## Novel and extendable genotyping system for Human Respiratory Syncytial Virus based on whole-genome sequence analysis

Jiani Chen<sup>1</sup>, Xueting Qiu<sup>2</sup>, Samuel Shepard<sup>3</sup>, Do-Kyun Kim<sup>4</sup>, James Hixson<sup>4</sup>, Pedro Piedra<sup>5</sup>, Vasanthi Avadhanula<sup>5</sup>, and Justin Bahl<sup>2</sup>

<sup>1</sup>University of Georgia <sup>2</sup>University of Georgia College of Veterinary Medicine <sup>3</sup>Centers for Disease Control and Prevention <sup>4</sup>The University of Texas Health Science Center at Houston <sup>5</sup>Baylor College of Medicine

June 1, 2021

## Abstract

Background: Human respiratory syncytial virus (RSV) is one of the leading causes of respiratory infections, especially in infants and young children. Previous RSV sequencing studies have primarily focused on partial sequencing of G gene (200-300 nucleotides) for genotype characterization or diagnostics. However, the genotype assignment with G gene has not recapitulated the phylogenetic signal of other genes and there is no consensus on RSV genotype definition. Methods: We conducted Maximum Likelihood phylogenetic analysis with 10 RSV individual genes and whole-genome sequence (WGS) that are published in GenBank. RSV genotypes were assigned by the statistical support monophyletic clusters with at least 10-year detection time from the WGS phylogeny. Results: In this study, we first statistically examined the phylogenetic incongruence, rate variation for each RSV gene sequence and WGS. We then proposed a new RSV genotyping system based on a comparative analysis of WGS and the spatial and temporal distribution of each lineage. We also provided an RSV classification tool to perform RSV genotype assignment. Conclusions: This revised RSV genotyping system will provide important information for disease surveillance, epidemiology, and vaccine development.

## Hosted file

Chen[irv]\_2021\_rsv\_genotype\_manuscript\_clean-FINAL.docx available at https://authorea. com/users/417154/articles/524348-novel-and-extendable-genotyping-system-for-humanrespiratory-syncytial-virus-based-on-whole-genome-sequence-analysis





