NURLYANA AQILAH HAMIDON
Bachelor of Science (Biomedical Sciences)
Faculty of Medicine and Health Sciences
Universiti Putra Malaysia

Nurlyana Aqilah Bt Hamidon was born in Kuala Lumpur on 16th September 1997. She is the only daughter of Hamidon B Musa and Rosni Bt Sulaiman. She received her secondary education from SM Sains Kuala Selangor in 2010. Later, she continued her study on Foundation of Agricultural Science at Universiti Putra Malaysia. After nearly a year, she decided to pursue her study in health sciences field. She chose to further in Bachelor of Science (Biomedical Sciences), and she will be graduated in November 2019. From her study, she obtained opportunities to perform various laboratory practices through most of the courses offered in the department. Her final year project entitled Bioinformatic Analysis of Malaysian Isolated Torque Teno Virus from Hepatitis Patient, has extremely related to molecular biology and bioinformatics. The research allows her to broaden her knowledge on the molecular properties and structural protein of the virus. She is passionate, self-motivated, and very organized. She resides in Bangi, Selangor and can be contacted at lyanaqilah13@yahoo.com.

ABSTRACT

Bioinformatic Analysis of Malaysian Isolated Torque Teno Virus from Hepatitis Patient

Nurlyana Aqilah Hamidon and Zulkefley Othman

Introduction: First isolation of Torque Teno Virus (TTV) has been unearthed two decades ago from a Japanese patient with post transfusion hepatitis of unidentified etiology. Studies showed that TTV is a circular genome with a size range from 3700 bp to 3900 bp. TTV is unenveloped, single stranded DNA and belongs to Anelloviridae family. TTV have an extremely high prevaience rate and their distribution worldwide were identified. Research in Malaysia regarding the genomic characterization of TTV is vital as there is a limited study about TTV in this country. Objective: To analyse sequence of TTV isolated from Malaysian hepatitis patient by bioinformatic software. Methodology: DNA extraction from HCV-infected patient by using QlAamp DNA Mini kit. Amplification of TTV DNA by a long standard PCR is applied, foliowed by separating DNA fragments by agarose gel electrophoresis, and visualized it under UV illumination. TTV DNA sequence was cloned into pJET vector, and sequenced by primer walking. Sequence analysis by BLAST NCBI and MUSCLE software, as well as phylogenetic analysis by MEGA software. ORFfinder software was used to determine the open reading frames proteins. Bioinformatic analysis on the sequence of TTV DNA was performed by using ProtParam and ProtScale webtools. Results and Discussion: The size of the isolated TTV DNA is 3265 bp. TTV sequence was 99% of query sequence matched with isolated KAV (AF435014.1). Phylogenetic analysis poses five major group of TTV genotypes from 50 published TTV isolated, and it has been revealed that our isolated TTV sequence was in group 2. There are ORF1, ORF2 and ORF3 present, which encodes 720, 153 and 137 amino acids, respectively. For bioinformatic analysis by ProtParam, both ORFs are unstable, with molecular weights, 85.34 kDa, 16.47 kDa and 14.25 kDa, respectively. In ProtScale, all ORFs represented different scale on each amino acid parameters computed, such as the first 85 positions of amino acid in ORF 1 protein represent low hydrophobic, while there are several regions in ORF2 and ORF3 are found to be low hydrophobic, including the 10 th and 90 th position of amino acids, respectively. Conclusion: The physical and chemical properties of ORFs protein are determined in ProtParam, while in ProtScale, different amino acids constitution display different scales based on the structure of the protein, thus the functional segments of the protein can be identified.