

4.28×10^9 cells/L, a hemoglobin level of 86 g/L, and a leukocyte count of 8.28×10^9 cells/L with 17% neutrophils and 78% lymphocytes.

The patient was given symptomatic supportive treatment, methylprednisolone sodium succinate, and 5 g of γ -globulin. He was not given any antimicrobial drugs. On August 4, he was discharged from hospital after symptoms had resolved.

In conclusion, our results confirm that mimivirus is an unlikely cause of human respiratory infections in China, as reported in other countries (5–9). Sporadic detection of mimivirus in 1 child who was born with a compromised respiratory system and had numerous hospitalizations was most likely caused by colonization of the child with this virus during numerous hospitalizations and critical care stays. In addition, parainfluenza virus 3 and bocavirus were detected in the mimivirus-positive child. Because parainfluenza virus 3 causes pneumonia and bocavirus causes infections with respiratory symptoms, particularly in children of his age, these 2 pathogens probably caused the illness in the child.

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Severe Pneumonia Associated with Adenovirus Type 55 Infection, France, 2014

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To the Editor: Human adenoviruses (HAdVs) comprise 70 recognized genotypes (as of February 15, 2016; <http://hadvwg.gmu.edu/>) and are frequently associated with mild and acute upper respiratory tract infections, depending on virus type and host immune status (1). HAdV type 55 (HAdV-55) has recently reemerged as a highly virulent pathogen, causing severe and sometimes fatal pneumonia among immunocompetent adults, particularly in Asia (2–4). Formerly known as HAdV-11a, HAdV-55 is a genotype resulting from recombination between HAdV-11 and HAdV-14 (5). We report 2 cases of severe pneumonia associated with HAdV-55 infection in France.

In November 2014, two immunocompetent women, 71 (patient A) and 36 (patient B) years of age, sought care 4 days apart at the emergency unit of the University

Hospital of Clermont-Ferrand, France, for an influenza-like syndrome characterized by fever, cough, and dyspnea. Laboratory investigations at admission revealed thrombocytopenia (98 and 88×10^9 thrombocytes/L for patients A and B, respectively; reference range $150\text{--}450 \times 10^9$ thrombocytes/L) and elevated C-reactive protein concentrations (71.6 and 45.8 mg/L, respectively; reference range <3 mg/L). Chest radiographs and thoracic tomodensitometry images showed acute left lobar pneumonia in each patient. Therapy with intravenous antimicrobial drugs (cefepime and levofloxacin) and oxygen was initiated. Patient A was transferred to the intensive care unit 4 days after admission because of unimproved respiratory function; patient B was transferred 5 days after admission because of acute respiratory distress syndrome.

Results for all bacteriologic analyses were negative (blood cultures, bronchoalveolar lavage fluid cultures, PCR for *Mycobacterium tuberculosis* [Xpert MTB/RIF; Cepheid, Sunnyvale, CA, USA] of bronchoalveolar lavage fluid, and urinary antigen testing [BinaxNOW *Legionella* and *Streptococcus pneumoniae*; Alere, Scarborough, ME, USA]). No specific antibodies were detected against *Chlamydia pneumoniae* (Anti-*C. pneumoniae*; Euroimmun,

Lübeck, Germany) and *Mycoplasma pneumoniae* (Plate-*lia M. pneumoniae* IgM; Bio-Rad, Hercules, CA, USA). For each patient, HAdV was the only pathogen detected in nasopharyngeal secretions collected at admission and in bronchoalveolar lavage fluids collected while in the intensive care unit (molecular multiplex assay [FilmArray Respiratory Panel; bioMérieux, Durham, NC, USA]). HAdV DNA was also detected in whole blood (Adenovirus R-gene; bioMérieux); viral load was $280,524$ copies/mL for patient A 9 days after hospital admission and $951,146$ copies/mL for patient B 4 days after admission. During hospitalization, transient hepatitis developed in each patient; serum aspartate aminotransferase levels were elevated up to 6–10 times reference range, and leukocyte counts indicated leukopenia (2.17 and $1.28 \times 10^9/L$ for patients A and B, respectively; reference range $4\text{--}10 \times 10^9/L$). Patient B had acute pancreatitis and hyperlipasemia (lipase $1,697$ UI/L; reference range $73\text{--}393$ UI/L). Healthy respiratory function was restored for both patients, who were discharged 26 (patient A) and 19 (patient B) days after admission.

