABV variants into gray foxes; however, the question will remain open until the reservoir is determined. After rabies was recognized in the gray fox during 2015, an active surveillance program was enacted in Lincoln County and surrounding counties; however, no rabid terrestrial animals were detected during this 6-month effort. To increase the robustness of this analysis, isolates from additional rabid foxes or bats either in Lincoln County or neighboring areas are

clearly needed. In nature, bats inhabit diverse ecological niches (41). Migratory tree bats usually travel long distances, which opens the possibility that this novel RABV variant might be present in other states or countries (42).

Although migratory tree bats are a major rabies reservoir in the United States, other species of migratory bats, such as *N. macrotis* (big free-tailed bats), commonly travel long distances, covering a range from South America to North America (43). Detecting rabies in *N. macrotis* bats is uncommon, and the availability of genetic data in GenBank is limited to 2 partial nucleoprotein gene sequences (300 bp): AY170304 (Arizona) and AY960093 (Colorado). The surveillance system in the United States detected 18 rabid *N. macrotis* bats during 2008–2018; the highest incidences were in 2015 ($n = 9$) and 2010 ($n = 4$) (10,34,44–46).

In this study, we found an *N. macrotis* bat RABV variant in a domestic dog and a skunk separated by 11 years. Analysis of the full nucleoprotein gene provided high posterior support that the RABV variant detected in United States shared a recent ancestor with a RABV variant found in Brazil in *N. laticaudatus* bats (47). The finding of a relatively rare RABV variant in a migratory bat species represents a reminder that RABVs can be carried long distances by reservoir species and could represent a method of introduction of exotic RABVs into the United States, yet another example of the need for adequate surveillance, routine species identification, and RABV characterization (48).

Antigenic characterization is useful to rapidly identify the common RABV variants in the United States (49). The antigenic patterns of the isolates from Lincoln County gave conflicting results; the isolates showed different patterns, despite having 99.9% genetic similarity. These discrepancies in the interpretation of the mAb results demonstrate the limitation of that method to differentiate RABVs within certain bat species. In comparison, the amplicon sequences generated by the LN34 assay (50), which target a highly conserved lead sequence of RABV genome, are able to confirm the distinct sequences for this novel RABV. This study highlights the need for RABV characterization when there are concerns about epidemiologic shifts to inform public health and animal health interventions. Despite extensive surveillance systems in the United States for RABV, virus characterization is not routinely performed. As genetic virus characterization becomes more routine, additional cryptic RABV transmission cycles probably will be recognized.

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Divergent Rabies Virus Variant of Probable Bat Origin in 2 Gray Foxes, New Mexico, USA

Appendix 2 Table. Isolates sequenced this study and reference sequences used for the analysis*

Isolate	Country	State	County	City	Host source	Year	GenBank accession no.	RABV lineage	Reference
A15-0755; 2015012162	USA	New Mexico	Lincoln	Alto	<i>Urocyon cinereoargenteus</i>	2015	OM202983	Novel New Mexico	This study
A15-1836; 2008000832	USA	New Mexico	Sierra		<i>Urocyon cinereoargenteus</i>	2008	OM202984	Cosmopolitan (AZFX)	This study
A15-1837; 2009000595	USA	New Mexico	Chaves		<i>Mephitis mephitis</i>	2009	OM202985	South-central skunk	This study
A15-1838; 2009001979	USA	New Mexico	Sierra		Bat	2009	OM202986	<i>Eptesicus fuscus</i> -W1	This study
