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Community-acquired pneumonia (CAP) refers to pneumonia acquired outside of hospital or long-term care facilities. The overall annual incidence of CAP ranges from five to 20 per 1,000 adults. Many microbial pathogens can cause CAP, and the role of viruses may have been underestimated thus far because of a lack of appropriate diagnostic methods. Modern molecular techniques have revealed that respiratory viruses account for about 22% of adult CAP cases. The most common viruses are influenza, parainfluenza, respiratory syncytial virus, metapneumovirus, and adenovirus.

We previously reported 18 sporadic CAP cases caused by human adenovirus (HAdV) from our single center between August 2008 and April 2011. Polymerase chain reaction (PCR) analysis using type-specific primers targeting the hexon gene revealed that they all belonged to species B (HAdV-11, HAdV-7, HAdV-3, and HAdV-14), and HAdV-11 accounted for 58.8% (10 of 17) of them. However, further genome sequence analysis proved that these 10 HAdV-11 strains were actually HAdV type 55 (HAdV-55). HAdV-55, an intertypic recombinant described originally as genome type 11a, was identified from an outbreak of acute pneumonia in China.

**Background:** Since 2008, severe cases of emerging human adenovirus (HAdV) type 55 (HAdV-55) were reported sporadically in China. But no comparative studies had been conducted to discern the differences in epidemiologic and clinical abnormalities between HAdV-55 and other types (HAdV-7, HAdV-3, HAdV-14, HAdV-50, and HAdV-C).

**Methods:** A multicenter surveillance study for adult and adolescent community-acquired pneumonia (CAP) was conducted prospectively in Beijing and Yan Tai between November 2010 and April 2012. A standardized data form was used to record clinical information. The viral DNA extracted from the clinical samples or adenovirus viral isolates was sequenced.

**Results:** Among 969 cases, 48 (5%) were identified as adenovirus pneumonia. Six branches were clustered: HAdV-55 in 21, HAdV-7 in 11, HAdV-3 in nine, HAdV-14 in four, HAdV-50 in two, and HAdV-C in one. Most HAdV-55 cases were identified during February and March. All the hypervariable regions of the hexon genes of the 21 HAdV-55 strains were completely identical. Patients who had HAdV-55 were about 10 years older ($P = .027$) and had higher pneumonia severity index scores ($P = .030$) compared with those with other types (HAdV-7, HAdV-3, HAdV-14, HAdV-50, and HAdV-C). Systemic BP was also higher among patients in the HAdV-55 group ($P = .006$). Unilateral or bilateral consolidations were the most common radiologic findings in both patients with HAdV-55 and those with other types (57.9% vs 36%). More than one-half of the patients were admitted to hospital; oxygen therapy was given to 29.2% of the 48 patients, and two needed mechanical ventilation.

**Conclusions:** HAdV-55 has established itself as a major pneumonia pathogen in the Chinese population, and further surveillance and monitoring of this agent as a cause of CAP is warranted.
respiratory tract infection in Shandong Province, China, in 2006. It exhibited a neutralizing antigen epitope of HAdV-11 and the pathogenic properties of HAdV-14. The whole-genome sequencing analysis showed that HAdV-55 had an HAdV-14 chassis with a partial HAdV-11 in the hexon gene. For this reason, it was renamed HAdV-55.

Our previous case series indicated that HAdV-55 apparently emerged in Beijing. Adenovirus 14 is an emerging agent of concern that has been causing outbreaks of pneumonia not just in China, but worldwide. Adenovirus 55, which is related to adenovirus 14, is now also emerging as an agent of concern. We investigated whether HAdV-55 has a different clinical profile from the profiles of other adenovirus types circulating in China.

**Materials and Methods**

**Beijing Network for Adult CAP**

The Beijing Network for Adult Community-Acquired Pneumonia (BNACAP), which consists of 11 general hospitals from nine different districts in Beijing and one teaching hospital in Yan Tai, is a clinic-based, multicenter, prospective surveillance system for adults and adolescents with CAP. Yan Tai is a city by the sea in Shan Dong Province, located about 770 km southeast of Beijing.

