

00287 Laboratory-based Survey of Human Adenovirus Infections in a Pediatric Medical Centre in Singapore From 2015 to 2016

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Aims: Human adenoviruses (HAdV) are non-enveloped, double-stranded DNA viruses with seven difference species (A-G) and more than 60 genotypes. HAdVs cause infections in all age groups, but children are particularly affected due to their increased susceptibility to common viral infections. HAdV infections may occur in the form of periodic peaks or outbreaks in the community, and severe infections can manifest themselves in the respiratory tract. Here, we studied the seasonal distribution of HAdVs through the submission base of a Singapore-based laboratory.

Methodology: A total of 773 clinical specimens such as blood, respiratory tracts specimens, conjunctival, and rectal swabs were submitted to HAdV-specific real-time polymerase chain reaction (PCR). All positive specimens were sent to National Public Health Laboratory (NPHL) for genotyping.

Result: In 2015, there were 43 (13.7%) positive cases of HAdV detected among 315 specimens. There was a noticeable increase of positive cases in the month of November. In 2016, the total positive cases increased to 109 cases (23.8%) among 458 specimens. In that year, there was a steady increase of positive cases from March until December. From this study, HAdV type 3 was the most prevalent genotype. HAdV infections appear to show a distinct seasonal pattern which peaks at the end of each year (November and December) in 2015 and 2016 in Singapore.

Conclusion: This study provides an overview of the seasonal patterns of HAdV infections in children in Singapore. Early detection and monitoring of HAdV detected in children can be a valuable tool to improve patient management and to develop prevention strategies, especially in outbreak situations.