

# Molecular Epidemiology of Common Respiratory Adenovirus Infection of Children in Northern Taiwan Circulating between 2009 and 2013

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## Background/Objective

Respiratory infections caused by human adenoviruses (HAdV) of species B, C, and E are worldwide. The most common genotypes are HAdV B3 and B7. We conducted this study to understand molecular epidemiology of HAdV B3 and B7 in northern Taiwan.

## Method

HAdV isolated from pediatric patients hospitalized in a medical center in northern Taiwan between 2009 and 2013. Partial hexon and fiber genes were amplified and sequenced for further phylogenetic analysis to evaluate genotype and evolutionary dynamics. The nucleotide substitution and codon partitioning model were selected by Bayesian information criterion and compare the Bayesian factor respectively. Phylogenetic trees and evolutionary patterns of HAdV were reconstructed by Maximum likelihood (ML) and Bayesian Markov chain Monte Carlo approach respectively.

## Result

During these 4 years, 96 strains of HAdV B3 and 12 strains of HAdV B7 were analyzed. The hexon fragments of both genotypes are not sufficient to conduct the evolutionary dynamics due to lack of enough substitutions pattern in studied region. For the fiber gene fragments, the mean substitution rate in HAdV B3 and B7 was  $5.36 \times 10^{-4}$  and  $2.6 \times 10^{-4}$  nucleotide substitutions per site per year (95% HPD  $3.5 \times 10^{-8}$ - $1.5 \times 10^{-3}$  and  $1.5 \times 10^{-5}$  –  $5.2 \times 10^{-4}$ ) respectively; however, the substitution rate of HAdV B3 represented a bimodal distribution with peaks at about  $1.2 \times 10^{-4}$  and  $7.9 \times 10^{-4}$ . Despite the mean substitution rate of fiber gene is similar between B3 and B7; interestingly, it has very different that the relative substitution rate of each codon position.

## Conclusion

The hexon gene is relative stable than fiber gene in both genotypes. The evolutionary rate of fiber gene of HAdV B3 and B7 is similar. These observations might be useful for vaccine design and further epidemiological studies.