**Study Population**

Clinical information collected by investigators with a standardized data form included the following: age, sex, comorbidities, smoking history, vaccination against influenza and Streptococcus pneumoniae in the past year, symptoms (fever, cough, sputum, dyspnea, chest pain), GI symptoms (nausea, vomiting, diarrhea, and abdominal pain), and neurologic symptoms (headache, dizziness). Clinical signs (body temperature, heart rate, respiratory frequency, BP, and crackles) and treatments (antibiotics, antiviral therapy, or oxygen use) were also recorded. The pneumonia severity index (PSI) was used to assess the severity of illness on the day of enrollment.

Symptoms and signs of all patients were followed up, either during their hospitalization or after discharge, until all symptoms disappeared. For outpatients, the same information was gathered. All the information collected from the patients was input into a computerized database.

**Microbiologic Diagnostic Tests Undertaken**

The nasal or throat swab specimens collected by the attending physicians were collected in 2-mL viral transport media, transported at 2°C to 8°C, and preserved at −80°C. The viral RNA was extracted from the clinical samples using a QiAamp RNA mini kit (QIAGEN). Following this, a commercially available Seeplex RV 15 ACE Detection kit (Seegene Inc), a multiplex, one-step, reverse transcriptase PCR, was used to screen for 15 different viruses as the cause of the respiratory illness. The kit included assays for adenovirus, influenza A and B viruses, human metapneumovirus, rhinovirus, respiratory syncytial virus (groups A and B), coronavirus, parainfluenza virus (type 1, 2, 3, 4), bocavirus, and enterovirus.

Blood cultures were performed for patients presenting with chills and shivering. If pleural fluid and sputum samples were available, Gram stain and culture were performed. Urinary antigen tests for Legionella pneumophila and S pneumoniae (Binx) were also performed on all urine specimens. Atec sera (1-3 days after onset) and convalescent sera (2-4 weeks after onset) were collected for testing of the antibody for HAdV or other respiratory viruses.

**Criteria for Viral Pneumonia**

Viral pneumonia was diagnosed based on one of the following criteria: (1) the presence of HAdV or other respiratory viruses detected in sputum or throat swab samples by molecular methods or (2) seroconversion, defined as a fourfold or greater increase in titers of antibodies to HAdV or other respiratory viruses.

**Cell Culture and Virus Isolation**

Nasal or throat swab specimens were inoculated onto Hep-2 cells and cultured in a maintenance medium for detection of a
cytopathic effect (CPE). Cells were observed for CPE every 7 days. Cultures exhibiting adenovirus-like CPE were processed again to confirm the presence of the virus.

**Results**

**Epidemiology**

Between November 2010 and April 2012, 1,013 cases with CAP were enrolled in the BNACAP study. Forty-four cases were ruled out: In 30, no throat/nasal specimen was obtained, and clinical information was missing in 14. Therefore, 969 cases were available for the etiology study. Among them, 393 were positive for at least one pathogen: respiratory viruses in 262, *Mycoplasma pneumoniae* in 168, typical bacteria in 47, *Mycobacterium tuberculosis* in 15, and *Legionella pneumophila* in four. Dual causes were found in 65 patients (e-Table 1).

**Types of HAdV**

Forty-eight patients (48 of 969 [5%]) were identified as having adenovirus pneumonia, and 26 of the 48 adenovirus-positive samples showed characteristic adenovirus-like CPE. Basic Local Alignment Search Tool analysis based on the hypervariable region of the hexon genes from all 48 adenovirus-positive samples was performed. Among the 48 samples, 21 (43.8%) were HAdV-55, 11 (22.9%) were HAdV-7, nine (18.8%) were HAdV-3, four (8.3%) were HAdV-14, two (4.2%) were HAdV-50, and one (2.1%) was HAdV-C. Most HAdVs were identified in February and March. No adenovirus was found in November or December (Fig 1). The type distribution was similar between Beijing and Yan Tai City (Table 1).

**Statistical Analysis**

Data analysis was performed using SPSS 15.0 (IBM). A two-tailed independent-samples t test or a Mann-Whitney U test (in the case of nonnormal distributions) was used to compare continuous variables between the two groups. For the categorical data, univariate analysis was carried out using the χ² test or Fisher exact test. Significance was fixed at P < .05.

