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Severe Pediatric Adenovirus 7 Disease in Singapore Linked to Recent Outbreaks across Asia

Oon Tek Ng, Koh Cheng Thoon, Hui Ying Chua, Natalie Woon Hui Tan, Chia Yin Chong, Nancy Wen Sim Tee, Raymond Tzer Pin Lin, Lin Cui, Indumathi Venkatachalam, Paul Anantharajah Tambyah, Jonathan Chew, Raymond Kok Choon Fong, Helen May Lin Oh, Prabha Unny Krishnan, Vernon Jian Ming Lee, Boon Huan Tan, Sock Hoon Ng, Pei Jun Ting, Sebastian Maurer-Stroh, Vithiagaran Gunalan, Wei Xin Khong

During November 2012–July 2013, a marked increase of adenovirus type 7 (Ad7) infections associated with severe disease was documented among pediatric patients in Singapore. Phylogenetic analysis revealed close genetic links with severe Ad7 outbreaks in China, Taiwan, and other parts of Asia.

Human adenoviruses (HAdVs) are classified into >50 types and are associated with clinical manifestations that include respiratory, gastrointestinal, ocular, genitourinary, and neurologic disease (1). HAdV infections have been estimated to cause 5%–10% of acute respiratory illnesses in children <5 years of age. Although most infections are subclinical or result in mild upper respiratory tract illnesses, HAdVs can also cause severe pneumonia. Among the HAdV types, type 7 (Ad7) has most often been associated with severe respiratory disease (2).

Recent reports have noted increased incidence of severe Ad7 disease in Asia: among the general population and pediatric inpatients in Taiwan; among persons in a military training camp in Shaanxi, China; and among those in a police training center in Kuala Lumpur, Malaysia (2–4). During January–June 2013, physicians in Singapore noted an increase in HAdV pediatric inpatients. Here we characterize the clinical and molecular epidemiology of this outbreak by reviewing data from government hospitals, the military, and a nationwide influenza-like illness (ILI) laboratory surveillance network in Singapore.

The Study

We retrospectively reviewed demographic and clinical information of adenovirus infections reported in Singapore during January 2011–July 2013 in 3 populations: 1) pediatric inpatients at KK Women’s and Children’s Hospital (formerly known as Kandang Kerbau Hospital) and National University Hospital, which are the only government hospitals in Singapore that have pediatric departments; 2) military personnel; and 3) outpatients reported to the nationwide ILI surveillance network housed in the National Public Health Laboratories (NPHL). Institutional review boards of the participating hospitals approved this study.

Cases of HAdV infection among military personnel were detected by a sentinel surveillance program in 5 military camps in which occurrences of febrile respiratory illnesses, defined as presence of acute respiratory symptoms (cough, sore throat, or both) and fever (oral temperature ≥37.5°C) (5), are monitored. All male citizens of Singapore undergo 2 years of conscripted military service upon turning 18–19 years of age; new personnel continuously enter the camps. To identify cases among the civilian population, the NPHL ILI laboratory surveillance network processes upper respiratory tract samples from patients with acute onset of fever (oral temperature ≥38°C) and respiratory symptoms referred by physicians at 23 sentinel clinics (6).

HAdV infection cases were defined by the detection of adenovirus by PCR assay, immunofluorescence, viral culture, or antigen detection in clinical samples (respiratory specimens, including nasal wash, bronchoalveolar lavage, endotracheal tube aspirate, oropharyngeal, nasopharyngeal, throat, and nasal swab; or urine or eye swab specimens). HAdV typing was performed by sequencing...
of HAdV hexon gene hypervariable regions 1–6 (HVR
1–6) (Ad7 reference Gomen AY594255 hexon gene nt 324–
1123) (7). To assess whether Ad7 was associated with se-
vere disease, diagnoses of inpatients were dichotomised
as invasive (pneumonia, gastroenteritis, disseminated dis-
ease, or hemorrhagic cystitis) and noninvasive (upper re-
spiratory tract infection, acute laryngotracheobronchitis,
bronchitis, bronchiolitis, tonsillitis, otitis media, or con-
junctivitis) on the basis of clinical syndromes identified
by physicians.

During January 2011–July 2013, samples from 421 pedi-
atric inpatients, 752 military personnel, and 85 pedi-
atric outpatients from the NPHL ILI surveillance network
were positive for adenovirus. During August 2011–July
2013, a total of 289 (96.0%) pediatric inpatient cases were
genotyped. The number of pediatric inpatients increased
from 32 during January–July 2012 to 200 cases during
January–July 2013 (Figure 1). This increase was predomi-
nantly related to Ad7 infections, which were first detected
in November 2012 and represented 48.5% (n = 97) of all
genotyped adenovirus cases in the first 7 months of 2013.
The increase in Ad7 pediatric inpatients was accompanied
by a smaller increase in detection of subgroup B HAdV
infections (n = 47) among military personnel, from Sep-
tember 2012 to July 2013; all patients recovered with out-
patient treatment. Of the samples from military personnel,
35 (74.5%) were genotyped; all were Ad7. During Septem-
ber 2012–July 2013, of 19 HAdV cases among pediatric
patients (<16 years of age) detected and genotyped by the
community ILI surveillance, none were Ad7; of 17 HAdV
cases identified among adults, 3 (17.6%) were Ad7.

