University of Nebraska - Lincoln DigitalCommons@University of Nebraska - Lincoln

USDA National Wildlife Research Center - Staff Publications U.S. Department of Agriculture: Animal and Plant Health Inspection Service

2019

Isolation of Rabies Virus from the Salivary Glands of Wild and Domestic Carnivores during a Skunk Rabies Epizootic

Cornell University Jimenez Cornell University

Terry R. Spraker Colorado State University, terry.spraker@colostate.edu

Jessica Anderson Colorado State University

Richard Bowen Colorado State University, Richard.Bowen@colostate.edu

Amy Gilbert USDA National Wildlife Research Center, Amy.T.Gilbert@aphis.usda.gov

Follow this and additional works at: https://digitalcommons.unl.edu/icwdm_usdanwrc

Commons, Natural Resources and Conservation Commons, Natural Resources Management and Policy Commons, Veterinary Infectious Diseases Commons, and the Veterinary Preventive Medicine, Epidemiology, and Public Health Commons

Cornell University Jimenez; Spraker, Terry R.; Anderson, Jessica; Bowen, Richard; and Gilbert, Amy, "Isolation of Rabies Virus from the Salivary Glands of Wild and Domestic Carnivores during a Skunk Rabies Epizootic" (2019). USDA National Wildlife Research Center - Staff Publications. 2247. https://digitalcommons.unl.edu/icwdm_usdanwrc/2247

This Article is brought to you for free and open access by the U.S. Department of Agriculture: Animal and Plant Health Inspection Service at DigitalCommons@University of Nebraska - Lincoln. It has been accepted for inclusion in USDA National Wildlife Research Center - Staff Publications by an authorized administrator of DigitalCommons@University of Nebraska - Lincoln.

Journal of Wildlife Diseases, 55(2), 2019, pp. 473–476 © Wildlife Disease Association 2019

Isolation of Rabies Virus from the Salivary Glands of Wild and Domestic Carnivores during a Skunk Rabies Epizootic

Isabel Jimenez,¹ **Terry Spraker**,² **Jessica Anderson**,³ **Richard Bowen**,³ **and Amy Gilbert**^{4,5} ¹College of Veterinary Medicine, Cornell University, 602 Tower Road, Ithaca, New York 14853, USA; ²Department of Microbiology, Immunology, and Pathology, College of Veterinary Medicine and Biomedical Sciences, Colorado State University, 300 W Drake Road, Fort Collins, Colorado 80526, USA; ³Department of Biomedical Sciences, Colorado State University, 3107 Rampart Road, Fort Collins, Colorado 80523, USA; ⁴National Wildlife Research Center, US Department of Agriculture, Animal and Plant Health Inspection Service, Wildlife Services, 4101 Laporte Avenue, Fort Collins, Colorado 80521, USA; ⁵Corresponding author (email: amy.t.gilbert@aphis.usda.gov)

ABSTRACT: Rabies is a fatal zoonotic disease of global importance. Rabies virus is shed in the saliva of infected hosts and is primarily transmitted through bite contact. Canine rabies has been eliminated from the US, but wildlife constitutes more than 90% of the reported cases of animal rabies in the US each year. In the US, several wild carnivore species are reservoirs of distinct variants of rabies virus (RV). After decades of apparent absence, the south-central skunk (SCSK) RV variant was detected in Colorado in 2007 and resulted in a large-scale epizootic in striped skunk (Mephitis mephitis) populations in northern Colorado starting in 2012. We attempted isolation of RV from salivary gland tissues from confirmed rabid carnivores, comprising 51 striped skunks and seven other wild and domestic carnivores collected during 2013 through 2015 in northern Colorado. We isolated RV from 84.0% (158/188; 95% confidence interval=78.1-88.6%) of striped skunk and 71% (17/24; 95% confidence interval=51-85%) of other carnivore salivary glands. These data suggested that infected reservoir and vector species were equally likely to shed the SCSK RV variant and posed a secondary transmission risk to humans and other animals.

Key words: Carnivore, rabies virus, reservoir, salivary gland, skunk, vector.

Rabies lyssavirus (RV) is a neuroinvasive and neurotropic single-stranded negative sense RNA virus and is the only lyssavirus currently documented in the Americas (Rupprecht et al. 2011). Globally, two main evolutionary lineages of RV are associated with canids and bats, and each further comprises diverse variants that naturally circulate in wildlife (Troupin et al. 2016). Wildlife is an important source of human and domestic animal RV exposures and constitutes 92.4% of the 5,508 animal rabies cases in the US reported during 2015 through public health surveillance (Birhane et al. 2017). The majority of human exposures in the US are associated with circulation of the raccoon (*Procyon lotor*) RV variant, and postexposure prophylaxis is administered to an estimated 23,000 persons each year (Christian et al. 2009). Spillover infections occur when RV is transmitted from a reservoir host to another mammal species. Repeated spillover to competent vector species may lead to a host shift, in which RV can be perpetuated within a novel host (Kuzmin et al. 2012; Borucki et al. 2013).

