# BIOINFORMATICS DIVISION

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Bioinformatics Division is involved in Hepatitis B Virus (HBV), Respiratory Syncytial Virus (RSV) research area and health informatics. Bioinformatics Division is also involved in DNA sequencing services for research in tuberculosis, malaria, HBV and other infections.

## RESEARCH PROJECTS

## 1. COMMUNICABLE DISEASES

### 1.1 RESPIRATORY SYNCYTIAL VIRUS INFECTION

#### 1.1.1 Phylogenetic analysis of Myanmar human Respiratory Syncytial Virus from under five children with acute respiratory infection admitted to Yangon Children Hospital (YCH)

Human respiratory syncytial virus (HRSV) is one of the most important respiratory viruses responsible for annual epidemic ARI outbreaks in infants and pre-school children worldwide and it is frequently causing bronchiolitis and pneumonia in infants less than six months old. RSV is a member of the family *Paraxymoviridae* that is differentiated into two groups (A and B) based on antigenic and genetic variability.

To date, 11 genotypes for RSV group A and 23 for RSV group B have been described based on changes in the G gene coding for the attachment glycoprotein. In this study, nasopharyngeal swab samples were collected from 160 hospitalized pediatric ARI cases at Yangon Children Hospital between January to September 2014. Out of 160 cases, Non – structural protein 1 (NS1) gene of RSV was detected in 16.25% (26/160).Among 26 NS1 gene positive samples,21 samples can proceed for gene sequencing and they showed RSV - A strains 52% (11/21) and RSV- B strains 48% (10/21). The genetic analysis based on the Non-structural protein (NS 1) is relatively stable and has low immunogenicity. G protein, a surface-expressed glycoprotein that is associated with attachment of the virus, shows the largest antigenic and genetic differences between the two HRSV subgroups and is one of the targets for neutralization and protective antibody responses. The G protein contains two hypervariable regions(HVR); the second variable region, which corresponds to the C-terminal region of the G protein, reflects overall G protein gene variability and has been analyzed in molecular epidemiological studies. Therefore, the 21 NS1 gene positive nasopharyngeal swab samples were processed for genotyping by reverse transcription-PCR and sequencing of C terminal of the G gene, second variable region. RSV G gene was found in 61.9% (13/21) of samples. RSV-A was the larger group, accounting for 53.8% (7/13),

followed by RSV-B, 38.5% (5/13) and one case (7.7%)(1/13) was a mixed infection. The phylogenetic analysis revealed that all group A strains clustered as the ON1 genotype. This RSV ON1 genotype in subgroup A has a characteristic of a 72 nucleotide duplication in the second highly variable region of attachment G gene. The phylogenetic pattern of tested samples were found to be closely related to Canada, Japan, China, Korea and Thailand. Other studies reported the association of ON 1 genotype with less severe cases such as bronchiolitis and the present study also showed the similar findings. The 8 RSV-A sequences of the present study was submitted at GenBank, NCBI and the accession numbers were shown in the following table.

| No. | Sample | GenBank Accession No. |
|---|---|---|
| 1. | RSV-A 083 | KY320500 |
| 2. | RSV-A 100 | KY320501 |
| 3. | RSV-A 102 | KY320502 |
| 4. | RSV-A 105 | KY320503 |
| 5. | RSV-A 119 | KY320504 |
| 6. | RSV-A 122 | KY320505 |
| 7. | RSV-A 135 | KY320506 |
| 8. | RSV-A 137 | KY320507 |

## 2. ACADEMIC AND TECHNOLOGY DEVELOPMENT

### 2.1 HEALTH INFORMATICS

#### 2.1.1 Clinical Decision Support System

##### 2.1.1.1 Knowledge-Based approach to clinical decision support system for dengue fever, dengue haemorrhagic fever, dengue shock syndrome, measles, rubella and congenital rubella syndrome (2016)

Clinical decision support systems (CDSSs) reflect active knowledge systems which use two or more items of patient's data to generate case-specific advice. A computer-aided CDSS for diagnosis and treatment often plays a vital role and brings essential benefits. This research consists of three parts, the knowledge base, inference engine, and mechanism to communicate. The knowledge base contains the rules and associations of compiled data which most often take the form of IF-THEN rules. The inference engine combines the rules from the knowledge base with the patient's data. The communication mechanism allows the system to show the results to the user as well as to have input into the system. Knowledge acquisition is very important starting procedure for this research. The knowledge base is obtained from the domain expert (e.g. pediatrician). This CDSS incorporates signs and symptoms and discusses solutions for diagnosis, treatment and description of dengue fever, dengue haemorrhagic fever, dengue shock syndrome, measles, rubella and congenital rubella syndrome. Data is collected only for six conditions: dengue fever, dengue haemorrhagic fever, dengue shock syndrome, measles, rubella and congenital rubella syndrome. Total number of 50 patient records (clinical data) is collected from Yangon Children Hospital, Yankin Children Hospital, Mandalay Children Hospital and Pyin Oo Lwin Hospital.

Laboratory data was extracted from the Department of Medical Research. Performance measurement is calculated by using Microsoft Excel. The CDSS diagnostic accuracy was shown to be correct classification rate with a value of 98% to 50 patient records compared to known diagnosis by laboratory testing. The result values showed satisfactory agreement; 1 for five diseases and 0.8 for one disease by using Kappa method. This research is Knowledge-Based CDSS, constructed for dengue fever, dengue haemorrhagic fever, dengue shock syndrome, measles, rubella and congenital rubella syndrome. It can be used for automated diagnosis by using clinical data, with accompanying description and treatment for these diseases.

## 3. RESEARCH CAPACITY STRENGTHENING

3.1 Maintenance of DNA Sequencer

Weekly instrument maintenance tasks
- Checking of storage conditions of the used arrays
- Washing the pump and capillary channels using conditioning reagent and Polymer.

Monthly instrument maintenance tasks
- Flushing the pump trap with distilled water
- Emptying the condensation container and the water trap waste container
- Replacing the Cathode Buffer container septa

Quarterly instrument maintenance task
- Running the performance check by using sequencing standard kit.

## SERVICES PROVIDED

1. ACADEMIC

| Sr. | Name | Course | Responsibility |
|---|---|---|---|
| 1.1 | Daw Kay Thi Aye | 1st Year Diploma Molecular Biology, DSMA | Demonstration of DNA sequencer and sequence data analysis |

2. LABORATORY

| Sr. | Laboratory tests | No. of tests |
|---|---|---|
| 1.1 | DNA sequencing of the requested samples (*Mycobacterium tuberculosis*, Hepatitis B virus, *Plasmodium falciparum*, Respiratory Syncytial Virus, RT-HBV, Epstein-Barr virus (EBV), Dengue virus and Rotavirus) | 1646 |