A15-1841; 2010039542	USA	New Mexico	Chaves		<i>Mephitis mephitis</i>	2010	OM202987	South-central skunk	This study
A15-1842; 2011021732	USA	New Mexico	Lincoln		<i>Mephitis mephitis</i>	2011	OM202988	South-central skunk	This study
A15-1843; 2011030508	USA	New Mexico	Chaves		<i>Mephitis mephitis</i>	2011	OM202989	South-central skunk	This study
A16-0745; 2004003088	USA	New Mexico	San Juan		<i>Mephitis mephitis</i>	2004	OM202990	<i>Nyctinomops macrotis</i>	This study
A16-0746; 2008003514	USA	New Mexico	Dona Ana		<i>Urocyon cinereoargenteus</i>	2008	OM202991	Cosmopolitan (AZFX)	This study
A16-0747; 2009002276	USA	New Mexico	Dona Ana		<i>Antrozous pallidus</i>	2009	OM202992	<i>Antrozous pallidus</i>	This study
A16-0748; 2009002549	USA	New Mexico	Dona Ana		<i>Tadarida brasiliensis</i>	2009	OM202993	<i>Tadarida brasiliensis</i>	This study
A16-0749; 2011031485	USA	New Mexico	Dona Ana		<i>Eptesicus fuscus</i>	2011	OM202994	<i>Tadarida brasiliensis</i>	This study
A16-0750; 2012026146	USA	New Mexico	Eddy		<i>Urocyon cinereoargenteus</i>	2012	OM202995	South-central skunk	This study
A16-0751; 2012034852	USA	New Mexico	Eddy		<i>Tadarida brasiliensis</i>	2012	OM202996	<i>Tadarida brasiliensis</i>	This study
A16-0752; 2012036136	USA	New Mexico	Eddy		Bat	2012	OM202997	<i>Tadarida brasiliensis</i>	This study
A16-0753; 2013038564	USA	New Mexico	Valencia		<i>Canis familiaris</i>	2013	OM202998	<i>Nyctinomops macrotis</i>	This study
A16-0754; 2009002942	USA	New Mexico	Otero		Bat	2009	OM202999	<i>Antrozous pallidus</i>	This study
A16-0755; 2015013805	USA	New Mexico	Dona Ana	La Mesa	<i>Tadarida brasiliensis</i>	2015	OM203000	<i>Tadarida brasiliensis</i>	This study
A16-0756; 2015016381	USA	New Mexico	Bernalillo	Albuquerque	<i>Lasiurus cinereus</i>	2015	OM203001	<i>Lasiurus cinereus</i>	This study
A16-0757; 2015018259	USA	New Mexico	Bernalillo	Albuquerque	<i>Tadarida brasiliensis</i>	2015	OM203002	<i>Tadarida brasiliensis</i>	This study
A16-0758; 2015018808	USA	New Mexico	Rio Arriba	Dixon	<i>Lasiurus cinereus</i>	2015	OM203003	<i>Lasiurus cinereus</i>	This study
A16-0759; 2015020795	USA	New Mexico	Rio Arriba	Espanola	<i>Myotis sp</i>	2015	OM203004	<i>Lasiurus cinereus</i>	This study
A16-0760; 2015024056	USA	New Mexico	Taos	Taos	<i>Lasiurus cinereus</i>	2015	OM203005	<i>Lasiurus cinereus</i>	This study
A16-0761; 2015025510	USA	New Mexico	Taos	El Prado	<i>Myotis sp</i>	2015	OM203006	<i>Myotis californicus</i>	This study
A16-0762; 2015027394	USA	New Mexico	Bernalillo	Albuquerque	<i>Myotis sp</i>	2015	OM203007	<i>Myotis californicus</i>	This study
A16-0763; 2015028251	USA	New Mexico	Bernalillo	Albuquerque	<i>Tadarida brasiliensis</i>	2015	OM203008	<i>Tadarida brasiliensis</i>	This study
A16-0764; 2015031004	USA	New Mexico	Eddy	Carlsbad	<i>Lasiurus cinereus</i>	2015	OM203009	<i>Lasiurus cinereus</i>	This study
A16-0765; 2013021240	USA	New Mexico	Eddy		<i>Lasiurus cinereus</i>	2013	OM203010	<i>Lasiurus cinereus</i>	This study
A16-0766; 2015019329	USA	New Mexico	Quay	San Jon	<i>Lasiurus cinereus</i>	2015	OM203011	<i>Lasiurus cinereus</i>	This study
A17-0179; 2011031282	USA	New Mexico	Bernalillo		Bat	2011	OM203012	<i>Myotis californicus</i>	This study
A17-0180; 2011034775	USA	New Mexico	San Miguel		<i>Lasionycteris noctivagans</i>	2011	OM203013	<i>Lasionycteris noctivagans</i>	This study
A19-2238; 2019027361	USA	New Mexico	Lincoln	Capitan	<i>Urocyon cinereoargenteus</i>	2019	OM202982	Novel New Mexico	This study
2015030671	USA	New Mexico	Eddy	Carlsbad	<i>Bassariscus astutus</i>	2015	OM203014	<i>Tadarida brasiliensis</i>	This study
2016005216	USA	New Mexico	De Baca	Fort Sumner	<i>Mephitis</i>	2016	*	South-central skunk	This study
2016008511	USA	New Mexico	De Baca	Fort Sumner	<i>Mephitis mephitis</i>	2016	OM203015	South-central skunk	This study
2016022033	USA	New Mexico	De Baca	Fort Sumner	<i>Mephitis mephitis</i>	2016	OM203016	South-central skunk	This study
