second patient were within the same subgroup, but similarity in nucleotide sequences was only 82.5%. This result suggests that this patient was infected with 2 different virus strains of HRV-A and a strain of HRV-C.

Comparison of the HRV-A strains with the HRV-C strain showed that they belonged to different subgroups and had low similarity for nucleotide sequences. The second patient had 3 distinct rhinovirus infections over 3 months, and each was associated with illness requiring hospitalization. Both patients had underlying diseases, reactive airway diseases, and repeated episodes of RTI that may have rendered them vulnerable to reinfection, compromising their immune responses.

Complete coding sequences of HRV-A and HRV-C have been determined (4, 7). However, little is known about their involvement in the pathogenesis of recurrent wheezing in young children. According to recent reports, HRV-C has been detected in hospitalized children with lower RTI in the People’s Republic of China (5). Possible association of novel infection with HRV and exacerbation of asthma in children has also been reported (6). We report HRV-A and HRV-C co-infections in conjunction with other respiratory viruses, such as RSV, as a potential cause of recurrent wheezing in infants with acute lower RTIs. Co-infections with HRV-A and HRV-C may contribute to increased virulence and subsequent pathogenesis of other respiratory viruses. Additional studies will be required to further explore the clinical role of novel HRVs.

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Drug therapy, graphic response to the antimicrobial though the pneumonia showed radiographic response to the antimicrobial drug therapy, *A. baumannii* continued to be isolated from respiratory secretions on numerous occasions. Despite another course of therapy with colistin and ceftazidime, the patient never recovered from respiratory failure. She eventually died of sepsis caused by vancomycin-resistant *E. faecium*. An *A. baumannii* isolate obtained just before she died lacked susceptibility to all commercially available antimicrobial drugs (Table).

Multidrug-resistant *A. baumannii* has emerged as a substantial problem worldwide (2). Such strains are typically resistant to all β-lactams and fluoroquinolones and require salvage therapy with colistin, amikacin, or tigecycline. Unfortunately, notably high-level resistance to colistin and amikacin was found in the isolate we have described (Table). Tigecycline, a newly available glycylcycline antimicrobial drug, showed intermediate susceptibility. No randomized trials have been performed to specifically evaluate combination antimicrobial drug therapy for treatment of infection with *A. baumannii*.

Considerable media attention has been paid to extensively drug-resistant (XDR) strains of *Mycobacterium tuberculosis* (3). Infections with XDR strains are extremely difficult to treat and pose considerable infection control issues. We recently proposed that gram-negative bacilli lacking susceptibility to all commercially available antimicrobial drugs also be referred to as XDR because no therapeutic options are available (4).

Numerous outbreaks of *A. baumannii* infection have been reported worldwide (5). Unfortunately, multidrug-resistant *A. baumannii* strains have become endemic in some institutions. Experimental and clinical isolates lacking susceptibility to colistin, often considered the drug of last resort, are increasingly being reported (6–8). Therefore, we alert healthcare workers to the need for stringent care in adhering to infection control precautions when caring for patients infected with XDR *A. baumannii*. Use of contact isolation precautions, enhanced environmental cleaning, removal of sources of infection from the hospital environment, and prudent use of antimicrobial drugs can contribute to control of such outbreaks (5). Fortunately, no spread of the XDR strain affecting this patient occurred. A crisis is looming should XDR *A. baumannii* become established pathogens in hospitals.

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Cryptosporidium Pig Genotype II in Immunocompetent Man

To the Editor: Protozoan parasites from the genus Cryptosporidium have been described as a cause of diarrheal disease in immunodeficient and immunocompetent humans worldwide. Although C. hominis and C. parvum (cattle genotype) cause most infections, humans can be infected by several other Cryptosporidium species or genotypes: C. meleagrisid; C. felis; C. canis; C. suis; C. muris; C. andersoni; C. hominis monkey genotype; C. parvum (mouse genotype); and Cryptosporidium rabbit genotype, deer genotype, skunk genotype, horse genotype, and chipmunk genotype I (1–4). Wild and domestic animals are sources of infection for humans (and other animals) and important contributors to contamination of food and drinking water; many nonhuman Cryptosporidium species or genotypes are detected in untreated water (5). We examined the diversity of Cryptosporidium spp. in immunocompetent persons in South Bohemia in the Czech Republic.

Diarrheal fecal samples (n = 457) from 203 anonymous immunocompetent patients ≤69 years of age with suspected cryptosporidiosis (at least 2 samples/patient/3-day period) were obtained from local health departments and public hospitals in South Bohemia during 2005–2007. Samples were examined for Cryptosporidium oocysts by using aniline-carbol-methyl violet staining and light microscopy at × 1,000 magnification (6). The microscopically positive samples were confirmed by DNA sequencing of the small subunit (SSU) rRNA gene. Total DNA was extracted from 200–300 mg stool by using the QIAamp DNA Stool Mini Kit (QIAGEN, Hilden, Germany), following the manufacturer’s instructions, after previous homogenization and disruption of oocysts with the Mini-BeadBeater (Biospec Products, Bartlesville, OK, USA). An ≈830-bp fragment of the SSU rRNA gene was amplified by nested PCR according to Jiang et al. (7). Purified PCR products were sequenced in both directions on an ABI3130 sequencer analyzer (Applied Biosystems, Foster City, CA, USA) by using the secondary PCR primers and the BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems). Sequences were assembled by using Chromas Pro (www.techneleyium.com/au/chromas.html) and aligned with reference sequences using ClustalX (ftp://ftp-igbmc.u-strasbg.fr/pub/ClustalX). The BLAST server (www.ncbi.nlm.nih.gov/BLAST) was used for DNA database searches. The SSU rRNA gene partial sequences of the 7 patient isolates have been submitted to GenBank (Table).

Of the 203 patients, 7 (3.4%) (6 children and 1 adult) had positive results for Cryptosporidium spp. Moreover, all samples obtained from these persons during the 3-day period were Cryptosporidium spp. positive; partial sequences of the Cryptosporidium SSU rRNA gene were obtained from all positive samples identifying 3 different species or genotypes of Cryptosporidium. Five were C. parvum (bovine genotype), I was C. hominis, and I contained the Cryptosporidium pig genotype II (Table). Cryptosporidium pig genotype II was found in stool samples from a 29-year-old man who also was infected with Giardia intestinalis (assemblage A) (data not shown).

Only C. parvum (bovine genotype), C. hominis, and Cryptosporidium rabbit genotype have been implicated in waterborne outbreaks of cryptosporidiosis in humans. Further studies are needed to determine the potential of other cryptosporidia of animal origin. Recent genetic and biologic characterization studies have identified 2 distinct host-adapted cryptosporidia in pigs, C. suis and Cryptosporidium pig genotype II. Furthermore, both above-mentioned cryptosporidia have been identified in untreated water (8). Pigs could be sources of Cryptosporidium water and food pollution and a consequent risk to public health.

Although human infection with C. suis has been previously described (9), human infection with Cryptosporidium pig genotype II has been never reported. This genotype was found in diarrheal stool of 1 adult patient in this study. However, onset of diarrhea could have been caused by co-infection with G. intestinalis (assemblage A), which recently also has been described in pigs (10). Contact with infected animals and ingestion of contaminated food or water could be