**Figure 1.** Epidemiologic distribution of different types of human adenoviruses. Most human adenovirus type 55 was identified during February and March, and it had epidemiologic characteristics similar to other types. No adenovirus pneumonia was found in November and December, the typical influenza season months.
Forty percent of the patients had bilateral involvement on chest radiography (Table 2). Consolidation, patchy infiltrate, and ground-grass opacity were the most common findings in pneumonia caused by HAdV. Patients infected by HAdV-55 presented consolidation more commonly than did those infected by other types (57.9% vs 36%) (Fig 2), but the difference was not significant.

Complications, Management, and Prognosis of Patients With HAdV Pneumonia

More than one-half of the patients were admitted to hospital, but there was no difference between HAdV-55 and other types (Table 3). No case was proved to have a coinfection with bacteria, but coinfections with other respiratory viruses (25%) or M pneumoniae (12.5%) were common. Oxygen therapy was given to 29.2% of the patients, and only two needed mechanical ventilation. Antibiotics were given to all the patients, but only four were prescribed antiviral drugs (all from Beijing Chao-Yang Hospital). The clinical outcomes, including duration of fever and other respiratory symptoms, length of stay in hospital, and hospitalization...
of HAdV strains were compared with the sequences of HAdV-B species in GenBank (e-Fig 1B); 21 of the 47 HAdV-Bs formed a dependent branch and revealed 100%, 96.7%, and 80% homologies with HAdV-55 (FJ643676), HAdV-11 (AF532578), and HAdV-14 (AY803294), respectively. Another phylogenetic tree was then conducted based on the partial fiber gene of the 15 HAdVs, hexon genes which were homologous to HAdV-55 (e-Fig 1C). The partial fiber gene had 99.8% to 100%, 99.4% to 99.5%, and 94.2% to 94.3% nucleotide identity with HAdV-55 (FJ643676),

Table 2—Laboratory Findings and Chest Radiologic Characteristics of Patients With CAP Caused by Adenoviruses (Comparison Between HAdV-55 and Other Types)

| Characteristic | Total (N = 48) | HAdV-55 (n = 21) | Other Types (n = 27) | P Value |
|---------------|---------------|-----------------|---------------------|--------|
| WBC, 10^9/L   | 7.19 ± 3.59   | 6.70 ± 3.31     | 7.33 ± 3.84         | .749   |
| Leukocyte < 4,000/mm³, % | 4 (8.3) | 2 (9.5) | 2 (7.4) | 1.0 |
| Leukocyte > 10,000/mm³, % | 5 (12.2) | 3 (14.3) | 4 (14.8) | .715 |
| Neutrophil, % | 68.7 ± 12.3   | 69.9 ± 11.8     | 67.7 ± 12.9         | .553   |
| Lymphocyte, % | 21.9 ± 9.3    | 20.9 ± 9.0      | 22.8 ± 9.8          | .484   |
| Hemoglobin, g/L | 141.4 ± 14.8 | 139.0 ± 15.0    | 143.3 ± 14.7        | .327   |
| Platelet, 10^12/L | 186.9 ± 77.4 | 196.2 ± 76.7    | 179.7 ± 69.3        | .469   |
| AST, μL       | 26.5 (14-176) | 25 (14-130)     | 26 (17-176)         | .975   |
| ALT, μL       | 23 (6-122)    | 26.5 (9-122)    | 22 (6-109)          | .511   |
| ALB, g/L      | 36 (24.5-45.9)| 34.6 (30.7-43.7)| 36.4 (24.5-45.9)   | .600   |
| LDH, μL       | 201 (120-794)| 193 (120-467)   | 217 (129-794)       | .771   |
| CK, μL        | 47 (34-1944)  | 70.5 (41-345)   | 87 (34-1944)        | .659   |
| Tbil, μmol/L  | 9.9 (4.3-39.4)| 11.8 (6.0-39.4) | 8.9 (4.3-38.4)      | .063   |
| Cr, μmol/L    | 68.9 (1.9-148.7)| 77.5 (1.9-148.7)| 62 (3.6-110.2)      | .372   |
| K, mmol/L     | 3.92 ± 0.42   | 3.91 ± 0.46     | 3.93 ± 0.40         | .845   |
| Na, mmol/L    | 136.2 ± 4.1   | 135.1 ± 4.2     | 137.0 ± 5.9         | .102   |
| PaO₂, mm Hg   | 83.4 ± 23.8   | 91.8 ± 31.3     | 77.1 ± 14.7         | .167   |
| FSAO₂, mm Hg  | 32.6 ± 6.5    | 32.3 ± 7.3      | 32.9 ± 6.1          | .827   |
| ESR, mm/h     | 27 (8-70)     | 32 (8-66)       | 23.5 (9-70)         | .212   |
| CRP, mg/L     | 11.1 (2-147)  | 11.1 (2-147)    | 12 (2-104)          | .728   |
| PCT, ng/mL    | 10 (4-35.5)   | 10 (4-35.5)     | 1 (2-28.6)          | 1.0    |
| Chest radiographya | 19 (39.6) | 9 (47.4) | 10 (40) | .761 |
| Interventionsb | 20 (45.5) | 11 (57.9) | 9 (36) | .223 |
| Patchy infiltration | 18 (40.9) | 7 (36.8) | 11 (44) | .760 |
| Ground-grass opacity | 12 (27.3) | 5 (26.3) | 7 (28) | 1.0 |
| Pleural effusion | 3 (6.8) | 1 (5.3) | 2 (8) | 1.0 |
| Coinfectionsc | 8 (16.7) | 4 (19.1) | 4 (14.8) | .715 |