2016023718	USA	New Mexico	De Baca	Fort Sumner	<i>Mephitis mephitis</i>	2016	*	South-central skunk	This study
2017017313	USA	New Mexico	Colfax	Raton	<i>Myotis thysanodes</i>	2017	OM203017	<i>Myotis californicus</i>	This study
2017017380	USA	New Mexico	Dona Ana	Las Cruces	<i>Tadarida brasiliensis</i>	2017	*	<i>Tadarida brasiliensis</i>	This study
2017018982	USA	New Mexico	Roosevelt	Portales	<i>Urocyon cinereoargenteus</i>	2017	OM203018	South-central skunk	This study
2017020232	USA	New Mexico	Santa Fe	Edgewood	<i>Eptesicus fuscus</i>	2017	*	<i>Eptesicus fuscus</i> -W1	This study
2017020434	USA	New Mexico	Curry	Clovis	<i>Mephitis mephitis</i>	2017	OM203019	South-central skunk	This study
2017020702	USA	New Mexico	Santa Fe	Espanola	<i>Myotis sp</i>	2017	OM203020	<i>Myotis californicus</i>	This study
2017025341	USA	New Mexico	Colfax	Raton	<i>Mephitis mephitis</i>	2017	*	South-central skunk	This study
2017027177	USA	New Mexico	Santa Fe	Santa Fe	<i>Tadarida brasiliensis</i>	2017	*	<i>Tadarida brasiliensis</i>	This study
2017027736	USA	New Mexico	Hidalgo	Lordsburg	<i>Lynx rufus</i>	2017	*	Cosmopolitan (AZFX)	This study

Isolate	Country	State	County	City	Host source	Year	GenBank accession no.	RABV lineage	Reference
2017029131	USA	New Mexico	Lincoln	Ruidoso	<i>Urocyon cinereoargenteus</i>	2017	OM203021	<i>Eptesicus fuscus</i> -W1	This study
2017029692	USA	New Mexico	Hidalgo	Rodeo	<i>Lynx rufus</i>	2017	OM203022	Cosmopolitan (AZFX)	This study
2017034789	USA	New Mexico	Colfax	Maxwell	<i>Canis latrans</i>	2017	OM203023	South-central skunk	This study
2018001861	USA	New Mexico	Santa Fe	Santa Fe	<i>Mephitis mephitis</i>	2018	OM203024	South-central skunk	This study
2018011578	USA	New Mexico	Colfax	Cimarron	<i>Mephitis mephitis</i>	2018	OM203025	South-central skunk	This study
2018015102	USA	New Mexico	Santa Fe	Santa Fe	<i>Antrozous pallidus</i>	2018	OM203026	<i>Antrozous pallidus</i>	This study
2018015202	USA	New Mexico	Santa Fe	Santa Fe	<i>Mephitis mephitis</i>	2018	*	South-central skunk	This study
2018015604	USA	New Mexico	San Juan	Farmington	<i>Antrozous pallidus</i>	2018	OM203027	<i>Antrozous pallidus</i>	This study
2018018118	USA	New Mexico	De Baca	Fort Sumner	<i>Mephitis mephitis</i>	2018	OM203028	South-central skunk	This study
2018018773	USA	New Mexico	Bernalillo	Albuquerque	<i>Myotis lucifugus</i>	2018	*	<i>Tadarida brasiliensis</i>	This study
2018019209	USA	New Mexico	Santa Fe	Santa Fe	<i>Urocyon cinereoargenteus</i>	2018	OM203029	South-central skunk	This study
2018021859	USA	New Mexico	Dona Ana	Las Cruces	<i>Antrozous pallidus</i>	2018	OM203030	<i>Antrozous pallidus</i>	This study
2018026719	USA	New Mexico	San Juan	Aztec	<i>Nyctinomops macrotis</i>	2018	*	<i>Nyctinomops macrotis</i>	This study
2018028298	USA	New Mexico	Santa Fe	Santa Fe	<i>Mephitis mephitis</i>	2018	OM203031	South-central skunk	This study
2018029020	USA	New Mexico	Eddy	Carlsbad	<i>Tadarida brasiliensis</i>	2018	OM203032	<i>Tadarida brasiliensis</i>	This study
2018029317	USA	New Mexico	Curry	Clovis	<i>Felis catus</i>	2018	OM203033	South-central skunk	This study
2018029975	USA	New Mexico	Rio Arriba	Dulce	<i>Mephitis mephitis</i>	2018	OM203034	<i>Eptesicus fuscus</i> -W1	This study
2018032217	USA	New Mexico	San Juan	Bloomfield	<i>Mephitis mephitis</i>	2018	OM203035	<i>Nyctinomops macrotis</i>	This study
2019002104	USA	New Mexico	Santa Fe	Santa Fe	<i>Urocyon cinereoargenteus</i>	2019	OM203036	<i>Eptesicus fuscus</i> -W1	This study
2019005171	USA	New Mexico	Santa Fe	Santa Fe	<i>Urocyon cinereoargenteus</i>	2019	OM203037	<i>Eptesicus fuscus</i> -W1	This study
2019006128	USA	New Mexico	Santa Fe	Santa Fe	<i>Urocyon cinereoargenteus</i>	2019	OM203038	<i>Eptesicus fuscus</i> -W1	This study
2019007630	USA	New Mexico	Santa Fe	Santa Fe	<i>Mephitis mephitis</i>	2019	*	South-central skunk	This study