The south-central skunk (SCSK) RV variant has geographically widespread circulation in striped skunks (*Mephitis mephitis*) in the US (Oertli et al. 2009; Kuzmina et al. 2013). Following decades of apparent absence in the state, it was detected in eastern Colorado in 2007 and spread to multiple counties in subsequent years (Gilbert et al. 2014). Epizootics of SCSK RV occurred in two counties in northern Colorado during 2012. During 2012– 14, spillover cases in wild carnivores and domestic animals represented 13.1% (21/160) of all terrestrial rabid animals and 3.4% (21/625) of all terrestrial submissions from three counties in northern Colorado (Pepin et al. 2017).

The primary mode of RV transmission is by inoculation of contaminated saliva into bite wounds. Viral replication may occur within muscle at the site of inoculation but is not required prior to viral entry into the central nervous system (CNS; Harrison and Murphy 1978; Charlton and Casey 1979; Shankar et al. 1991). After replicating in the CNS, RV spreads to highly innervated peripheral sites including the salivary glands (SGs). Additional viral replication may occur in the SGs, and viral particles are shed intermittently in the saliva immediately prior to and during the clinical stage of the disease. In this study, we collected brain, as well as mandibular and parotid SG, tissues from rabid wild and domestic carnivores in three counties in northern Colorado for attempted RV isolation to evaluate the risk of secondary transmission. Reports of suspect rabid animals were made by the public to local health departments, and animals were euthanatized by local authorities prior to sampling. Rabies testing of brainstem and cerebellar tissues was performed at one of two diagnostic laboratories in the state using the direct fluorescent antibody test (Centers for Disease Control and Prevention 2018). We immediately stored subsamples of brainstem and bilateral mandibular and parotid SGs at -80 C until isolation. We attempted virus isolation from SG tissues of 51 rabid striped skunks (reservoir) and seven other carnivores (vectors).

We homogenized tissues with stainless steel beads to 10% suspensions in 2 mL Dulbecco's Modified Eagle Medium (DMEM; Sigma-Aldrich, St. Louis, Missouri, USA) supplemented with 5% fetal bovine serum (FBS), decanted into labeled vials, and then clarified homogenates by centrifugation for 5-10 s at $500 \times G$. For each sample, we stored one vial of homogenate at -80 C and used the other for cell culture inoculation. For inoculation, we incubated 0.1 mL of homogenate for 30 min on an 80-90% confluent monolayer of mouse neuroblastoma cells in 25 cm² tissue culture flasks at 37 C. Each batch of inoculated flasks included one that was not inoculated and served as a negative control. Following incubation, we decanted media and washed the cell monolayer twice with 2-3 mL of sterile phosphate-buffered saline (PBS). We added 5 mL fresh DMEM plus 5% FBS to each flask and continued incubation for 2-4 d at 37 C and 5% carbon dioxide in air.

After incubation, we decanted supernatants into 15 mL centrifuge tubes and stored them at -80 C. We washed the cell monolayer once with 2-3 mL PBS, prior to the addition of 1 mL of trypsin solution to dislodge the cells. We transferred a 0.1 mL aliquot of trypsinized cell suspension into a new flask with 5 mL DMEM plus 5% FBS. We centrifuged the remaining 0.4 mL aliquot for 5–10 s at 500 × G and resuspended cells in 0.1 mL of PBS. We prepared spot slides, air dried, and fixed in acetone for staining. We stained slides using a FITC-labeled RV antibody conjugate (Fujirebio Diagnostics, Malvern, Pennsylvania, USA) and estimated the infection rate based on observation of 20 fields under 200× magnification using fluorescence microscopy.

We considered cells that had reached greater than 50% infection rate (i.e., greater than 10 of 20 fields infected) positive and assigned the sample a score based on the passage number. We scored positive cells on the first passage 3, second passage 2, and third passage 1. If positive cells were not observed by the third passage, we considered the sample negative and scored 0. For a positive passage, we added 1 mL of supernatant to duplicate tubes containing 0.1 mL of FBS and stored them at -80 C. We washed the cell monolayer with 1 mL of PBS, split into two 0.5 mL tubes, and centrifuged for 30 s at $8,000 \times G$. We aspirated the supernatant, dried the pellet, and then stored it at -80 C. If cells were not positive upon first passage, we transferred a 0.1 mL aliquot of trypsinized cell suspension into a new flask with 5 mL DMEM plus 5% FBS to repeat the process for up to two additional serial passage attempts.