A partial region of the hexon gene was amplified and sequenced from DNA extracts of respiratory and blood

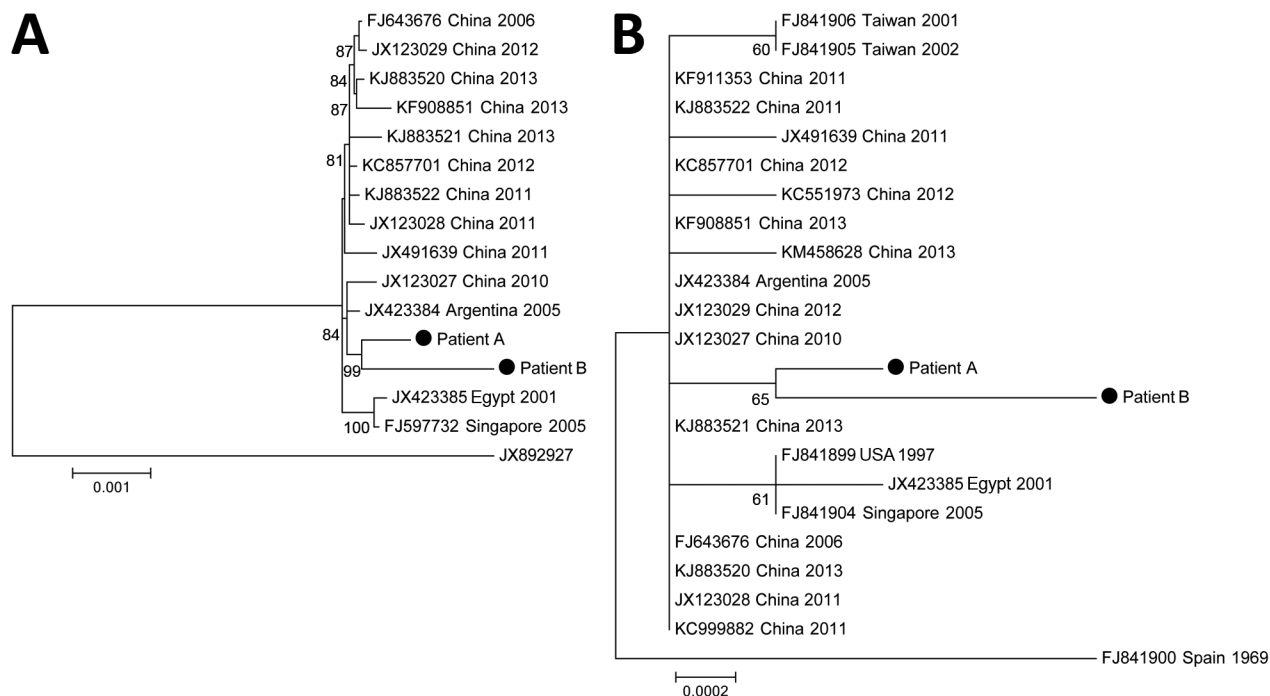


Figure. Phylogeny of 13 complete-genome sequences of human adenovirus type 55 (A) and of 21 sequences of hexon genes (B). The complete genome tree (A) is rooted to a human adenovirus type 14 isolate (GenBank accession no. JX892927). The strains from patients A and B (immunocompetent women with human adenovirus infection) reported in this study are indicated. The phylogenetic tree was calculated by using the maximum-likelihood method in MEGA6 (<http://www.megasoftware.net>). The best algorithm was chosen by the criterion score of the Bayesian information criteria. The statistical robustness of branches was estimated by 1,000 bootstraps. Only bootstrap values $>70\%$ are indicated. The tree is drawn to scale; branch lengths are measured in number of substitutions per site (scale bar). All positions containing gaps and missing data were eliminated. The sequence of the hexon gene from patient B was partially complete (2,821/2,841, 99.3%).