2019009072	USA	New Mexico	Santa Fe	Santa Fe	<i>Mephitis mephitis</i>	2019	*	South-central skunk	This study
2019009563	USA	New Mexico	De Baca	Fort Sumner	<i>Mephitis mephitis</i>	2019	*	South-central skunk	This study
2019009681	USA	New Mexico	De Baca	Fort Sumner	<i>Mephitis mephitis</i>	2019	*	South-central skunk	This study
2019010065	USA	New Mexico	Quay	Tucumcari	<i>Mephitis mephitis</i>	2019	*	South-central skunk	This study
2019011895	USA	New Mexico	Bernalillo	Albuquerque	<i>Mephitis mephitis</i>	2019	*	South-central skunk	This study
2019012604	USA	New Mexico	De Baca	Fort Sumner	<i>Urocyon cinereoargenteus</i>	2019	OM203039	South-central skunk	This study
2019013575	USA	New Mexico	De Baca	Fort Sumner	<i>Procyon lotor</i>	2019	*	South-central skunk	This study
2019014195	USA	New Mexico	Curry	Clovis	<i>Urocyon cinereoargenteus</i>	2019	*	South-central skunk	This study
2019015395	USA	New Mexico	Curry	Clovis	<i>Mephitis mephitis</i>	2019	OM203040	South-central skunk	This study
2019016184	USA	New Mexico	Roosevelt	Portales	<i>Mephitis mephitis</i>	2019	*	South-central skunk	This study
2019017081	USA	New Mexico	Curry	Clovis	<i>Mephitis mephitis</i>	2019	*	South-central skunk	This study
2019019506	USA	New Mexico	Colfax	Angel Fire	<i>Eptesicus fuscus</i>	2019	*	<i>Eptesicus fuscus</i> -W1	This study
2019020776	USA	New Mexico	Curry	Clovis	<i>Mephitis mephitis</i>	2019	*	South-central skunk	This study
2019022292	USA	New Mexico	Roosevelt	Portales	<i>Mephitis mephitis</i>	2019	*	South-central skunk	This study
2019022293	USA	New Mexico	Roosevelt	Portales	<i>Felis catus</i>	2019	*	South-central skunk	This study
2019023945	USA	New Mexico	Santa Fe	Santa Fe	Bat	2019	OM203041	<i>Eptesicus fuscus</i> -W1	This study
2019024119	USA	New Mexico	Santa Fe	Santa Fe	<i>Antrozous pallidus</i>	2019	*	<i>Antrozous pallidus</i>	This study
2019025160	USA	New Mexico	San Miguel	Las Vegas	Bat	2019	*	<i>Eptesicus fuscus</i> -W1	This study
2019026915	USA	New Mexico	Colfax	Angel Fire	<i>Mephitis mephitis</i>	2019	*	South-central skunk	This study
2019027778	USA	New Mexico	Rio Arriba	Abiquiu	<i>Nyctinomops macrotis</i>	2019	*	<i>Nyctinomops macrotis</i>	This study
2019027923	USA	New Mexico	Santa Fe	Santa Fe	<i>Urocyon cinereoargenteus</i>	2019	*	<i>Tadarida brasiliensis</i>	This study
2019033570	USA	New Mexico	Curry	Clovis	<i>Mephitis mephitis</i>	2019	*	South-central skunk	This study
SM870	USA	Florida			<i>Lasiurus intermedius</i>	1988	OM203047	<i>Lasiurus intermedius</i>	This study
SM871	USA	Florida			<i>Lasiurus intermedius</i>	1988	OM203048	<i>Lasiurus intermedius</i>	This study
SM873	USA	Florida			<i>Lasiurus intermedius</i>	1988	OM203049	<i>Lasiurus intermedius</i>	This study
A17-0022	USA	Arizona	Pima		<i>Urocyon cinereoargenteus</i>	2017	OM203042	Cosmopolitan (AZFX)	This study
A17-0026	USA	Arizona	Pima		<i>Urocyon cinereoargenteus</i>	2017	OM203043	Cosmopolitan (AZFX)	This study
A17-4105	USA	Arizona	Gila		<i>Urocyon cinereoargenteus</i>	2017	OM203044	Cosmopolitan (AZFX)	This study
A18-0242	USA	Arizona			<i>Canis latrans</i>	2018	OM203045	Cosmopolitan (AZFX)	This study
A19-0377	USA	Arizona			<i>Urocyon cinereoargenteus</i>	2019	OM203046	Cosmopolitan (AZFX)	This study

Isolate	Country	State	County	City	Host source	Year	GenBank accession no.	RABV lineage	Reference
EF31; 89RABL1461	Canada	Saskatchewan			<i>Eptesicus fuscus</i>	1989	AF351831	<i>Eptesicus fuscus</i> - E2	Nadin-Davis, S.A., et al 2001
ML7; 79RABL1020	Canada	Alta			<i>Myotis lucifugus</i>	1979	AF351837	<i>Lasionycteris noctivagans</i>	Nadin-Davis, S.A., et al 2001
LAN13; 80RABN4398	Canada	Ontario			<i>Lasionycteris noctivagans</i>	1980	AF351841	<i>Lasionycteris noctivagans</i>	Nadin-Davis, S.A., et al 2001
EF72; V570	USA	Connecticut			<i>Eptesicus fuscus</i>	1998	AF351854	<i>Eptesicus fuscus</i> - E1	Nadin-Davis, S.A., et al 2001
