Detection of Vaccinia Virus in Urban Domestic Cats, Brazil

Galileu Barbosa Costa, Júlia Bahia Miranda, Gregório Guilherme Almeida, Jaqueline Silva de Oliveira, Mariana Siqueira Pinheiro, Steffanye Aparecida Gonçalves, Jenner Karlsson Pimenta dos Reis, Ricardo Gonçalves, Paulo César Peregrino Ferreira, Cláudio Antônio Bonjardim, Jônatas Santos Abrahão, Erna Geessien Kroon, Giliane de Souza Trindade

Author affiliation: Universidade Federal de Minas Gerais, Belo Horizonte, Brazil

DOI: http://dx.doi.org/10.3201/eid2302.161341

We investigated possible vaccinia virus (VACV) in urban house cats in Brazil. Serum samples from 6 cats were positive for VACV by PCR, indicating likely VACV circulation among house cats in urban areas of Brazil. This finding highlights the importance of epidemiologic surveillance to avoid outbreaks among urban human populations.

Vaccinia virus (VACV) outbreaks, first reported in Brazil in 1999, affect dairy cattle and humans in rural areas (1). Although studies have shown evidence of VACV circulation among several mammal species (1–3), no consensus exists regarding the role of these animals in the VACV transmission chain or which animal is the natural reservoir. In fact, domestic or wild mammals could be asymptomatic hosts and also contribute to VACV transmission (3).

In contrast to VACV, cowpox virus (CPXV) circulates in urban environments in Europe but also in surrounding wild and rural areas (4). CPXV is transmitted to humans mainly by cats, which play a link between the natural reservoir and humans in the urban environment (4,5). In cats, the clinical course of CPXV infection varies from no symptoms to widespread skin necrotic lesions and can ultimately lead to death (6). Some studies have shown serologic evidence of orthopoxvirus infection in cats from Europe and have addressed the role of these animals in orthopoxvirus transmission to humans (7,8).

Because VACV and CPXV share some epidemiologic features and cats have a prominent role in the urban CPXV transmission chain, we decided to investigate whether urban domestic cats have evidence of exposure to VACV in Brazil. This study was approved by the Animal Experiments Committee of the Universidade Federal de Minas Gerais (registration protocol 315/2014).

We performed a retrospective study of serum samples from 277 house cats, collected during September 2012–December 2014 in 5 states in Brazil (online Technical Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/23/2/16-1341-Techapp1.pdf). The states in this study were those whose veterinary clinics agreed to submit samples. We screened serum samples for neutralizing antibodies by using a ≥70% plaque-reduction neutralization test (9). To detect VACV DNA in serum samples, we performed real-time PCR targeting the C11R and A56R genes (9). We directly sequenced A56R fragments in both orientations and in triplicate by using the Mega-BACE sequencer (GE Healthcare, Buckinghamshire, UK). We used ClustalW (http://www.genome.jp/tools/clustalw) and MEGA7 soft-
ware (http://www.megasoftware.net) to align nucleotide sequences and construct a phylogenetic tree (neighbor-joining method with 1,000 bootstraps).

The cats’ ages ranged from 3 months to 15 years; 150 (54.2%) of the cats were female. Thirteen cats (4.7%) had outdoor access, and 37 (13.4%) were admitted to the veterinary clinic for ≥1 night. Some cats had clinical illness inconsistent with orthopoxvirus infection, which can overlap with other common dermatologic diseases affecting cats (online Technical Appendix Table). Most (8/53 [15.1%]) seropositive cats were from the Pampulha region of the city of Belo Horizonte (Minas Gerais State) (online Technical Appendix Figure 1), followed by the eastern region of the city. We detected neutralizing antibodies in 16 animals (5.8%), with titers ranging from 100 to 1,600 neutralizing units/mL; of these, 13 (4.7%) were positive for C11R gene and 6 for A56R gene (online Technical Appendix Table). Alignment of the A56R fragments showed high similarity to the homologous gene of VACV isolates from Brazil (online Technical Appendix Figure 1). For the phylogenetic tree, we grouped sequences with VACV group 1 and 2 isolates (Figure).

We describe evidence of VACV circulation in cats in an urban environment in Brazil. Many studies have attempted to elucidate VACV outbreaks and risk factors in rural and wild areas (1–3). Our findings reveal a seropositivity rate of...
Financial support was provided by the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG), and Pró-Reitoria de Pesquisa/UFMG (PRPq). C.A. Bonjardim, J.S. Abrahão, E.G. Kroon, J.K.P. Reis, and G.S. Trindade are researchers from CNPq.

Mr. Costa is a PhD candidate in biomedicine at the Laboratório de Vírus, Microbiology Department, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais. His research is focused on the diagnosis, epidemiology, control, and prevention of orthopoxviruses and other emerging viruses.

Acknowledgments

We thank Associação Bichos Gerais, who provided some cat serum samples from Belo Horizonte. We also thank colleagues from the Laboratório de Vírus (ICB-UFMG) for their excellent technical support.

Financial support was provided by the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG), and Pró-Reitoria de Pesquisa/UFMG (PRPq). C.A. Bonjardim, J.S. Abrahão, E.G. Kroon, J.K.P. Reis, and G.S. Trindade are researchers from CNPq.

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Address for correspondence: Giliane de Souza Trindade, 6627 Avenida Presidente Antônio Carlos, Pampulha, Belo Horizonte – MG, 31270-901, Brazil; email: giliane@icb.ufmg.br