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. VIRAL HEPATITIS

1.1.1. Whole genome sequencing of Hepatitis B Virus (HBV) strains from Myanmar

Hepatitis B virus (HBV) is an important etiological agent of acute or chronic hepatitis, liver cirrhosis and hepatocellular carcinoma. It is estimated that there are currently more than 350 million chronically infected people worldwide and this poses major health problems worldwide, especially in Asian Pacific countries. To date, 10 HBV genotypes, scattered across different geographical regions, have been identified. HBV genotyping with surface (s) gene sequence in general is consistent with the genotyping of the full genomic sequence. However, it is not applicable for sub genotyping. Therefore complete genome sequences are more reliable for the analysis of genotype and sub genotyping. In addition to this, certain mutations which may affect the diagnostic detection, drug resistance, disease progression and effective vaccination of HBV can also be detected. In this study we successfully sequenced the 15 full-length genetic sequences of HBV isolate from HBV infected Myanmar peoples who were not taking antiviral therapy. GenBank accession number of the 15 HBV genome sequences were shown in the table. Genotyping was done by using HepSEQ web based program, and drug resistant mutations were detected by geno2pheno web based analytical tools. All 15 sequences revealed genotype C and no drug resistant mutations were seen among these isolates. There were also no mutations in pre core region and no known vaccine escape mutation among these isolates. This is the first time to sequence the whole genome of Myanmar HBV isolates by Department of Medical Research, and these whole genome sequences will act as baseline data for further exploring other genetic studies regarding HBV.

Table. GenBank accession number of 15 HBV genome sequences

No.	Sample	GenBank Accession No.
1.	MMHBV001	KT307718
2.	MMHBV002	KU051427
3.	MMHBV003	KT307719
4.	MMHBV004	KT364718
5.	MMHBV005	KT364719
6.	MMHBV006	KT364720
7.	MMHBV007	KT364721
8.	MMHBV008	KT987423
9.	MMHBV009	KT987426
10.	MMHBV010	KT987424
11.	MMHBV011	KT987425
12.	MMHBV012	KU051423
13.	MMHBV014	KU051424
14.	MMHBV017	KU051426
15.	MMHBV018	KU051425

2. ACADEMIC AND TECHNICAL 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 (2015)

In the medical area, clinical decision support systems (CDSSs) are a class of active knowledge systems which use two or more items of patients' data to generate case-specific advice. A computer-aided Clinical Decision Support System (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 will allow the system to show the results to the user as well as to have input into the system. Construction a software programme to explore signs and symptoms for discussion of solutions for diagnosis, treatment and description of dengue fever, dengue haemorrhagic fever and dengue shock syndrome was completed.

SERVICES PROVIDED

1.   ACADEMIC

Sr.	Name	Course	Responsibility
1.	Dr. Nyi Nyi Win	Training Workshop on molecular and liquid drug susceptibility testing methods for detection of pyrazinamide and second line anti-TB drug resistance	Demonstration of DNA sequencer and sequence data analysis
2.	Daw Kay Thi Aye	Training Workshop on molecular and liquid drug susceptibility testing methods for detection of pyrazinamide and second line anti-TB drug resistance	Demonstration of DNA sequencer and sequence data analysis

2.   LABORATORY

Sr.	Subject	Tested samples
1.	DNA sequencing of the requested samples (*Mycobacterium tuberculosis*, hepatitis B virus, *Plasmodium falciparum*, Respiratory Syncytial Virus, Rhino virus, Dengue virus and Rotavirus)	700

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.

3.2. Services for internet server and others
- Checking and installation and maintenance of internet server and AMRC Wi-Fi
- System maintenance, software installation and trouble shooting of computers, scanners and photocopier of AMRC
- Data entry and data management of results of research projects