South America, mainly for their fleece, with estimated numbers in 2014 reaching 230,000 in the United States (http://lib.icimod.org/record/23682), 35,000 in the United Kingdom (http://www.bas-uk.com), and 150,000 in Australia (http://www.alpaca.asn.au). Although MERS-CoV has not been found in camels other than dromedaries outside the Arabian Peninsula so far (9), our observations raise the question of whether other camels could become infected if MERS-CoV were introduced to regions with large populations of alpacas and possibly other closely related camels of the genera *Lama, Vicugna,* and *Camelus.*

Because the date of infection of the alpacas and camels in this study is not known, we cannot speculate on the level of susceptibility of alpacas versus dromedaries based on the observed differences in antibody titers, which were lower in alpacas. It remains to be determined whether alpacas, in parallel with dromedaries, will actually shed MERS-CoV and are capable of independent maintenance of the virus in their population. Differences in susceptibility to viral pathogens between New and Old World camels have been observed before (10). Therefore, understanding the risk requires further assessment of the reservoir competence of alpacas for MERS-CoV (e.g., through experimental infections) and an assessment of MERS-CoV–related viruses present in alpacas and other camels in different parts of the world.

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Address for correspondence: Chantal B.E.M. Reusken, Viroscience Department, Erasmus Medical Center, PO Box 2040, Rotterdam 3000 CA, the Netherlands; email: c.reusken@erasmusmc.nl

Cryptococcus gattii
VGIIb-like Variant in White-Tailed Deer, Nova Scotia, Canada

David P. Overy,1 Scott McBurney,1 Anne Muckle, Lorraine Lund, P. Jeffery Lewis, Robert Strang

Author affiliations: Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, Prince Edward Island, Canada (D.P. Overy, S. McBurney, A. Muckle, L. Lund, P.J. Lewis); Department of Health and Wellness, Halifax, Nova Scotia, Canada (R. Strang)

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To the Editor: Cryptococcus gattii is a fungal pathogen that is emerging in the Pacific Northwest of North America. In Nova Scotia, Canada, previously not recognized as a C. gattii–endemic area, a variant strain similar to VGIIb caused cryptococcosis with nasopulmonary, lymph node and central nervous system involvement in a free-ranging, yearling white-tailed deer (Odocoileus virginianus). The deer was found in the village of Greenwood (latitude 44.971724; longitude –64.9341295) on July 14, 2014. The deer exhibited behavioral and neurologic abnormalities, including

1These authors contributed equally to this article.
loss of fear of humans, ataxia, circling, high-stepping gait, torticollis, and a fixed stare. Additional clinical signs were ptalism with frothing from the mouth and dyspnea with gurgling respiration. The animal was euthanized, and the head, lungs, heart, gastrointestinal tract, liver, and kidneys were submitted for pathologic examination.

Gross examination revealed multifocal, soft, round, expansile, pale tan masses of variable sizes that had replaced or effaced the normal architecture of the tracheobronchial lymph nodes and pulmonary parenchyma. The center of the largest lymph node mass was necrotic and filled with viscous yellow material. Similar yellow gelatinous material obliterated the right ethmoturbinates rostral to the cribriform plate. In the brain, cerebellar coning was prominent. Several small, pitted lesions with dark rims were noted in the neuropil of the thalami, superior colliculi, and hippocampus. Gross lesions were absent in the liver, kidney, and gastrointestinal tract (online Technical Appendix, http://wwwnc.cdc.gov/EID/article/22/6/16-0081-Techapp1.pdf).

Microscopically, the nasal cavity, lung, tracheobronchial lymph node, and brain lesions were similar, consisting of variably sized, cystic spaces supported by various thicknesses of well-differentiated fibrovascular septa or remaining normal parenchyma. The cystic spaces, immediately adjacent tissues, meninges, and ependyma contained variable numbers of yeast associated with a granulomatous inflammatory response or a pleocellular population of lymphocytes, plasma cells, macrophages, and neutrophils (Figure). The yeast were round to oval, 15–33 μm in total diameter, with poorly staining central portions (5–12 μm in diameter) surrounded by a pale acidophilic or basophilic capsule (5–21 μm thick), which stained positively with a mucicarmine stain. Some yeast were dematiaceous, and Fontana-Masson staining was consistent with presence of melanin. Very rarely, narrow-based budding was observed in the yeast. All aforementioned morphologic characteristics, staining affinities, and lesion distributions are consistent with an infection with fungi in the genus Cryptococcus (1,2).

