

WHOLE GENOME SEQUENCING OF AN *ENTEROCOCCUS FAECALIS* ISOLATED FROM A PATIENT WITH CHOLECYSTITIS IN A TERTIARY HOSPITAL IN KOTA KINABALU, SABAH, MALAYSIA

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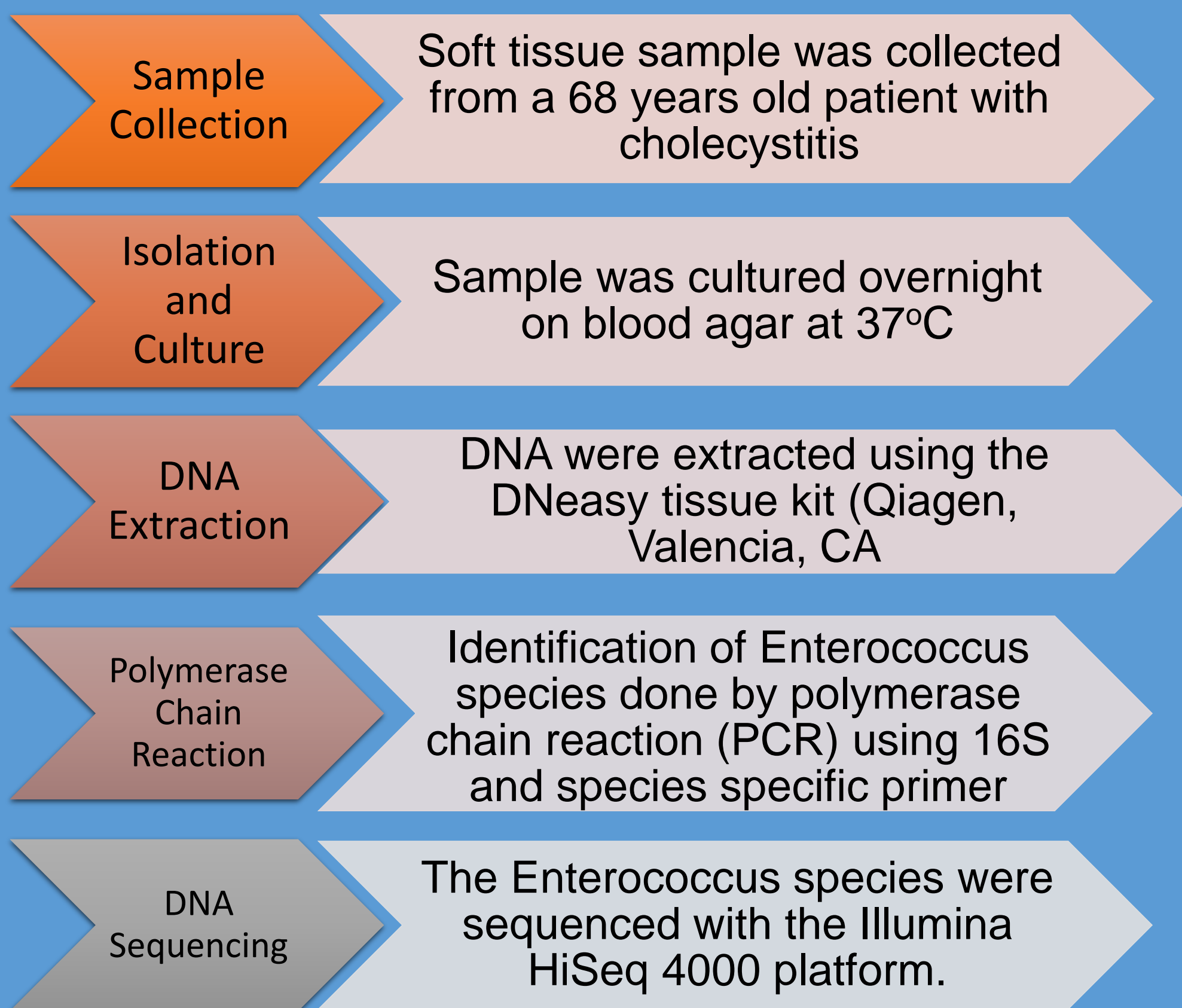
INTRODUCTION

Enterococcus faecalis is a gram-positive bacterium that causes various human nosocomial infections including urinary tract infection, endocarditis, wound infection, and bacteremia. The ability of Enterococci to survive in adverse conditions, presence of virulence factors and possession of intrinsic and acquired antibiotic resistance traits poses a therapeutic challenge in health care settings.

OBJECTIVES

This study aims to investigate the molecular characterization of local *Enterococcus* bacteria (*Enterococcus faecalis*) in a tertiary hospital in Kota Kinabalu, Sabah, using whole-genome sequencing.

MATERIALS & METHOD



CONCLUSION

The molecular characterization data from our study might be helpful to understand the insights of the pathogenic *E. faecalis* molecular characteristics presence in cases of acute cholecystitis

ETHICS STATEMENT

This research was approved by the Medical Research Ethics Committee (MREC), Ministry of Health, Malaysia (No. NMRR-19-1770-48622)..

REFERENCES

1. World Health Organization. Global Priority List of Antibiotic-Resistance Bacteria to Guide Research, Discovery, and Development of New Antibiotics. Geneva: World Health Organization; 2017.
2. Z. Zhong, W. Zhang, W. Liu, H. Xu, X. Xi, B. Menghe, H. Zhan, Z. Sun. Comparative genomic analysis of genus enterococcus. Microbiological Research 196 (2017) 95-105.

