Evolutionary analysis of Human Respiratory Syncytial Virus in Myanmar, 2015-2018

Wint Wint Phyu1, Khin Thuzar Htwe4, Clyde deapat5, Reiko Saito1, Irina Chon1,2, Hidekazu Osada1,2, Hisami watanabe2, Htay Htay Tin3

1*Division of International Health, Graduate School of Medical and Dental Sciences, Niigata University, Niigata, Japan; Infectious Diseases Research Center (IDRC) of Niigata University in Myanmar, Graduate School of Medical and Dental Sciences, Niigata University, Niigata, Japan; National Health Laboratory, Department of Medical Services, Ministry of Health and Sports, Myanmar; NUNiversity of Medicine, Mandalay, Myanmar; 2Department of Virology, Graduate School of Medicine, Tohoku University, Japan

**Background**

- Genetic evolution of Human Respiratory syncytial virus (HRSV), especially G gene encoding attachment protein, plays a crucial biological role for faster viral replication, which may elicit strong resistance to herd immunity.
- In Myanmar, there are no previous studies done to characterize genotypes and to assess evolution of HRSV.

**Aim**

- To clarify the clinical manifestations of HRSV infections in outpatients, and seasonality of HRSV in Myanmar.
- To assess the evolution of HRSV in Myanmar by studying genetic variations of the 2nd hypervariable region (HVR) of the G gene of the virus.

**Materials & Methods**

- Collection of nasal swabs from patients suspected of HRSV infection.
- Rapid diagnostic test: Multiplex PCR using primers targeting the G and F genes.
- Phylogenetic analysis using Maximum likelihood method.
- BEAST software version 1.8.4.

- Table 1: Positivity of HRSV subgroups by year in Myanmar, 2015-2018

<table>
<thead>
<tr>
<th>Year</th>
<th>HRSV-A Positive by RT-PCR</th>
<th>HRSV-B Positive by RT-PCR</th>
<th>Total (n=140)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2015</td>
<td>35 (100)</td>
<td>60 (100)</td>
<td>195 (100)</td>
</tr>
<tr>
<td>2016</td>
<td>60 (100)</td>
<td>30 (100)</td>
<td>90 (100)</td>
</tr>
<tr>
<td>2017</td>
<td>38 (100)</td>
<td>52 (100)</td>
<td>90 (100)</td>
</tr>
<tr>
<td>2018</td>
<td>28 (100)</td>
<td>160 (100)</td>
<td>188 (100)</td>
</tr>
<tr>
<td>Total</td>
<td>195 (100)</td>
<td>188 (100)</td>
<td>383 (100)</td>
</tr>
</tbody>
</table>

- Table 2: Base line characteristics of HRSV-A & HRSV-B subgroups in Myanmar, 2015-2018

- Figure 2: Phylogenetic trees of G gene of HRSV-A and HRSV-B strains from Myanmar and reference strains, 2015-2018

- Figure 3: Time scaled phylogenetic tree of ONI of HRSV-A and HRSV-B using Bayesian Markov Chain Monte Carlo (MCMC) method

- Figure 4: Effective population size of HRSV-A and HRSV-B strains in Myanmar, 2015-2018

**Summary**

- During the study period, 464 (24.5%) out of 1837 nasopharyngeal swabs were identified by RT-PCR. Out of these, 246 samples were positive by real time PCR, 84 (34.6%) were HRSV A, and 162 (65.4%) were HRSV B and 1 (0.8%) were mixed infection.
- HRSV-A was predominant in 2016. However, HRSV-B became predominant in two consecutive years of 2017 and 2018.
- Higher proportion rate of HRSV-A cases were found in 1 year old and above than children less than 1 year old (76.53 vs 29.53).
- Cough and rhinitis were the main symptoms, observed in 89.0% and 70.9% of HRSV infected children.
- The main distribution of HRSV-A positive samples showed that HRSV-A epidemic in Myanmar occurred between July through October and peaked during August and September.

- Phylogenetic analysis showed that HRSV-ONI strain in HRSV-A and BA9 in HRSV-B type is likely to circulate during 2015-2018 in Myanmar.

- According to Bayesian Markov Chain Monte Carlo (MCMC) method by using Beast software, the time to the most recent common ancestor (MRCA) was estimated since 1993 (95% HPD: 1935-2010) for HRSV-A and since 1999 (95% HPD: 2000-2010) for HRSV-B.

- The mean evolutionary rate for HRSV-A (1.23 x 10^-7 substitutions/year; 95% HPD: 1.83 x 10^-7 to 1.5 x 10^-7) and HRSV-B (2.31 x 10^-3 to 2.5 x 10^-3) were highly faster than HRSV-A (1.9 x 10^-3 substitutions/year; 95% HPD: 3.5 x 10^-3 to 2.6 x 10^-3).

- The estimated effective population size (diversity) of HRSV-A increased from 2015 to 2016, whereas, ONI was the dominant genotype and declined in the middle of 2018. In contrast, the diversity of HRSV-B was constant in 2015-2016, and increased in the middle of 2017.

**Conflict of Interest**

We have no conflict of interest.

**Acknowledgement**

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