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Short-Finned Pilot Whale Strandings Associated with Pilot Whale Morbillivirus, Brazil

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Cetacean morbillivirus (CeMV) causes illness and death in cetaceans worldwide; the CeMV strains circulating in the Southern Hemisphere are poorly known. We detected a pilot whale CeMV strain in 3 short-finned pilot whales (*Globicephala macrorhynchus*) stranded in Brazil during July–October 2020. Our results confirm this virus circulates in this species.

Cetacean morbillivirus (CeMV; family Paramyxoviridae, genus *Morbillivirus*) is an important cause of illness and death in cetaceans (*1*). The genus *Morbillivirus* comprises 2 lineages: CeMV-1, which includes dolphin morbillivirus (DMV), porpoise morbillivirus (PMV), pilot whale morbillivirus (PWMV), and beaked whale morbillivirus (BWMV) strains; and CeMV-2, comprising the strain detected in Indo-Pacific bottlenose dolphins (*Tursiops aduncus*) in western Australia, the Fraser's dolphin morbillivirus (FDMV), and Guiana dolphin morbillivirus (GDMV) strains (*1*,*2*). GDMV has been the only strain reported in cetaceans in Brazil (*3*). Four cases of PWMV have been recorded in pilot whales of the Northern Hemisphere, on the Atlantic coast of the United States and in the Canary Islands, Spain (*4*,*5*).

During July–October 2020, four short-finned pilot whales (*Globicephala macrorhynchus*) stranded in Brazil: 2 in Ceará state (cases 1 and 2) and 2 in Santa Catarina state (cases 3 and 4). All the animals stranded alive and died within 24 hours (Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/29/1/22-1549-App1.pdf). We performed standard necropsies and collected tissue samples, which we fixed in 10% buffered formalin for histopathology or froze at –20°C or –80°C for molecular analysis.

We performed RNA extractions of all available tissues with TRIzol-LS (Life Technologies Corporation, https://www.thermofisher.com). We performed a morbillivirus 2-step reverse transcription nested PCR to amplify the phosphoprotein gene (*6*). After DNA extraction with the QIAGEN Blood & Tissue Kit (QIAGEN, https://www.qiagen.com), we performed herpesvirus detection in lung (n = 2) and liver (n = 4) samples by nested pan-PCRs to amplify DNA polymerase and glycoprotein B genes (*7*); when those were positive, we tested the remaining

available tissues using the same protocols. We calculated percentage of identity among the obtained sequences and the closest ones from GenBank/EMBL/DDBJ based on p-distance. We used MEGA7 (https://www.megasoftware.net) to construct the phylogram (Figure).

Three animals, cases 1, 3 and 4, were morbillivirus-positive, amplified in central nervous system, lung, and pulmonary lymph node samples (Table, https://wwwnc.cdc.gov/EID/article/29/1/22-1549-T1.htm); sequences were submitted to GenBank (case 1, accession no. OP375347; case 3, OP375348; case 4, OP375349). Sequences from case 1 and 3 were identical and had a single nucleotide missense mutation (99.7% nt identity, 99.2% aa identity) when compared to the sequence from case 4. The sequences from cases 1 and 3 presented the highest nucleotide (99%) and amino acid identities (96.9%) with a PWMV sequence identified in 2 pilot whales in the Canary Islands, Spain (GenBank accession nos. KT006289 [animal 1], KT006290, and KT006291 [animal 2]). The sequence from case 4 had the highest nucleotide (99.2%) and amino acid similarities (97.7%) to the same PWMV sequences. Our sequences clustered with other PWMV sequences (Figure). In addition, we detected an alphaherpesvirus by the DNA polymerase protocol in a lung sample from case 3 (GenBank accession no. OP341880). The remaining tissue samples of case 3 (cerebellum, kidney, mesenteric lymph node, spleen, and liver) were