We used generalized linear models to analyze the data, including mixed models where repeated observations from a single animal were used (e.g., left and right SGs). We treated the identification number of the animal as a random effect and then species (skunk or other carnivore) and SG type (parotid or mandibular) as fixed effects. We used a logistic regression model to assess the relationship between the fixed effects and isolation of RV in any SGs tested for a given animal (presence or absence) and a multinomial regression model to assess the relationship of fixed effects with increasing passage score in any of the SGs tested (scale of 0 to 3). We performed statistical analysis using SAS

Carnivore	No. of animals	No. of sampled salivary glands			
		Mandibular		Parotid	
		Left	Right	Left	Right
Striped skunk Mephitis mephitis	51	41/49	42/51	35/42	40/46
Raccoon Procyon lotor	2	2/2	1/2	1/1	0/2
Red fox Vulpes vulpes	3	2/3	2/3	2/2	1/2
Coyote Canis latrans	1	1/1	1/1	1/1	1/1
Domestic cat Felis catus	1	1/1	0/1	n.t.	1/1

TABLE 1. Rabies virus isolation attempts from salivary glands of rabid wild and domestic carnivores in northernColorado, USA during 2013–15.

9.4 software (SAS Institute, Cary, North Carolina, USA). We evaluated significance at α =0.05.

We isolated RV from 84.0% (158/188; 95% confidence interval=78.1-88.6%) of SGs from rabid skunks and 71% (17/24; 95% confidence interval=51-85%) of SGs from other rabid carnivores (Table 1). There was no species effect on the isolation of RV from SGs (F=2.2, P=0.14) or effect of SG type (F=0.02, P=0.90), indicating that RV isolation from mandibular or parotid SGs of rabid reservoir and vector animals was equally likely. The mean passage score for all SGs was 1.99 (SE ± 0.08) in skunks and 1.71 (SE ± 0.25) in other carnivores. No association was found between species (F=1.5, P=0.23) or SG type (F=0.5, P=0.47) and increasing passage score, suggesting similar passage success from mandibular and parotid SGs of rabid reservoir and vector animals.

While spillover events during this epizootic were relatively infrequent, a pattern consistent with skunk RV circulation in the US (Wallace et al. 2014), our data suggested that exposure to a confirmed rabid skunk or other domestic or wild carnivore carried an equal risk of RV exposure. The factors that predispose certain species to be RV reservoir hosts are not well understood but are thought to include anatomical, physiological, ecological, and phylogenetic factors, as well as viral genetic adaptations (Rupprecht et al. 2011; Mollentze et al. 2014). A decreased ability of skunk RV to infect heterologous species has been demonstrated experimentally (Hill and Beran 1992; Hill et al. 1993), where raccoons but not skunks are resistant to infection. Pathophysiological differences such as the presence and density of appropriate receptors at the bite location, immune response, and ability of the virus to infect the CNS and then spread to the SGs may influence vector competence. While similar RV shedding capacity was observed among rabid carnivores in this study, some vector species may still have reduced susceptibility to SCSK RV infection. Other limitations of these data included the low number of vectors sampled and lack of titration for individual SGs.

This study has implications for public education, exposure prevention, and postexposure recommendations (Manning et al. 2008). In the event of a potential exposure, one should seek immediate medical attention and contact the local public health department. Domestic companion animals are at risk of RV exposure through contact with wildlife and may become clinically infected and shed RV, posing a secondary transmission risk to humans. Routine vaccination of domestic animals is thus an important barrier to human infection. Most wild carnivores involved in a potential human or pet exposure should be regarded as rabid unless proven negative by laboratory testing.

We would like to thank C. Wickham, N. Walker, S. Eaton, D. Wostenberg, M. Diefenbach, J. Kanine, D. Madden, T. Garcia, and T. Rigg for assistance with sample collection. The state of Colorado Department of Natural Resources permitted this carcass tissue sampling under scientific collection licenses (14SALV2060, 15SALV2060). The findings and conclusions in this report have not been formally disseminated by the US Department of Agriculture and should not be construed to represent any agency determination or policy.