RESULTS

Figure 1 : Phylogenetic tree showing the position of *Enterococcus faecalis* (labelled as SHH039) based on the core-SNP sequences with other 36 *Enterococcus faecalis* extracted from the GenBank public database and *Enterococcus termitis* (JXLF01) and *Enterococcus gallinarum* (EGR748) as an outgroup. The tree was constructed using MEGA 8.0 with 1000 bootstrap iterations

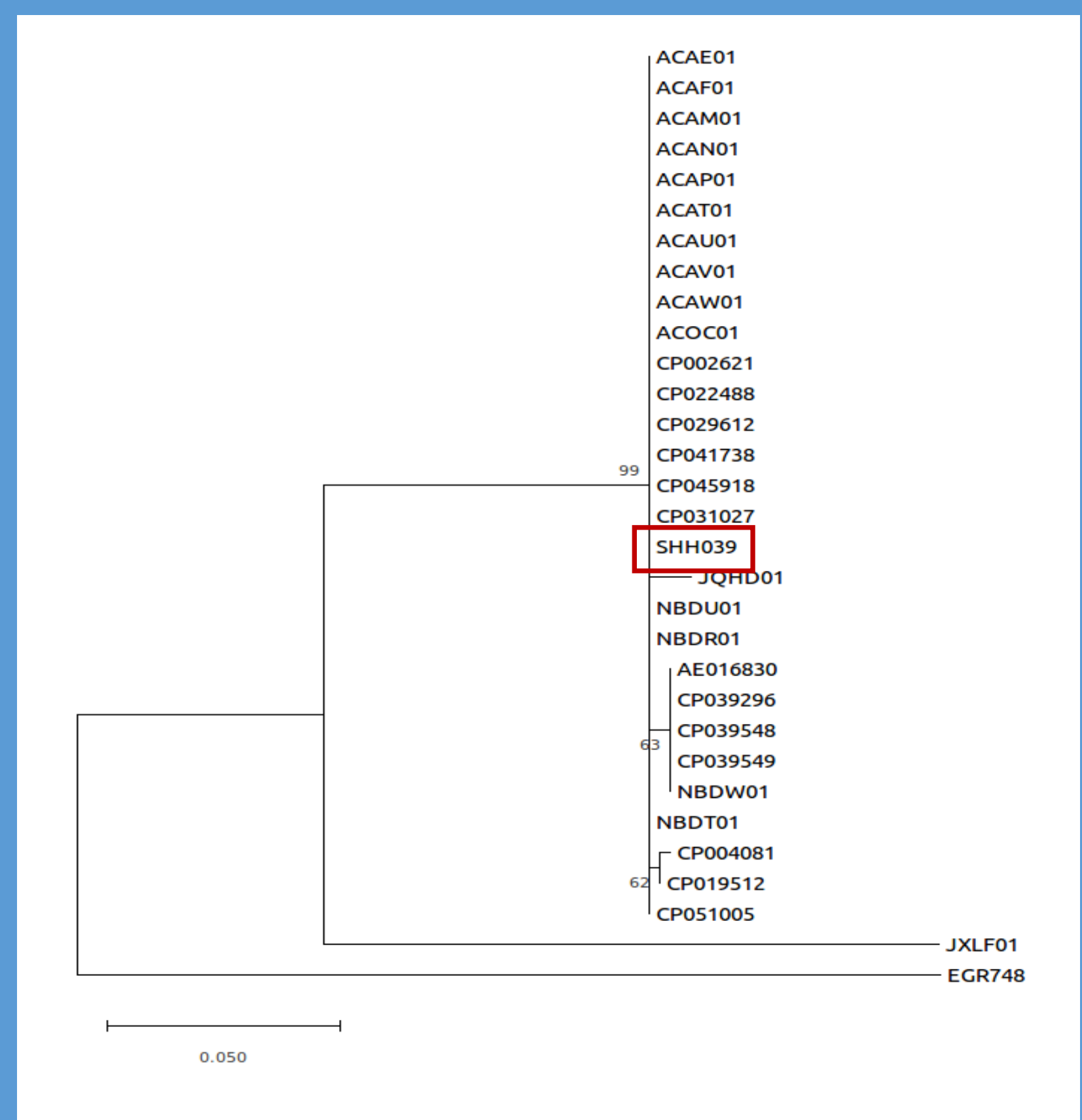


Table 1: List of *Enterococcus faecalis* extracted from GeneBank public database used in this study

Accession No	Source of <i>Enterococcus faecalis</i>
1 ACAE01	Urine
2 ACAF01	Urine
3 ACAM01	Blood
4 ACAN01	Wound
5 ACAP01	Clinical isolate
6 ACAT01	Pig
7 ACAU01	Urine
8 ACAV01	Liver clinical isolate
9 ACAW01	Infant faecal
10 ACOC01	Urine
11 CP002621	Human oral isolate
12 CP029612	Dog
13 CP029612	No information source
14 CP041738	Human blood
15 CP045918	Tilapia fish
16 CP031027	Fish
17 JQHD01	Sputum
18 NBDU01	Urine tract infections
19 NBDR01	Chicken
20 AE016830	Human blood
21 CP039296	Human blood
22 CP039548	Human blood
33 CP039549	Human blood
34 NBDW01	Chicken
35 NBDT01	Clinical isolate
36 CP004081	Sputum
37 CP019512	Clinical isolate
38 CP051005	Urine



Photo 1: *Enterococcus faecalis* strain on blood agar after 24 hours incubation at 37°C

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.