

## **Whole genome sequencing of an *Enterococcus faecalis* isolate from a patient with cholecystitis in a tertiary hospital in Kota Kinabalu, Sabah, Malaysia**

### **ABSTRACT**

**Introduction:** *Enterococcus faecalis* is a gram-positive bacterium that causes various human nosocomial infections including urinary tract infection, endocarditis, wound infection, and bacteremia. **Objectives:** This study aims to investigate the molecular characterization of local *Enterococcus* bacteria (isolate no. SHH039) isolated from a patient in a tertiary hospital in Kota Kinabalu, Sabah, using whole-genome sequencing. **Methodology:** A Tissue sample collected from a patient with cholecystitis was cultured for bacteria onto blood agar and identified and characterized by molecular methods. Bacterial DNA was extracted by using the Qiagen DNeasy Tissue Kit (Qiagen, Valencia, CA). The quantification of DNA was done using Qubit fluorometer (Qubit 3.0, Thermo Fisher Scientific). The sample was then sequenced using the Illumina HiSeq 4000 system. In addition, the 16S rRNA sequence was aligned with reference sequences using CLUSTAL W and subsequently, a phylogenetic tree was obtained using the maximum-likelihood method in MEGA 8.0. This research was approved by the Medical Research Ethics Committee (MREC), Ministry of Health, Malaysia (No. NMRR-19-1770-48622) and University Malaysia Sabah ethical committee (JKEtika 1/19(26)). **Result:** Our phylogenetic tree analysis showed the isolate belongs to *Enterococcus faecalis*. The estimated whole genome size of the strain was 2,990,081 bp with a G + C content of 37.30%. The de novo assembly of the genome generated 77 contigs with an N50 of 270,652 bp. The genome dataset has been deposited at DDBJ/ENA/GenBank under the accession number JAEFCX000000000. The raw data were deposited as sequence read archive (SRA) number SRR13153714. **Conclusion:** The molecular characterization data from our study might be helpful to understand the insights of the *E. faecalis* infection mechanism and molecular characteristics of the pathogen.