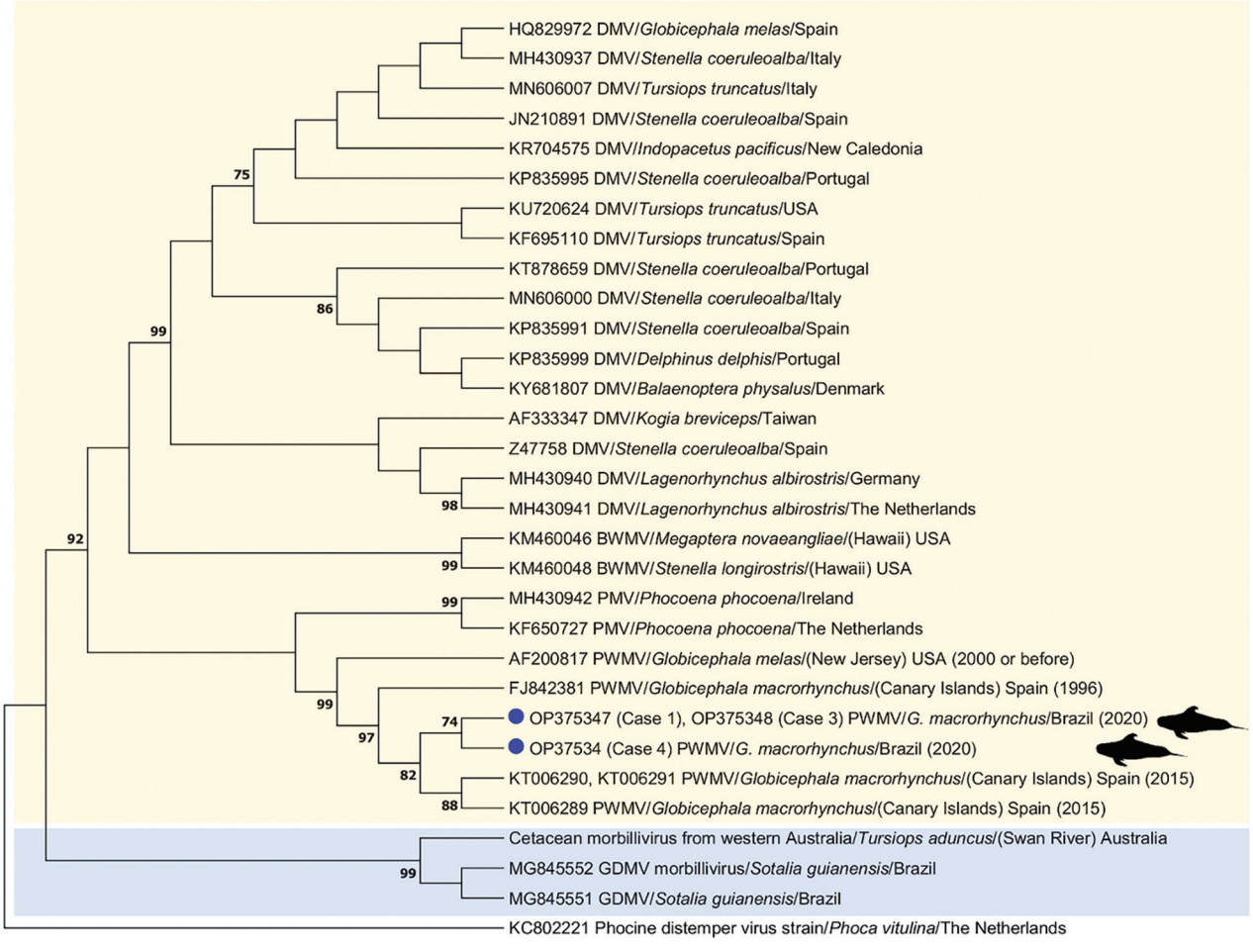

Figure. Maximum-likelihood phylogenetic tree based on Hasegawa-Khisino-Yano model with inversions gamma distribution and invariant sites of the phosphoprotein gene nucleotide sequences of cetacean morbillivirus PWMV obtained in Brazil (this study, blue circles), PWMV sequences previously described, and other morbillivirus strains described in cetaceans available from the GenBank/DDBJ/EMBL databases. Phocine distemper virus was selected as outgroup. The sequence identifier shows GenBank accession number, virus type, and location. Yellow shading indicates strains comprised in *Cetacean morbillivirus* lineage 1; blue shading indicates strains in lineage 2. Numbers at nodes indicate the bootstrap value; 1,000 bootstrap replications were selected, and bootstrap values <70 were omitted. BWMV, beaked whale morbillivirus; DMV, dolphin morbillivirus; GDMV, Guiana dolphin morbillivirus; PMV, porpoise morbillivirus; PWMV, pilot whale morbillivirus.

herpesvirus-negative by PCR. The obtained herpesvirus has the highest similarity (99.5% nt identity, 100% aa identity) to an alphaherpesvirus obtained in a striped dolphin (*Stenella coeruleoalba*) from Spain (GenBank accession no. GQ888671).

The general health of the CeMV-positive animals was poor, and all were undernourished. We compared the main pathologic findings in these animals to all other cases of PWMV strain reported in the literature (Table).