One species of Cryptococcus was isolated from a tracheobronchial lymph node aspirate. Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry fingerprinting of the isolate (Biotyper RTC software; Bruker Daltonics Ltd, Bremen, Germany) yielded 8 diagnostic signals consistent with C. gattii VGIIb and VGIIc; therefore, the isolate was further classified by multilocus sequence typing based on 7 genetic loci, following the International Society for Human and Animal Mycology consensus multilocus sequence typing scheme for the C. neoformans/C. gattii species complex (3). Further discrimination based on allele congruence with established C. gattii VGII genotypes (4) classified the isolate as being most similar to genotype C. gattii VGIIb (CAP59 allele no. 2, GPD1 allele no. 6, LAC1 allele no. 4, PLB1 allele no. 2, URA5 allele no. 2, IGSl allele no. 10). However, because of a slight difference in the SOD1 allele (99.5% similarity with allele no. 15), this strain is considered to be a unique variant strain, most similar to that of the VGIIb genotype. Whole-genotyping studies have provided evidence of multiple distinct introductions of the VGIIb genotype to North America (5). Because of the observed difference in the SOD1 allele, the VGIIb-like variant strain may represent a fourth introduction or a different VGII genotype altogether.

The white-tailed deer represents a new host species for C. gattii in North America. Because white-tailed deer are nonmigratory, generally exhibiting only minor seasonal

![Figure. Tissue from white-tailed deer (Odocoileus virginianus), showing microscopic lesions caused by a unique Cryptococcus gattii VGIIb-like variant strain most similar to that of the VGIIb genotype; etiology was confirmed by molecular sequencing.](image-url)
movements (6), this infection was considered to be autochthonous, indicating endemicity of the C. gattii VGIIb-like variant in Nova Scotia and highlighting the value of non-migratory animals as sentinels for emerging diseases (7). Incidence for this disease is highest in the Pacific Northwest, where the primary agents are C. gattii VGII genotypes (2,4). A pertinent literature review and consultation with regional public and veterinary health authorities determined that Québec was the most eastern province in Canada where cryptococcosis associated with C. gattii VGII has caused clinical disease that was not potentially travel related in humans (Philippe Dufresne, pers. comm.). In eastern North America, the C. gattii VGIIb genotype is reported to have caused disseminated cryptococcosis in a human in Florida, USA (8,9). Because C. gattii is potentially pervasive in the environment, the Nova Scotia Department of Health has alerted provincial infectious disease specialists and the provincial public health laboratory to ensure availability of the diagnostic capacity to test for the fungus.

The C. gattii VGIIb genotype causes substantial, life-threatening disease in otherwise healthy hosts (2), and a unique VGIIb-like variant is endemic to Atlantic Canada. Therefore, continued surveillance by physicians and veterinarians in the region is warranted.

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Address for correspondence: David P. Overy, Department of Pathology and Microbiology, Atlantic Veterinary College, University of Prince Edward Island, 550 University of Prince Edward Island, Charlottetown, PEI, Canada; email: dovery@upei.ca

Zika Virus in a Traveler Returning to China from Caracas, Venezuela, February 2016

Jiandong Li, Ying Xiong, Wei Wu, Xiaoqing Liu, Jing Qu, Xiang Zhao, Shuo Zhang, Jianhua Li, Weihong Li, Yong Liao, Tian Gong, Lijing Wang, Yong Shi, Yanfeng Xiong, Daxin Ni, Qun Li, Mifang Liang, Guoliang Hu, Dexin Li

Author affiliations: National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China (Jiandong Li, W. Wu, J. Qu, X. Zhao, S. Zhang, L. Wang, M. Liang, D. Li); Jiangxi Provincial Center for Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Nanchang, China (Y. Xiong, X. Liu, T. Gong, Y. Shi, G. Hu); Ganzhou Municipal Center for Disease Control and Prevention, Ganzhou, China (Jianhua Li, Y. Liao, Y. Xiong); Office of Emergence Response, Chinese Center for Disease Control and Prevention, Beijing (D. Ni, Q. Li); Beijing Center for Disease Prevention and Control, Beijing (W. Li)

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To the Editor: Zika virus, a member of the Flaviviridae family, is primarily transmitted through Aedes spp. mosquitoes, and evidence of vertical, sexual, and blood

*These authors contributed equally to this article.*