LITERATURE CITED

- Birhane MG, Cleaton JM, Monroe BP, Wadhwa A, Orciari LA, Yager P, Blanton J, Velasco-Villa A, Petersen BW, Wallace RM. 2017. Rabies surveillance in the United States during 2015. J Am Vet Med Assoc 250:1117–1130.
- Borucki MK, Chen-Harris H, Lao V, Vanier G, Wadford DA, Messenger S, Allen JE. 2013. Ultra-deep sequencing of intra-host rabies virus populations during cross-species transmission. *PLoS Negl Trop Dis* 7:e2555.
- Centers for Disease Control and Prevention. 2018. Protocol for postmortem diagnosis of rabies in animals by direct fluorescent antibody testing. https://www.cdc.gov/rabies/pdf/RabiesDFASPv2.pdf. Accessed April 2018.
- Charlton KM, Casey GA. 1979. Experimental rabies in skunks: Immunofluorescence light and electron microscopic studies. *Lab Invest* 41:36–44.
- Christian KA, Blanton JD, Auslander M, Rupprecht CE. 2009. Epidemiology of rabies post-exposure prophylaxis—United States of America, 2006–2008. Vaccine 27:7156–7161.
- Gilbert A, Kohler D, Rigg T, Fischer JW, Spraker T, Fox K, Vercauteren KC. 2014. A recent epizootic of skunk rabies and associated spillover in northern Colorado, USA. In: Proceedings of the 26th vertebrate pest conference 2014, Waikoloa, Hawaii, 3–6 March, pp. 323–327.
- Harrison AK, Murphy FA. 1978. Lyssavirus infection of muscle spindles and motor end plates in striated muscle of hamsters. Arch Virol 57:167–175.
- Hill RE Jr, Beran GW. 1992. Experimental inoculation of raccoons (*Procyon lotor*) with rabies virus of skunk origin. *J Wildl Dis* 28:51–56.
- Hill RE Jr, Smith KE, Beran GW, Beard PD. 1993. Further studies on the susceptibility of raccoons (*Procyon lotor*) to a rabies virus of skunk origin and comparative susceptibility of striped skunks (*Mephitis mephitis*). J Wildl Dis 29:475–477.

- Kuzmin IV, Shi M, Orciari LA, Yager PA, Velasco-Villa A, Kuzmina NA, Streicker DG, Bergman DL, Rupprecht CE. 2012. Molecular inferences suggest multiple host shifts of rabies viruses from bats to mesocarnivores in Arizona during 2001–2009. PLoS Pathog 8:e1002786.
- Kuzmina NA, Lemey P, Kuzmin IV, Mayes BC, Ellison JA, Orciari LA, Hightower D, Taylor ST, Rupprecht CE. 2013. The phylogeography and spatiotemporal spread of south-central skunk rabies virus. *PLoS One* 8:e82348.
- Manning SE, Rupprecht CE, Fishbein D, Hanlon CA, Lumlertdacha B, Guerra M, Meltzer MI, Dhankhar P, Vaidya SA, Jenkins SR, et al. 2008. Human rabies prevention—United States, 2008: Recommendations of the advisory committee on immunization practices. MMWR Recomm Rep 57(RR-3):1–28.
- Mollentze N, Biek R, Streicker DG. 2014. The role of viral evolution in rabies host shifts and emergence. *Curr Opin Virol* 8:68–72.
- Oertli EH, Wilson PJ, Hunt PR, Sidwa TJ, Rohde RE. 2009. Epidemiology of rabies in skunks in Texas. J Am Vet Med Assoc 234:616–620.
- Pepin KM, Davis AJ, Streicker DG, Fischer JW, Vercauteren KC, Gilbert AT. 2017. Predicting spatial spread of rabies in skunk populations using surveillance data reported by the public. *PLoS Negl Trop Dis* 11:e0005822.
- Rupprecht CE, Turmelle A, Kuzmin IV. 2011. A perspective on lyssavirus emergence and perpetuation. *Curr Opin Virol* 1:662–670.
- Shankar VI, Dietzschold BE, Koprowski HI. 1991. Direct entry of rabies virus into the central nervous system without prior local replication. J Virol 65:2736–2738.
- Troupin C, Dacheux L, Tanguy M, Sabeta C, Blanc H, Bouchier C, Vignuzzi M, Duchene S, Holmes EC, Bourhy H. 2016. Large-scale phylogenomic analysis reveals the complex evolutionary history of rabies virus in multiple carnivore hosts. *PLoS Pathog* 12: e1006041.
- Wallace RM, Gilbert A, Slate D, Chipman R, Singh A, Wedd C, Blanton JD. 2014. Right place, wrong species: A 20-year review of rabies virus cross species transmission among terrestrial mammals in the United States. *PLoS One* 9:e107539.

Submitted for publication 11 May 2018. Accepted 20 July 2018.