Title of dissertation			
Characterisation of Human Respiratory Syncytial Virus among Children with Severe Acute Respiratory Infection before and during the COVID-19 pandemic in Zambia			
RONPAKU Fellow			
Name	**Paul Simusika**		
Position	Technical Laboratory Scientist	ID No.	R12008
Department	Virology Laboratory, Pathology ＆Microbiology Department		
Institution	The University Teaching Hospital	Nationality	Zambia
Japanese Advisor			
Name	Hitoshi Oshitani		
Position	Professor	Institution	Tohoku University Graduate School of Medicine

Background:

Annual outbreaks of human respiratory syncytial virus (HRSV) are caused by newly introduced and locally persistent strains. During the COVID-19 pandemic, global and local circulation of HRSV significantly decreased. This study was conducted to characterize HRSV in 2018–2022 and to analyze the impact of COVID-19 on the evolution of HRSV.

Materials and Methods:

Combined oropharyngeal and nasopharyngeal swabs were collected from children hospitalized with severe acute respiratory infection (SARI) at two hospitals in Zambia. The second hypervariable region of the attachment gene G was targeted for phylogenetic analysis.

Results:

Out of 3,113 specimens, 504 (16.2%) were positive for HRSV, of which 131 (26.0%) and 66 (13.1%) were identified as HRSVA and HRSVB, respectively. In early 2021, an increase in HRSV was detected, caused by multiple distinct clades of HRSVA and HRSVB. Some were newly introduced, whereas others resulted from local persistence.

Conclusions:

This study provides insights into the evolution of HRSV, driven by global and local circulation. The COVID-19 pandemic had a temporal impact on the evolution pattern of HRSV. Understanding the evolution of HRSV is vital for developing strategies for its control.

Keywords: Respiratory syncytial virus; molecular evolution; severe acute respiratory infection; children; Zambia