Clinical information was available for 188 HAdV-pos-
itive pediatric inpatients (<16 years of age) admitted during
January–September 2013 (Table 1). A total of 54 patients
had invasive infections and 134 had noninvasive infections
(Table 2). More patients (n = 21, 38.9%) who had invasive
infections had comorbid conditions than did patients who
had noninvasive infections (n = 14, 10.5%; p<0.001). Ad7
was more frequently identified among patients who had in-
vasive infection (57.4% vs. 41.0%; p = 0.002). In univari-
ate analysis, invasive infection was significantly associated
with presence of comorbid conditions (crude odds ratio
[OR] 5.45, 95% CI 2.50–11.88) and Ad7 infection (crude
OR 6.95, 95% CI 1.98–24.41; p<0.001). After adjusting for
age and gender, presence of comorbid conditions (adjusted
OR 6.78, 95% CI 2.59–17.72) and Ad7 infection (adjusted
OR 9.00, 95% CI 2.34–34.59) remained significantly as-
sociated with invasive infection (p<0.001).

We used the maximum-likelihood method to compare
the phylogenetic relationships among representative Ad7
partial hexon gene sequences from pediatric inpatients (n =
9, November 2012–June 2013); the nationwide ILI labora-
tory surveillance network (n = 1 adult sample, January–June
2013); and military personnel (n = 34, September 2012–
May 2013) by using reference Ad7 sequences (GenBank
accession nos. KP729815–KP729824) (Figure 2) (8,9).
All Singapore Ad7 isolates except KK341 and KK342 had
100% nucleotide identity with strains reported from a 2011
adenovirus community outbreak in Taiwan (JX174430),
severe disease in infants in Shaanxi in 2009 (GU230898),
and a military training camp outbreak in Shaanxi in 2012
(KC689913) (2,3,10).
hexon gene sequences of the Singapore isolates had 100% nucleotide identity with sequences reported from outbreaks in Taiwan and China (2,3,10).

Ad7 has been reported to cause outbreaks in 3 main patterns: 1) severe disease among young children, especially during winter in temperate countries; 2) less severe disease in nonseasonal community outbreaks; and 3) outbreaks among military personnel (11). The outbreak we report was marked by severe disease among young children and mild disease among military personnel. In the 2 government-owned hospitals, 1–2 cases among pediatric patients were identified per month by using community ILI surveillance. Failure to detect an increase in Ad7 remains unexplained but might be related to the low number of samples collected and tested.

Ad7 can be subclassified by restriction enzyme analysis (12). The available Singapore partial hexon gene sequences were most closely related to Ad7d and Ad7d2 genome types, which have been associated with outbreaks of acute respiratory illness in Asia. Ad7d, the predominant Ad7 circulating virus in China since the early 1980s, was the cause of outbreaks in South Korea during 1995–1997; during a community and pediatric outbreak in Taiwan in 2011, Ad7d replaced Ad7b as the main Ad7 strain (2,13). The closely related Ad7d2 was described in Israel in 1992 and has caused outbreaks in the United States and Japan (14,15). Systematic HAdV typing in Singapore was initiated in late 2011, so it remains unknown if Ad7 sub-strain replacement, specifically the circulating pediatric HAdV strain in early 2011, was a factor in the outbreak we report.

Our findings indicate a need for improved vigilance for detection and surveillance of severe Ad7 disease in Asia, as well as whole-genome sequencing and seroprevalence studies to perform accurate typing of outbreak strains and to identify correlates of pathogenicity. These practices could facilitate effective, early deployment of vaccine prevention and antiviral therapy.

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Dr. Ng is an Infectious Disease Consultant at Tan Tock Seng Hospital. His primary research interests are pathogen molecular epidemiology, emerging infectious diseases, and HIV.

References


Figure 2. Phylogenetic analysis of adenovirus type 7 (Ad7) sequences from this study based on sequenced Ad7 hexon gene hypervariable regions 1–6 (Ad7 reference Gomen AY594255 hexon gene nt 324 to 1123). The phylogenetic relationships between Ad7 isolates in this study were inferred by using the maximum-likelihood method based on the Tamura-Nei model (8). Initial trees for the heuristic search were obtained by applying the neighbor-joining method to a matrix of pairwise distances estimated by using the maximum-composite likelihood approach. Tree is drawn to scale; branch lengths are measured in the number of substitutions per site, the rate of which was assumed to be uniformly distributed. The analysis involved 63 nt sequences. Green indicates isolates from military personnel, dark blue indicates isolates from patients in National University Hospital, pink indicates isolates from patients in KK Women’s and Children’s Hospital, and light blue indicates isolates from patients in Changi General Hospital. The sequence labeled as “AY594255_7_Gomen (USA 1954)” represents 1 of the published Gomen sequences (AY594255). “_7” is added to GenBank accession numbers to denote that these are Ad7 sequences. All other strains shown are published Ad7 reference isolates. Phylogenetic analyses were conducted by using MEGA6 (9). KK341 and KK342 had a single thymine-to-cytosine mutation (Ad7 reference Gomen AY594255 hexon gene nt 780). The remaining 41 isolates from Singapore had 100% nucleotide identity.


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