EF71; V569	USA	Connecticut			<i>Eptesicus fuscus</i>	1998	AF351860	<i>Eptesicus fuscus</i> - E1	Nadin-Davis, S.A., et al 2001
EF3; 72R4744	Canada	Ontario			<i>Eptesicus fuscus</i>	1972	AF351861	<i>Eptesicus fuscus</i> - E2	Nadin-Davis, S.A., et al 2001
2253	USA	California			<i>Antrozous pallidus</i>	1993	AF394869	<i>Antrozous pallidus</i>	Rodhe, R.E. et al, 2004
1566	USA	California	Pluma		<i>Myotis californicus</i>	1987	AF394871	<i>Myotis californicus</i>	Rohde, R.E., et al 2004
872	USA	Florida	Sarasota		<i>Lasiurus intermedius</i>	1988	AF394878	<i>Lasiurus intermedius</i>	Rodhe, R.E. et al, 2004
2247	USA	California			<i>Homo sapiens</i>	1994	AF394879	<i>Lasionycteris noctivagans</i>	Rodhe, R.E. et al, 2004
2152	USA	New York	Westchester		<i>Lasionycteris noctivagans</i>	1984	AF394880	<i>Lasionycteris noctivagans</i>	Rodhe, R.E. et al, 2004
1435	USA	Arkansas	Houston		<i>Pipistrellus subflavus</i>	1991	AF394881	<i>Perimyotis subflavus</i>	Rodhe, R.E. et al, 2004
2698	USA	Tennessee			<i>Homo sapiens</i>	1994	AF394882	<i>Perimyotis subflavus</i>	Rodhe, R.E. et al, 2004
446	USA	Georgia	Clayton		<i>Lasiurus cinereus</i>	1982	AF394884	<i>Lasiurus cinereus</i>	Rodhe, R.E. et al, 2004
885	USA	Florida	Escambia		<i>Lasiurus borealis</i>	1988	AF394885	<i>Lasiurus borealis</i>	Rodhe, R.E. et al, 2004
2085	USA	Texas	Walker		<i>Lasiurus borealis</i>	1986	AF394886	<i>Lasiurus borealis</i>	Rodhe, R.E. et al, 2004
804	USA	California	Lake		<i>Eptesicus fuscus</i>	1987	AF394887	<i>Eptesicus fuscus</i> -W2	Rodhe, R.E. et al, 2004
136	USA	Pennsylvania	Perry		<i>Eptesicus fuscus</i>	1984	AY039226	<i>Eptesicus fuscus</i> - E1	Rodhe, R.E. et al, 2004
2049	USA	Colorado	El Paso		<i>Eptesicus fuscus</i>	1985	AY039228	<i>Eptesicus fuscus</i> - E2	Rohde, R.E., et al 2004
132	USA	Pennsylvania	Adams		<i>Eptesicus fuscus</i>	1984	AY039229	<i>Eptesicus fuscus</i> - E2	Rohde, R.E., et al 2004
3659	USA	Arizona	Flagstaff		<i>Nyctinomops macrotis</i>	1997	AY170304	<i>Nyctinomops macrotis</i>	Leslie, M.J., et al 2006
SHBRV-18	USA					NA	AY705373	<i>Lasionycteris noctivagans</i>	Faber, M., et al 2004
conm5293	USA	Colorado			<i>Nyctinomops macrotis</i>	NA	AY960093	<i>Nyctinomops macrotis</i>	Shankar, V., et al 2005
A033756NYrac1584	USA	New York	Westchester		<i>Procyon lotor</i>	2003	DQ886041	Eastern raccoon	Biek, R., et al, 2007
PA23	USA	Pennsylvania	Fulton		<i>Procyon lotor</i>	2004	EF508139	Eastern raccoon	Biek, R., et al, 2007
V211	USA	Texas			<i>Mephitis mephitis</i>	1994	EU345002	South-central skunk	Szanto, A., et al, 2007, unpub. data
NewMexicoDG2006	USA	New Mexico			<i>Canis familiaris</i>	2006	FJ228487	<i>Tadarida brasiliensis</i>	Velasco-Villa, A., et al 2008
2153Salvhm02	USA				<i>Homo sapiens</i>	2002	FJ228492	<i>Desmodus rotundus</i>	Velasco-Villa, A., et al 2008
3901Mxmichbv03	Mexico	Michoacan			<i>Bos taurus</i>	2003	FJ228493	<i>Desmodus rotundus</i>	Velasco-Villa, A., et al 2008
412Mxyucdg02	Mexico	Yucatan			<i>Canis familiaris</i>	2002	FJ228525	Cosmopolitan (Dog)	Velasco-Villa, A., et al 2008
FLdg1994	USA	Florida			<i>Canis familiaris</i>	1994	FJ228528	Cosmopolitan (Dog)	Velasco-Villa, A., et al 2008
H2USTXWillcy98	USA	Texas			<i>Canis latrans</i>	1998	FJ228530	Cosmopolitan (Dog)	Velasco-Villa, A., et al 2008
DgNYKprwsky1950	USA	New York			<i>Canis familiaris</i>	1950	FJ228535	Cosmopolitan (Dog)	Velasco-Villa, A., et al 2008
TX692007	USA	Texas			<i>Canis latrans</i>	2007	FJ228536	Cosmopolitan (TXFX)	Velasco-Villa, A., et al 2008
TX672007	USA	Texas			<i>Urocyon cinereoargenteus</i>	2007	FJ228538	Cosmopolitan (TXFX)	Velasco-Villa, A., et al 2008
3148Mxchihbct94	Mexico	Chihuahua			<i>Lynx rufus</i>	1994	FJ228542	Cosmopolitan (AZFX)	Velasco-Villa, A., et al 2008
AZ1968	USA	Arizona			<i>Eptesicus fuscus</i>	2004	GU644642	<i>Eptesicus fuscus</i> -W1	Stricker, D.G., et al 2010
