In the last 12 years, newly recognized members of the morbillivirus family have caused many deaths among marine mammals, specifically cetaceans and pinnipeds (1). The first recognized marine mammal morbilliviral epizootic occurred in 1987-88 along the Atlantic coast of the United States (2,3). More than half the in-shore population of bottlenose dolphins (*Tursiops truncatus*) may have died. In 1988, thousands of harbor seals (*Phoca vitulina*) (4) and small numbers of harbor porpoises (*Phocoena phocoena*) (5) died in morbilliviral epizootics in northwestern Europe. A separate epizootic claimed thousands of striped dolphins (*Stenella coeruleoalba*) in the western Mediterranean (6). In 1993-94, another bottlenose dolphin epizootic occurred in the Gulf of Mexico (7,8). Recently, morbilliviral infection has been reported in cetaceans in the Pacific (9).

Viruses have been cultured from animals from some of the epizootics, and novel marine mammal morbilliviruses have been identified. Two cetacean morbilliviruses have been identified and named porpoise morbillivirus (PMV) and dolphin morbillivirus (DMV). PMV was isolated from harbor porpoises that died along the Irish coast. DMV was first identified in striped dolphins from the Mediterranean (10).

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A female long-finned pilot whale (*G. melas*) was stranded below the deck of a beach home on the Delaware Bay, New Jersey. The whale was inactive and appeared near death. The likelihood has shown that these animals were infected with PMV (Taubenberger et al., unpub. data).

We report a case of lethal morbilliviral infection in a long-finned pilot whale (*G. melas*). Sequence analysis of fragments of the morbillivirus phosphoprotein (P) and nucleoprotein (N) genes suggests that this is a novel morbillivirus, phylogenetically related to, but distinct from, the other cetacean morbilliviruses, PMV and DMV.

A female long-finned pilot whale (*G. melas*) was stranded below the deck of a beach home on the Delaware Bay, New Jersey. The whale was inactive and appeared near death. The likelihood
of recovery was remote, and euthanasia was considered appropriate. The animal was transported by truck to a veterinary diagnostic laboratory, where it died shortly after arrival.

At necropsy, body fat was found to be depleted. The lungs were dark red and congested. Nematodes were observed in the second stomach chamber. Significant histologic lesions were present in many organs. In the lung, alveoli and airways contained numerous neutrophils, histiocytes, and multinucleate cells, interspersed with cellular debris. Multifocal type 2 pneumocyte hyperplasia was observed. Many multinucleate cells and some bronchiolar epithelial cells contained eosinophilic intracytoplasmic and intranuclear inclusion bodies. An immunohistochemical stain demonstrated morbilliviral antigen (8) in bronchiolar epithelium, multinucleate (syncytial) cells, and type 2 pneumocytes (Figure 1). Syncytial cells, often containing eosinophilic intracytoplasmic and intranuclear inclusion bodies, were also observed in spleen, lymph nodes, and liver. Additionally, eosinophilic intracytoplasmic inclusion bodies were present in colonic and gastric epithelia and in transitional epithelium of the kidney. Intracytoplasmic and intranuclear inclusion bodies were seen in glossal epithelium. Other histologic lesions included nonsuppurative encephalomyelitis, necrotizing hepatitis, erosive colitis, necrotizing gastritis, ulcerative glossitis, and ulcerative esophagitis.

RT-PCR was performed on RNA isolated from formalin-fixed, paraffin-embedded lung and brain tissues (7,11). A 378 nucleotide fragment of the P gene (GenBank accession number AF200817 and a 230 nucleotide fragment of the N gene (GenBank accession number AF200818 were amplified and sequenced. In both cases the sequences were novel but related to the previously described cetacean morbillivirus sequences. We have tentatively named this virus “pilot whale morbillivirus” or PWMV.

Sequences of both the N and P gene fragments were analyzed by parsimony and neighbor-joining (Figure 2). Parsimony analyses (12) with Sendai virus as outgroup placed PWMV in the cetacean morbillivirus clade with PMV and DMV, with moderate-to-high bootstrap values (N sequence = 70; P sequence = 100). Neighbor-joining (13) also placed PWMV in the cetacean morbillivirus clade with high bootstrap values (N sequence = 97; P sequence = 100). Thus PWMV is clearly related to, but distinct from, PMV and DMV, and the latter two are more closely related to one another than either is to PWMV (Figure 2).

Both the origin of these cetacean morbilliviruses and the mechanism of spread to different parts of the world remain unknown. Recently, serologic evidence of morbilliviral infection was obtained from 11 of 15 species of odontocete cetaceans of the western Atlantic (14), suggesting that exposure to these viruses has been widespread. Serologic evidence of enzootic infection (with a seroprevalence of 86%) was also obtained from two species of pilot whales (G. melas and G. macrorhynchus) in the western Atlantic (15). Clinical disease consistent with morbilliviral pneumonia was detected in one G. melas calf, although the morbillivirus in that case was not characterized. Duignan et al. (15) speculated that pilot whales may serve as vectors of morbillivirus infection to other odontocete cetaceans.

The results from this case suggest that pilot whales may have their own species-adapted morbillivirus. Given that this is a single case, that no morbilliviral epizootic has been described for pilot whale species, and that seroprevalence is consistent with enzootic morbilliviral infection (15), lethal infection might be rare in these species. Nevertheless, it remains possible for pilot whales to serve as vectors by which
immmunologically naïve species are exposed to morbillivirus infection. The viruses in these hosts may have undergone species-adaptive changes, reflecting the genetic differences between DMV, PMV, and PWMV. While only partial sequences have been obtained from two of the morbilliviral genes in this case, the fact that it is closer to the root of the cetacean morbillivirus clade (Figure 2) suggests that PWMV resembles the common ancestor of the clade more closely than either DMV or PMV.

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