Molecular Typing of Human Adenovirus Infection among Paediatric Patients in Singapore from 2012 to 2014

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Background/Objective

Human Adenoviruses (HAdVs) are the common viruses causing acute respiratory infections in children, and certain types of HAdV have reported to be related with severe clinical presentations. As part of influenza-like illness (ILI) surveillance program, we characterized adenoviruses from clinical samples collected in Singapore between 2012 and 2014.

Method

Respiratory specimens were collected from children' s hospital and a private paediatric clinic. Identification of HAdV was carried out by IF and/or PCR. Sequencing of HAdV hexon gene HVR1-6 was performed before phylogenetic analysis.

Result

HAdV had been detected in 6.2% (104/1684) ILI samples collected in the outpatient clinic, which was the 3rd predominate one among respiratory viruses under our surveillance. A total of 777 samples were analysed, 91 were collected from outpatients and 686 were from inpatients. Among outpatients, HAdV-1, -2, -3, -4 and -5 were the most predominant types (24.2%, 22.0%, 26.4%, 15.4% and 8.8%, respectively, 96.7% in total) during 2012-2014. Among inpatients, HAdV-4 (47.8%) and -3 (26.9%) were the predominant genotypes in 2012, but increased HAdV-7 (39.5%) was detected during 2013 together with HAdV-3 (25.2%) and -4 (18.2%). In 2014, HAdV-3 became the predominant genotype (77.3%). Other types detected in inpatients included HAdV-1, -2 -5 and -8.

Conclusion

In our study, HAdV-1, -2, -3, -4 and -5 were commonly detected in both paediatric outpatients and inpatients. Although HAdV-7 was the predominant type in inpatients in 2013, it was seldom detected in outpatients during the same period and all patients in the other period of this study. These finding provided baseline data of circulating HAdVs in Singapore, which are important for ILI surveillance and early detection of outbreaks.