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Fatal Cronobacter sakazakii Sequence Type 494 Meningitis in a Newborn, Brazil

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We describe a case of infection with Cronobacter sakazakii sequence type 494 causing bacteremia and meningitis in a hospitalized late premature infant in Brazil. We conducted microbiological analyses on samples of powdered infant formula from the same batch as formula ingested by the infant but could not identify the source of contamination.

In September 2017, a healthy boy was born at 35 weeks’ gestation in Brazil. The newborn was fed breast milk and reconstituted powdered infant formula (PIF) while in the hospital. On postnatal day 4, he began sleeping more than usual and experienced hypoactivity, pallor, jaundice, seizures, metabolic acidosis, and finally respiratory insufficiency, necessitating mechanical ventilation and empiric treatment with cefepime and ampicillin. We obtained 2 blood cultures on postnatal day 4 that yielded Cronobacter spp. with resistance to cephalothin and cefoxitin, intermediate resistance to nitrofurantoin, and susceptibility to other antimicrobial drugs, including cefepime and ampicillin. A transfontanel ultrasound on postnatal day 6 showed grade 2 perinventricular hemorrhage with hypoxic-ischemic lesions. Subsequent computed tomography and nuclear magnetic resonance (NMR) imaging revealed biparietal cerebral abscess (Figure). Culture of the cerebral abscess on postnatal day 33 yielded Cronobacter spp., that had the same pattern of antimicrobial drug susceptibility as that found in blood isolates. Because of the

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PIF was analyzed in accordance with 2 standard procedures resulting in brain abscess formation. Virulence studies of C. sakazakii ST494 strains are needed to elucidate their pathogenicity and to compare with C. sakazakii CC4 strains.
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Introduction of Eurasian-Origin Influenza A(H8N4) Virus into North America by Migratory Birds

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We identified a Eurasian-origin influenza A(H8N4) virus in North America by sampling wild birds in western Alaska, USA. Evidence for repeated introductions of influenza A viruses into North America by migratory birds suggests that intercontinental dispersal might not be exceedingly rare and that our understanding of viral establishment is incomplete.

Research of and surveillance for influenza A viruses in wild birds inhabiting western Alaska have consistently provided support for the exchange of viruses between East Asia and North America via Beringia (1,2). Sampling of wild birds inhabiting Izembek National Wildlife Refuge (NWR) and surrounding areas in Alaska (≈55°N, 163°W) conducted during 2011–2015 has been used in recent research to identify the dispersal of influenza A(H9N2) viruses among China, South Korea, and Alaska (3); provide inference about the evolutionary pathways of economically important foreign-origin poultry pathogens introduced into North America (4); and identify sampling efficiencies for optimizing the detection of evidence for intercontinental virus exchange (5).

During September–October 2016, we collected 541 combined oral-pharyngeal and cloacal swab samples from hunter-harvested waterfowl (Anseriformes spp.) and 401 environmental fecal samples from monospecific flocks of either emperor geese (Chen canagica) or glaucous-winged gulls (Larus glaucescens) within and around Izembek NWR. Samples were deposited into viral transport media, placed in dry shippers charged with liquid nitrogen within 24 h, shipped, and stored frozen at −80°C before laboratory analysis. We screened samples for the influenza A virus matrix gene and subjected them to virus isolation; resultant isolates were genomically sequenced in accordance with previously reported methods (5). A total of 116 samples tested positive for the matrix gene, and 38 isolates were recovered of the following combined subtypes: H1N2, H3N2, H3N2/N6 (mixed infection), H3N8, H4N6, H5N2, H6N2, H7N3,