AZ7590	USA	Arizona			<i>Eptesicus fuscus</i>	2005	GU644643	<i>Lasiurus xanthinus</i>	Stricker, D.G., et al 2010
CA29	USA	California			<i>Eptesicus fuscus</i>	2002	GU644645	<i>Eptesicus fuscus</i> -W2	Stricker, D.G., et al 2010
IA381	USA	Iowa			<i>Eptesicus fuscus</i>	2005	GU644655	<i>Eptesicus fuscus</i> - E2	Stricker, D.G., et al 2010
MI1865	USA	Michigan			<i>Eptesicus fuscus</i>	2005	GU644667	<i>Eptesicus fuscus</i> - E2	Stricker, D.G., et al 2010
WA1833	USA	Washington			<i>Eptesicus fuscus</i>	2005	GU644693	<i>Eptesicus fuscus</i> -W2	Stricker, D.G., et al 2010
WA2017	USA	Washington			<i>Eptesicus fuscus</i>	2005	GU644695	<i>Eptesicus fuscus</i> - E2	Stricker, D.G., et al 2010
FL701	USA	Florida			<i>Lasiurus borealis</i>	2003	GU644698	<i>Lasiurus seminolus</i>	Stricker, D.G., et al 2010
TN33	USA	Tennessee			<i>Lasiurus borealis</i>	2004	GU644705	<i>Lasiurus borealis</i>	Stricker, D.G., et al 2010
TX6070	USA	Texas			<i>Lasiurus borealis</i>	2003	GU644707	<i>Lasiurus borealis</i>	Stricker, D.G., et al 2010
TX5276	USA	Texas			<i>Lasiurus borealis</i>	2004	GU644709	<i>Lasiurus borealis</i>	Stricker, D.G., et al 2010
AZ1838	USA	Arizona			<i>Lasiurus cinereus</i>	2005	GU644712	<i>Lasiurus cinereus</i>	Stricker, D.G., et al 2010

Isolate	Country	State	County	City	Host source	Year	GenBank accession no.	RABV lineage	Reference
ID7227	USA	Idaho			<i>Lasiurus cinereus</i>	2005	GU644715	<i>Lasiurus cinereus</i>	Stricker, D.G., et al 2010
FL1024	USA	Florida			<i>Lasiurus intermedius</i>	2001	GU644722	<i>Lasiurus intermedius</i>	Stricker, D.G., et al 2010
FL905	USA	Florida			<i>Lasiurus intermedius</i>	2001	GU644724	<i>Lasiurus intermedius</i>	Stricker, D.G., et al 2010
FL978	USA	Florida			<i>Lasiurus intermedius</i>	2001	GU644725	<i>Lasiurus intermedius</i>	Stricker, D.G., et al 2010
FL1165	USA	Florida			<i>Lasiurus intermedius</i>	2004	GU644726	<i>Lasiurus intermedius</i>	Stricker, D.G., et al 2010
TX5433	USA	Texas			<i>Lasiurus intermedius</i>	2003	GU644728	<i>Lasiurus xanthinus</i>	Stricker, D.G., et al 2010
ID7376	USA	Idaho			<i>Lasionycteris noctivagans</i>	2005	GU644730	<i>Lasiurus cinereus</i>	Stricker, D.G., et al 2010
GA7034	USA	Georgia			<i>Lasiurus seminolus</i>	2003	GU644732	<i>Lasiurus seminolus</i>	Stricker, D.G., et al 2010
TX5850	USA	Texas			<i>Lasiurus seminolus</i>	2002	GU644736	<i>Lasiurus borealis</i>	Stricker, D.G., et al 2010
TX6127	USA	Texas			<i>Lasiurus seminolus</i>	2003	GU644737	<i>Lasiurus borealis</i>	Stricker, D.G., et al 2010
CA06	USA	California			<i>Lasiurus xanthinus</i>	2004	GU644740	<i>Lasiurus xanthinus</i>	Stricker, D.G., et al 2010
ID7198	USA	Idaho			<i>Myotis californicus</i>	2005	GU644743	<i>Myotis californicus</i>	Stricker, D.G., et al 2010
WA1502	USA	Washington			<i>Myotis californicus</i>	2004	GU644745	<i>Myotis californicus</i>	Stricker, D.G., et al 2010
MI1100	USA	Michigan			<i>Myotis lucifugus</i>	2005	GU644748	<i>Lasionycteris noctivagans</i>	Stricker, D.G., et al 2010
AZ2857	USA	Arizona			<i>Myotis yumanensis</i>	2004	GU644751	<i>Myotis yumanensis</i>	Stricker, D.G., et al 2010
CA828	USA	California			<i>Myotis yumanensis</i>	2004	GU644752	<i>Myotis yumanensis</i>	Stricker, D.G., et al 2010
IN1657	USA	Indiana			<i>Pipistrellus subflavus</i>	2004	GU644757	<i>Perimyotis subflavus</i>	Stricker, D.G., et al 2010
TX5168	USA	Texas			<i>Pipistrellus subflavus</i>	2004	GU644758	<i>Perimyotis subflavus</i>	Stricker, D.G., et al 2010
MS076	USA	Mississippi			<i>Tadarida brasiliensis</i>	2004	GU644782	<i>Tadarida brasiliensis</i>	Stricker, D.G., et al 2010
NMBAT2007	USA	New Mexico			<i>Tadarida brasiliensis</i>	2007	GU991831	<i>Tadarida brasiliensis</i>	Velasco-Villa,A. and Rupperecht, C.E, 2016 unpub. data
TXdg1968	USA	Texas			<i>Canis familiaris</i>	1968	GU991837	South-central skunk	Velasco-Villa,A. and Rupperecht, C.E, 2016, unpub. data
H01/08	Colombia				<i>Homo sapiens</i>	2008	JF693456	<i>Desmodus rotundus</i>	Caicedo,Y., et al 2015
