

**Whole genome sequencing data of a clinical *Enterococcus gallinarum* strain EGR748 from Sabah, Malaysia**

**ABSTRACT**

*Enterococcus gallinarum* is a gram positive facultatively anaerobic bacteria that is typically found in mammalian intestinal tracts. It is generally not considered pathogenic to humans and is rarely reported. Here, we present the draft genome sequence data of *Enterococcus gallinarum* strain EGR748 isolated from a human clinical sample, and sequenced using the Illumina HiSeq 4000 system. The estimated whole genome size of the strain was 3,730,000 bp with a G + C content of 40.43%. The de novo assembly of the genome generated 55 contigs with an N50 of 208,509 bp. In addition, the Maximum Likelihood phylogenetic analysis based on the 16S rRNA sequence data accurately clustered EGR748 with other *E. gallinarum* strains. The data may be useful to demonstrate the capacity of this enterococcal species becoming the causal agents of nosocomial blood-stream infections. The genome dataset has been deposited at DDBJ/ENA/GenBank under the accession number JAABOR000000000.