samples, as previously described (6). Phylogenetic analysis with strains representing all HAdV genotypes identified the viruses as HAdV-55 (data not shown). We performed complete-genome sequencing, which is now recommended for confirmation of HAdV type, by using next-generation sequencing from blood samples (online Technical Appendix, <http://wwwnc.cdc.gov/EID/article/22/11/16-0728-Techapp1.pdf>). Genome coverage (34,755 nt) was 99.1% (patient A) and 96.1% (patient B). Phylogenetic analysis showed that the sequences of the isolates from the 2 patients clustered together (bootstrap 99%) and were genetically more closely related to the sequences of the CQ-814 strain isolated in China in 2010 and the strain from Argentina (GenBank accession no. JX423384) (Figure, panel A). To investigate genetic relationships with more strains from distant geographic areas, we performed phylogenetic analyses with all available sequences of the hexon gene of HAdV-55 strains. However, because diversity of this gene between strains was low, we could not determine the geographic origin of the strains from France, which were genetically distant from the strain isolated in Spain in 1969 (Figure, panel B).

Over the past 10 years, reports of HAdV-55 have been increasing in Asia during outbreaks of respiratory diseases that in some cases led to severe pneumonia and deaths in immunocompetent adults and children (2–4,7,8). Of the 969 cases of community-acquired pneumonia in adults, 48 (5%) were associated with HAdVs; HAdV-55 was identified in 21 (43.8%) of these patients (7). For the 2 patients we report, clinical features were similar to those described elsewhere (4,8). Neither patient had traveled recently, and the 2 patients had not had contact with each other. Analysis of complete genomic sequences showed that the viruses infecting the patients were distinguishable from strains previously isolated in other countries. HAdV-55 could thus have been circulating in France for several years. Since its first detection in Spain in 1969 (9), HAdV-55 has been reported only 1 time in Europe, in Germany in 2004 (10).

Because most HAdV infections are asymptomatic and respiratory virus screening in routine practice does not systematically include HAdV detection, the true prevalence and clinical effect of HAdV-55 infection has probably been underestimated. The involvement of virus of this genotype in severe pneumonia emphasizes the need to reinforce HAdV surveillance by including HAdV genome detection and genotyping (if positive) in the documentation of severe respiratory infections.

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Spotted Fever Group *Rickettsia* in the Pampa Biome, Brazil, 2015–2016

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Severe Pneumonia Associated with Adenovirus Type 55, France, 2014

Technical Appendix

HAdV Full-Genome Sequencing and Analysis

Because HAdV-55 isolation on A549 cells was unsuccessful for both patients, the full genome sequence was assessed directly from clinical samples by a metagenomic approach with the MiSeq Reagent kit v2 on a MiSeq 2000 Illumina system (Illumina, San Diego, CA). Three different strategies were used and combined to obtain maximum genome coverage. Except for nucleic acid purification steps, libraries were generated as previously described (Naccache S. et al., *Genome Res* 2014) with Nextera XT DNA Sample Preparation Kit (Illumina). Libraries were sequenced on an Illumina MiSeq 2000 according to standard Illumina protocols, creating 250-nt paired-end reads. 1) Total nucleic acids from plasma samples were extracted with EasyMag® (bioMérieux). 2) To remove most of the host DNA and thus to enrich the viral sequences, plasma samples were first incubated with Turbo DNase (Ambion). We then followed the protocol mentioned above. 3) After extraction of total nucleic acids from plasma samples as described in 1), host DNA was removed by MBD2-Fc-bound magnetic Bead and the remaining nucleic acids were purified with the Zymo DNA Clean and Concentrator kit.

For all MiSeq runs, after a quality filtering step with FastQ Quality Trimmer tool implemented on Galaxy (Blankenberg D. et al., *Bioinformatics* 2010), reads were aligned on HADV-55 JX491639 genome by Bowtie 2 (Langmead B. et al., *Nat methods* 2012). As no approach managed to obtain sufficient coverage of the reference genome, aligned reads of the three strategies were combined by Geneious R8 (Biomatters) (Kearse M. et al., *Bioinformatics* 2012) to process a reference-based assembly.