WA1185	USA	Washington			<i>Lasionycteris noctivagans</i>	2003	JQ595315	<i>Lasionycteris noctivagans</i>	Streicker, D.G., et al 2012
WA1066	USA	Washington			<i>Lasionycteris noctivagans</i>	2003	JQ595316	<i>Lasionycteris noctivagans</i>	Streicker, D.G., et al 2012
CA982	USA	California			<i>Mephitis mephitis</i>	1994	JQ685894	Cosmopolitan (CASK)	Kuzmin,I.V., et al 2012
WA1185	USA	Washington			<i>Lasionycteris noctivagans</i>	2003	JQ685895	<i>Lasionycteris noctivagans</i>	Kuzmin,I.V., et al 2012
SM5442	USA	Arizona	Flagstaff		<i>Eptesicus fuscus</i>	2001	JQ685897	<i>Eptesicus fuscus</i> -W1	Kuzmin,I.V., et al 2012
A10-0515	USA	Arizona			<i>Urocyon</i>	2009	JQ685899	Cosmopolitan (AZFX)	Kuzmin,I.V., et al 2012
FL769	USA	Florida			<i>cinereoargenteus</i>				
TN209	USA	Tennessee			<i>Lasiurus seminolus</i>	2003	JQ685900	<i>Lasiurus seminolus</i>	Kuzmin,I.V., et al 2012
CA04148	USA	California			<i>Lasiurus borealis</i>	2005	JQ685902	<i>Lasiurus borealis</i>	Kuzmin,I.V., et al 2012
CA100	USA	California			<i>Eptesicus fuscus</i>	2004	JQ685903	<i>Eptesicus fuscus</i> -W2	Kuzmin,I.V., et al 2012
TX5960	USA	Texas			<i>Eptesicus fuscus</i>	2005	JQ685909	<i>Eptesicus fuscus</i> -W1	Kuzmin,I.V., et al 2012
SM5077	USA	Arizona	Flagstaff		<i>Lasiurus xanthinus</i>	2002	JQ685910	<i>Lasiurus xanthinus</i>	Kuzmin,I.V., et al 2012
TX4904	USA	Arizona	Flagstaff		<i>Mephitis mephitis</i>	2001	JQ685911	<i>Eptesicus fuscus</i> -W1	Kuzmin,I.V., et al 2012
FL1010	USA	Texas			<i>Lasiurus intermedius</i>	2002	JQ685915	<i>Lasiurus intermedius</i>	Kuzmin,I.V., et al 2012
CO-Coyot-2010	USA	Florida			<i>Lasiurus intermedius</i>	2002	JQ685916	<i>Lasiurus intermedius</i>	Kuzmin,I.V., et al 2012
NJ2262	USA	Colorado			<i>Eptesicus fuscus</i>	2010	JQ685917	<i>Eptesicus fuscus</i> -W2	Kuzmin,I.V., et al 2012
EF	USA	New Jersey			<i>Lasiurus borealis</i>	2005	JQ685919	<i>Lasiurus borealis</i>	Kuzmin,I.V., et al 2012
TN186	USA	Pennsylvania			<i>Eptesicus fuscus</i>	1984	JQ685920	<i>Eptesicus fuscus</i> - E1	Kuzmin,I.V., et al 2012
WAEF03	USA	Tennessee			<i>Pipistrellus subflavus</i>	2005	JQ685922	<i>Perimyotis subflavus</i>	Kuzmin,I.V., et al 2012
2403	USA	Washington			<i>Eptesicus fuscus</i>	2004	JQ685925	<i>Eptesicus fuscus</i> - E2	Kuzmin,I.V., et al 2012
WA0173	USA	Arizona	Flagstaff		<i>Urocyon</i>	2009	JQ685928	<i>Eptesicus fuscus</i> -W1	Kuzmin,I.V., et al 2012
A10-0514	USA	<i>cinereoargenteus</i>			<i>Eptesicus fuscus</i>	2000	JQ685931	<i>Eptesicus fuscus</i> -W2	Kuzmin,I.V., et al 2012
AZBAT65094	USA	<i>Mephitis mephitis</i>			<i>Mephitis mephitis</i>	2009	JQ685938	South-central skunk	Kuzmin,I.V., et al 2012
A10-0511	USA	Arizona	Flagstaff		<i>Eptesicus fuscus</i>	1981	JQ685942	<i>Eptesicus fuscus</i> -W2	Kuzmin,I.V., et al 2012
NC839	USA	Arizona	Flagstaff		<i>Urocyon</i>	2009	JQ685943	Cosmopolitan (AZFX)	Kuzmin,I.V., et al 2012
SM4862	USA	<i>cinereoargenteus</i>			<i>Mephitis mephitis</i>	1984	JQ685944	Cosmopolitan (NCSK)	Kuzmin,I.V., et al 2012
TN310	USA	Arizona	Flagstaff		<i>Eptesicus fuscus</i>	1999	JQ685946	<i>Eptesicus fuscus</i> -W1	Kuzmin,I.V., et al 2012
A093504	USA	Tennessee			<i>Lasiurus cinereus</i>	2004	JQ685947	<i>Lasiurus cinereus</i>	Kuzmin,I.V., et al 2012
SM5101	USA	Arizona	Flagstaff		<i>Eptesicus fuscus</i>	2001	JQ685950	<i>Eptesicus fuscus</i> -W1	Kuzmin,I.V., et al 2012
SM4872	USA	Arizona	Flagstaff		<i>Mephitis mephitis</i>	2001	JQ685958	<i>Eptesicus fuscus</i> -W1	Kuzmin,I.V., et al 2012
A10-0512	USA	Arizona	Flagstaff		<i>Eptesicus fuscus</i>	2001	JQ685960	<i>Eptesicus fuscus</i> -W1	Kuzmin,I.V., et al 2012
CASK2	USA	Arizona			<i>Mephitis mephitis</i>	2009	JQ685968	South-central skunk	Kuzmin,I.V., et al 2012
AZ3003	USA	California			<i>Mephitis mephitis</i>	1974	JQ685970	Cosmopolitan (CASK)	Kuzmin,I.V., et al 2012