Pilot whales are susceptible to DMV and PWMV; DMV cause atypical pilot whale deaths in the Mediterranean Sea (*6*). By contrast, 4 cases of PWMV infections have been recorded; 1 in New Jersey, USA, and 3 in the Canary Islands, Spain (*4*–*6*,*9*,*10*). All of them had multiorgan infections (*4*,*5*). Case 1 likely had a subacute or systemic CeMV infection characterized by meningomyelitis with gliosis and lymphocytic bronchointerstitial pneumonia. Further studies are necessary to elucidate if cases 3 and 4 manifested an infection similar to the brain-only DMV form or a systemic infection with heterogenic dissemination. The poor nutritional condition observed in all PWMV-positive animals could be the result of decreased foraging capacity caused by encephalitis (*1*). Case 3 had alphaherpesvirus and CeMV co-infection, a comorbidity previously reported in cetaceans, including pilot whales (*5*,*10*); in this case, however, there were no associated herpesviral lesions. All PWMV-positive cetaceans we described were juveniles, which could be associated with maternal passive immunity loss.

The occurrence of pilot whale strandings in 2020 on the coast of Brazil could be considered atypical. Of interest, although case 1 was stranded >3,300 km away from case 3 along the coastline, it had the same PWMV sequence type, which suggests circulation of that type along the coast of Brazil. Further studies are necessary to understand the effects and epidemiology of morbillivirus in cetaceans in the South Atlantic Ocean. However, the high similarity between our sequences and the PWMV detected in the Northern Hemisphere confirms that this strain also circulates in South America pilot whales and might be enzootic in *Globicephala* sp. whales in the Atlantic Ocean.

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Dr. Costa-Silva, a veterinarian specialist in marine mammals, completed this project as part of her PhD project in the Department of Preventive Veterinary Medicine and Animal Health, School of Veterinary Medicine and Animal Science, University of São Paulo.

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Catheter-Related Bloodstream Infection Caused by *Mycolicibacterium iranicum*, California, USA

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We describe a case of catheter-related bacteremia caused by *Mycolicibacterium iranicum* in the United States. The case highlights the value of using next-generation sequencing to identify infrequent and emerging pathogens and the challenges associated with choosing appropriate treatments because of limited knowledge of drug resistance mechanisms in those emerging pathogens.

Mycolicibacterium iranicum is a rapidly growing mycobacterium (RGM) and emerging cause of respiratory, wound, blood, and central nervous system infections (*1*,*2*). Phylogenetic analyses have shown that *M. iranicum* is more closely related to environmental mycobacterial species than pathogenic species (*3*), and most outbreaks have been associated with exposure to contaminated water (*4*,*5*).

Reports of nontuberculous mycobacteria infections have been increasing worldwide (*6*,*7*), predominantly in immunocompromised patients with hematologic or oncologic medical conditions (*6*). The rise in RGM detection is likely because of increased prevalence of immunocompromising conditions and improved access to molecular diagnostics (*7*). Molecular techniques, especially sequencing multiple conserved genes, such as *rrs* (16S rRNA), *rpoB*, and *groEL* (*hsp65*) (*4*), have led to a dramatic increase in mycobacterial species identified during the past 30 years. We describe a case of *M. iranicum* bacteremia associated with a long-term percutaneous catheter in an immunocompromised patient.

A woman, 76 years of age, with a history of polymyositis and hypertrophic obstructive cardiomyopathy was admitted to an academic hospital in Los Angeles, California, USA, because of substernal chest pain and dyspnea that began 1 day before. Her medications included prednisone (15 mg/d) and intravenous immunoglobulin (20 g administered every 10 days through a port-a-cath that had been in place for several years). The patient had taken mycophenolate mofetil until a month before hospital admission. During each intravenous immunoglobulin infusion over the past 2 years, she had experienced fevers, which were attributed to an infusion reaction. The most recent infusion was 4 days before admission.

The patient reported fatigue and generalized weakness for several days and an unintentional 25-pound weight loss over the past year. On hospital day 2, she was febrile with a temperature of 101°F (Appendix Figure, https://wwwnc.cdc.gov/EID/article/29/1/22-0851-App1.pdf). Results of a preliminary work-up were unrevealing; however, after 4 days of incubation, multiple aerobic blood cultures (in BACTEC FX aerobic and F lytic media; Becton Dickinson, https://www.bd.com) taken from her port grew beaded, gram-positive rods with yellow mycobacteria-like colonies (Appendix Figure). Matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry failed to identify the isolate. We performed a laboratory-developed, next-generation sequencing-based test that identified the organism as *Mycolicibacterium iranicum*, which we further verified using k-mer–based phylogenic analysis (Figure) (*8*). Using a previously described method for detection of macrolide resistance in *Mycobacteroides abscessus* (*9*), we did not detect a functional *erm* gene.

When blood cultures demonstrated *Mycobacterium* sp., we changed therapy and administered