Data are presented as mean ± SD, No. (%), or median (range). ALB = albumin; ALT = alanine aminotransferase; AST = aspartate aminotransferase; CK = creatine kinase; Cr = creatinine; CRP = C reactive protein; ESR = erythrocyte sedimentation rate; LDH = lactate dehydrogenase; PCT = procalcitonin; Tbil = total bilirubin. See Table 1 legend for expansion of other abbreviations.

a n = 27.
b n = 23.
c n = 12.
d Total (N = 44), HAdV-55 (n = 19), and other types (n = 25).
e Eight HAdV cases involved coinfections, including HAdV-55 with Mycoplasma pneumoniae in three, HAdV-55 with parainfluenza virus 3 and influenza virus B in one, HAdV-7 with Mycoplasma pneumoniae in one, HAdV-2 with respiratory syncytial virus A in one, HAdV-14 and parainfluenza virus 4 in one, and HAdV-3 with human coronavirus in one.

expenses, were similar between HAdV-55 and other types (Table 3).

Genome Sequence and Analysis of HAdV-55

A phylogenetic analysis was conducted based on the hypervariable region of the hexon gene to demonstrate the genetic relationship between HAdVs strains and the other seven HAdVs species (A-G); 47 of 48 strains belonged to HAdV species B and only one was HAdV-C (e-Fig 1A). Further partial hexon gene of HAdV strains were compared with the sequences of HAdV-B species in GenBank (e-Fig 1B); 21 of the 47 HAdV-Bs formed a dependent branch and revealed 100%, 96.7%, and 80% homologies with HAdV-55 (FJ643676), HAdV-11 (AF532578), and HAdV-14 (AY803294), respectively. Another phylogenetic tree was then conducted based on the partial fiber gene of the 15 HAdVs, hexon genes which were homologous to HAdV-55 (e-Fig 1C). The partial fiber gene had 99.8% to 100%, 99.4% to 99.5%, and 94.2% to 94.3% nucleotide identity with HAdV-55 (FJ643676),
HAdV has been recognized as an important viral cause of ARDS. The HAdV types most frequently associated with ARDS include subspecies B1 HAdV-3, HAdV-7, and HAdV-21 and species E HAdV-4. The association of subspecies B2 HAdV (HAdV-11, HAdV-14, HAdV-34, HAdV-35) infection with ARDS has been rarely reported historically, with some of that documentation covering military trainees. 15,18,19 In China, HAdV-3 and HAdV-7 were the most common types of pathogens. 20-22 HAdV-11a associated with ARDSs can be traced back to the 1980s 23 and it reemerged as an ARDS pathogen in 2006. 12,16 HAdV-55 (formerly known as HAdV-11a) was renamed HAdV-55 based on complete genomic sequence data, 13 which clearly showed that HAdV-55 was a recombinant between the HAdV-11 and HAdV-14 ancestral strains. Adenovirus 14 is an emerging agent of concern that has been causing outbreaks of pneumonia not just in China but worldwide. 24,25 Tate et al 26 reported an outbreak of severe respiratory disease associated with HAdV-14 in a US Air Force training facility. Five hundred fifty-one of 1,147 trainees (48%) with febrile respiratory illness were infected with HAdV-14; 23 trainees were hospitalized with pneumonia; four of those required admission to an ICU, and one died. Subsequently,

