

SHORT REPORT

**Molecular Characterization of Human Respiratory Syncytial Virus among Children in Yangon Children's Hospital**

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Acute respiratory infection (ARI) is responsible for high morbidity and mortality rates, especially in developing countries.<sup>1</sup> Respiratory syncytial virus (RSV) is one of the most important respiratory viruses responsible for annual epidemic ARI outbreaks in infants and pre-school children worldwide, frequently causing bronchiolitis and pneumonia mostly in infants less than six months old.<sup>2</sup> RSV is differentiated into two groups (A and B) based on antigenic and genetic variability. In this study, firstly, the relative prevalence of RSV among other viruses causing ARI in children at Yangon Children's Hospital (YCH) was observed. After that, clinical and epidemiological features of RSV infection was proceeded to study and then genetic analysis was performed. One-hundred and sixty nasopharyngeal swabs were collected from children with ARI at the YCH from January to September, 2014. All 160 specimens were screened by Reverse Transcriptase PCR (RT-PCR) for the following viruses: RSV, influenza virus A (IFVA), influenza virus B (IFVB) and human metapneumo virus (HMPV). The first 67 specimen collected from January to July, 2014 were screened by RT-PCR for the following additional viruses: human rhinovirus (HRV), human coronaviruses (HCoV-229E), (HCoV-OC43), human adenovirus (HADV), human bocavirus (HBOV), parainfluenza virus type 1

(PIV1), parainfluenza virus type 2 (PIV2), parainfluenza virus type 3 (PIV3) and parainfluenza virus type 4 (PIV4).

During the study period (January to July), 39(58.2%) ARI children were found to be caused by HRV, 6(9.00%) was due to HADV, 5(7.40%) by PIV1, 2(2.98%) by PIV2 and 2(2.98%) by PIV3, but none was found to be caused by PIV4, human bocavirus (HBOV) nor coronavirus (HCoVs: strain 229E, OC43). During the study period (July to September, 2014), ARI was caused by RSV in 26 cases (16.25%); by IFVA in 12 cases (7.50%) but none by IFVB nor HMPV. Thus, RSV and HRV were major viral etiological agents of ARI in children at YCH, Yangon. RSV was detected in 26 samples obtained from January to September 2014 and the majority of the RSV cases (92.3%) were reported in the rainy season (July to September). Among RSV-positive patients, the ratio of boys to girls was 1.4: 1; the age range was 1 month to 44 months, the majority of patients (88%) were under one year old; and the diagnosis in the majority patients (46.2%) was severe pneumonia.

During the study period from January to July (cold and dry season), ARI was caused

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by RSV in 2 cases (3%), IFVA in 5 cases (7%), HRV in 39 cases (58%), HADV in 6 cases (9%), PIV1 in 5 cases (7%), PIV2 in 2 cases (3%), PIV3 in 2 cases (3%). But ARI was not caused by IFVB, HMPV, PIV4, human bocavirus (HBOV) and corona virus (HCoV: strains 229E, OC43). During the study period from July to September (rainy season), ARI was caused by RSV in 24 cases (26%) and by IFVA in 7 cases (8%) but not caused by HRV, IFB and HMPV. Tests for other viruses have not yet been done. Thus, based on the limited study done for 9 months of the year for one year only, RSV was a major viral cause of ARI in children during the rainy season; and rhinovirus was a major viral cause of ARI in children during early summer.

Out of the 26 non-structural proteins 1 (NS1) gene-positive samples for RSV among the total 160 specimen, 21 RSV strains were selected for further genetic analysis. DNA sequencing was done by using Applied Biosystems 3500 XL Nucleotide sequence at DMR. The sequences were aligned by Lasergene SeqMan sequence analysis software, and the aligned sequences were analyzed for relationships with other RSV strains by Nucleotide Blasting in Basic Local Alignment Software Tool (BLAST) available from National Centre for Biotechnology Information (NCBI).

This analysis revealed that 11 RSV isolates (52%) were RSV-A strains and 10 isolates (48%) were RSV-B strains. The 11 NS1 gene sequence of RSV-A strains when analyzed by nucleotide blasting showed 100% homology with the sequence of USA strains. The 10 sequences of RSV-B strain showed 98% homology with the sequences from Latin America. This study revealed previously known information about the relative frequency of the viruses causing ARI in children at YCH, Yangon, and showed that RSV and HRV were major

etiological agents causing ARI among the children.

Limitations of this study was that the study period was only for 9 months of the year and insufficient for any firm conclusion about the epidemiology and seasonal pattern. During analysis, the genes coding for Non-structural proteins 1 (NS1) which were the basis of the genetic analysis in this study are relatively stable and have low immunogenicity so that while differentiation into RSV group A and B can be revealed they are not suitable for further analysis or sequencing studies. The G protein is the most immunogenic protein of the RSV virus and is one of the targets for neutralization and antibody response. All other RSV genes show higher degree of conservation, suggesting that the impact of immune pressures on the evolution of these genes is minimal. The next step in the study of molecular characterization of human RSV among children with ARI at YCH will be to sequence the DNA of the G genes of RSV strains isolated from these cases.

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#### *Competing interests*

The authors declare that they have no competing interests.

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