	USA	Arizona			<i>Antrozous pallidus</i>	2009	JQ685971	<i>Antrozous pallidus</i>	Kuzmin,I.V., et al 2012

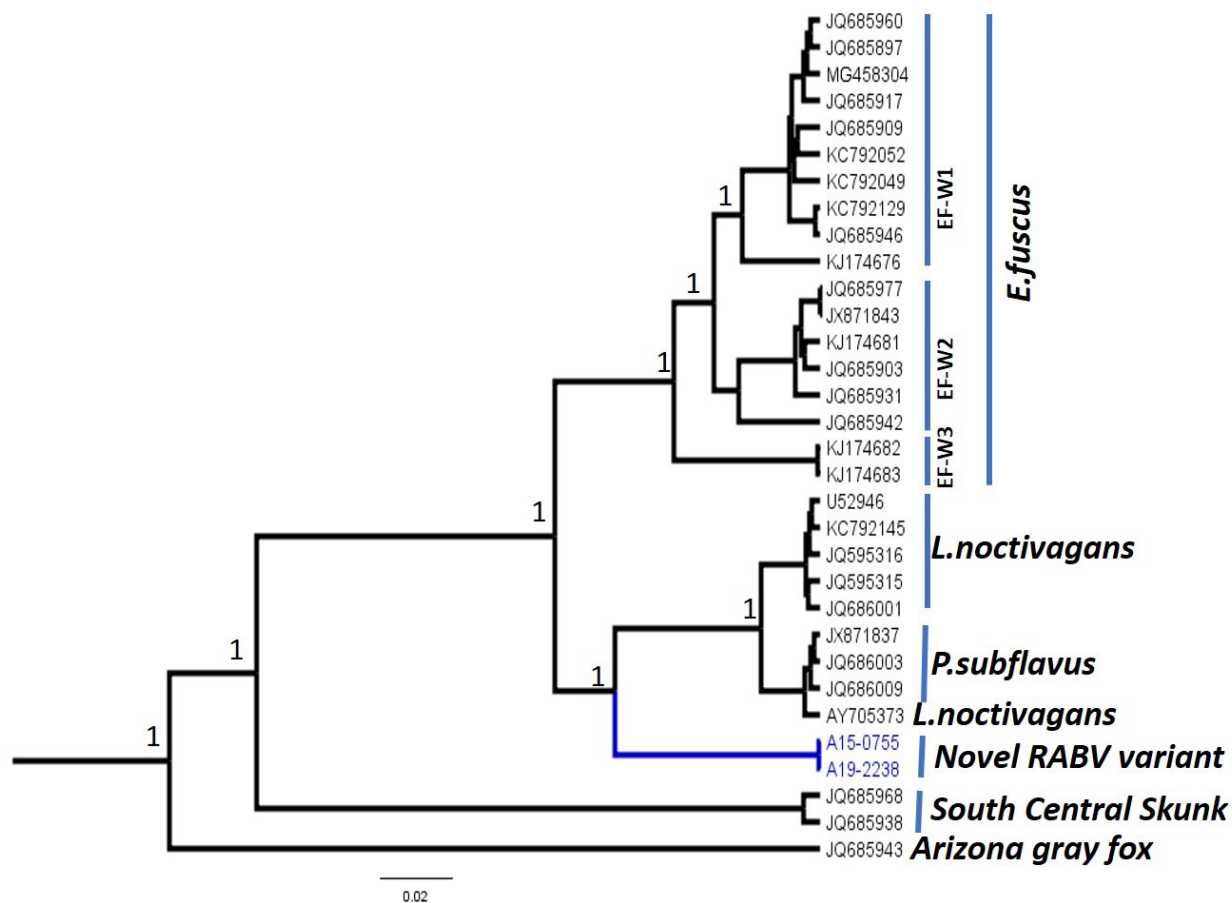
Isolate	Country	State	County	City	Host source	Year	GenBank accession no.	RABV lineage	Reference
OR58	USA	Oregon			<i>Urocyon cinereoargenteus</i>	2010	JQ685977	<i>Eptesicus fuscus</i> -W2	Kuzmin,I.V., et al 2012
AW3565	USA	Alabama			<i>Lasionycteris noctivagans</i>	2010	JQ686001	<i>Lasionycteris noctivagans</i>	Kuzmin,I.V., et al 2012
A10-5102	USA	North Carolina			<i>Perimyotis subflavus</i>	2010	JQ686003	<i>Perimyotis subflavus</i>	Kuzmin,I.V., et al 2012
A11-5737	USA	Virginia			<i>Vulpes vulpes</i>	2011	JQ686009	<i>Perimyotis subflavus</i>	Kuzmin,I.V., et al 2012
ARDG090042	USA	Arkansas			<i>Canis familiaris</i>	2009	JX855994	Cosmopolitan (NCSK)	Davis,R., et al, 2013
SDSK090045	USA	South Dakota			<i>Mephitis mephitis</i>	2009	JX855997	Cosmopolitan (NCSK)	Davis,R., et al, 2013
ARSK090068	USA	Arkansas			<i>Mephitis mephitis</i>	2009	JX856015	South-central skunk	Davis,R., et al, 2013
OKBV090073	USA	Oklahoma			<i>Bos taurus</i>	2009	JX856017	South-central skunk	Davis,R., et al, 2013
NEBV090102	USA	Nebraska			<i>Bos taurus</i>	2009	JX856036	South-central skunk	Davis,R., et al, 2013
A08-1210	USA				<i>Lasionycteris noctivagans</i>	2008	JX871837	<i>Perimyotis subflavus</i>	Ellison,J.A., et al 2013
A10-2057	USA				<i>Eptesicus fuscus</i>	2010	JX871843	<i>Eptesicus fuscus</i> -W2	Ellison,J.A., et al 2013
A12-0276	USA				<i>Urocyon cinereoargenteus</i>	2012	KC792049	<i>Eptesicus fuscus</i> -W1	Kuzmina,N.A., et al 2013
A12-0331	USA				Bat	2012	KC792052	<i>Eptesicus fuscus</i> -W1	Kuzmina,N.A., et al 2013
A12-4122	USA				<i>Eptesicus fuscus</i>	2012	KC792129	<i>Eptesicus fuscus</i> -W1	Kuzmina,N.A., et al 2013
A12-6377	USA				Bat	2012	KC792145	<i>Lasionycteris noctivagans</i>	Kuzmina,N.A., et al 2013
A13-3207	USA				<i>Eptesicus fuscus</i>	2012	KJ174676	<i>Eptesicus fuscus</i> -W1	Kuzmina,N.A., et al, unpub. data
A13-4551	USA				<i>Urocyon cinereoargenteus</i>	2012	KJ174681	<i>Eptesicus fuscus</i> -W2	Kuzmina,N.A., et al, unpub. data
A13-4546	USA				<i>Myotis lucifugus</i>	2012	KJ174682	<i>Eptesicus fuscus</i> -W3	Kuzmina,N.A., et al., unpub. data
A13-5626	USA				<i>Canis latrans</i>	2012	KJ174683	<i>Eptesicus fuscus</i> -W3	Kuzmina,N.A., et al, unpub. data
IP 350/10	Brazil				<i>Nyctinomops laticaudatus</i>	2010	KM594034	<i>Nyctinomops laticaudatus</i>	Oliveira, R.N. et al, 2014, unpub data
IP 542/10	Brazil				<i>Nyctinomops laticaudatus</i>	2010	KM594036	<i>Nyctinomops laticaudatus</i>	Oliveira, R.N. et al, 2014, unpub. data
05BC0708	Canada	Brackendale			<i>Myotis californicus</i>	2005	KY203100	<i>Myotis californicus</i>	Nadin-Davis,S.A., et al 2017
05BC0983	Canada	Summerland			<i>Myotis californicus</i>	2005	KY203103	<i>Myotis californicus</i>	Nadin-Davis,S.A., et al 2017
05ON2859	Canada				<i>Lasionycteris noctivagans</i>	2005	KY203107	<i>Lasionycteris noctivagans</i>	Nadin-Davis,S., et al, 2017
06ON0035	Canada				<i>Myotis leibii</i>	2006	KY203114	<i>Lasiurus seminolus</i>	Nadin-Davis,S., et al, 2017
RV50	USA				Bat	1975	MG458304	<i>Eptesicus fuscus</i> -W1	Fisher,S., et al 2018
A17-4052	USA	Oregon			Bat	2017	MW055098	<i>Eptesicus fuscus</i> - E2	Gigante,C.M., et al 2020
SHBRV	USA				<i>Lasionycteris noctivagans</i>	NA	U52946	<i>Lasionycteris noctivagans</i>	Morimoto,K., et al 1996

*Isolates not submitted to GenBank because of the length of the sequence was <200 bp. NA, not available; *numbers are not yet available.

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Appendix 2 Figure. Maximum clade credibility tree using full glycoprotein gene sequences of the novel rabies virus variant in blue and representative sequences of RABV associated with terrestrial mammals and bats (*Lasionycteris noctivagans*, *Perimyotis subflavus*, and *Eptesicus fuscus*). RABV, rabies virus.