**Discussion**

To our knowledge, this study is the first large cohort on the epidemiology and clinical features of CAP associated with HAdV-55, the emerging pathogen among immunocompetent adolescents and adults. Our data showed clearly that HAdV-55 has established itself as a major pneumonia pathogen in the Chinese population and that further surveillance and monitoring of this agent as a cause of CAP is warranted.

HAdV has been recognized as an important viral cause of ARDS. The HAdV types most frequently associated with ARDSs include subspecies B1 HAdV-3, HAdV-7, and HAdV-21 and species E HAdV-4. The association of subspecies B2 HAdV (HAdV-11, HAdV-14, HAdV-34, HAdV-35) infection with ARDS has been rarely reported historically, with some of that documentation covering military trainees. 15,18,19

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outbreaks associated with HAdV-14 were reported in other states, such as Oregon, Alaska, and so forth.27-28

Today, adenovirus 55, which is related to adenovirus 14, is also emerging as an agent of concern. Because of the absence of cases caused by other HAdV types, Vento et al29 could only compare pneumonia caused by HAdV-14 with HAdV-14-negative cases. Our study had the advantage of being able to compare the differences in clinical, laboratory, or radiographic abnormalities caused by HAdV-55 and other types of pathogens. We proved that patients with diseases due to HAdV-55 were about 10 years older (P = .027) and had higher PSI scores (P = .030).

Our study has several limitations. First, our case series mainly represents the relatively mild and moderate end of the disease. We believe a wider surveillance study is needed to evaluate the spectrum of the disease caused by this emerging pathogen in an affected area in China. In addition, virus isolates were typed only by amplification and sequencing of the hexon gene, and no seroneutralization was performed. More laboratory tests should be carried out to understand the genomics and pathogenic characteristics.

**Conclusions**

In conclusion, our data provide new insight into the epidemiology of HAdV-55 infection in China. Patients with HAdV-55 infection were about 10 years older and had higher PSI scores than did patients infected by other types (HAdV-3, HAdV-7, HAdV-14). Furthermore, because it is difficult to discern HAdV pneumonia from clinical symptoms and signs, viral cause determination and a good surveillance system are important.

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**Author contributions**: Drs Cao and Wang had full access to all of the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

Dr Cao: contributed to the design of the study, care of the adenovirus pneumonia cases, data gathering, analysis of clinical data, writing of the manuscript, and the decision to publish.

Dr Xu: contributed to the PCR analysis and genotyping and writing of the manuscript.

Dr Pu: contributed to data gathering and manuscript revision.

Dr Qu: contributed to the care of the adenovirus pneumonia cases, data gathering, clinical specimen collection, PCR analysis, and manuscript revision.

Dr Dong: contributed to the care of the adenovirus pneumonia cases, data gathering, analysis of clinical data, and manuscript revision.

Dr Zhang: contributed to the PCR analysis and genotyping and manuscript revision.

Dr Liu: contributed to the care of the adenovirus pneumonia cases, data gathering, analysis of clinical data, and manuscript revision.

Dr Wang: contributed to the care of the adenovirus pneumonia cases, data gathering, and manuscript revision.

Dr H. Li: contributed to the care of the adenovirus pneumonia cases, data gathering, and manuscript revision.

Dr X-H. Li: contributed to the care of the adenovirus pneumonia cases, data gathering, analysis of clinical data, and manuscript revision.

Dr Q. Xu: contributed to the care of the adenovirus pneumonia cases, data gathering, and manuscript revision.

Dr H. Li: contributed to the care of the adenovirus pneumonia cases, data gathering, and manuscript revision.

Dr W. Xu: contributed to the design of the study and the decision to publish and manuscript revision.

Dr C. Wang: contributed to the design of the study and the decision to publish and manuscript revision.
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Additional information: The e-Figure and e-Table can be found in the “Supplemental Materials” area of the online article.

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