Genome Report

Progress in Microbes and Molecular Biology

HH PUBLISHER

# Whole genome sequence of MUM116, a *Bacillus* species isolated from intertidal soil

Hooi-Leng Ser[1], Wen-Si Tan[2], Wai-Fong Yin[3], Kok-Gan Chan[3,4], Vengadesh Letchumanan[1*]

[1]Novel Bacteria and Drug Discovery (NBDD) Research Group, Microbiome and Bioresource Research Strength (MBRS), Jeffrey Cheah School of Medicine and Health Sciences, Monash University Malaysia, 47500, Bandar Sunway, Selangor Darul Ehsan, Malaysia
[2]Illumina Singapore Pte Ltd, Woodlands Industrial Park E1, Singapore
[3]Division of Genetics and Molecular Biology, Institute of Biological Sciences, Faculty of Science, University of Malaya, 50603 Kuala Lumpur, Malaysia
[4]Vice Chancellor Office, Jiangsu University, Zhenjiang 212013, PR China

**Abstract:** Over the past few years, mangrove-derived *Bacillus* sp. have been characterized frequently for their bioactive potential. *Bacillus* sp. MUM 116 was isolated from mangrove forest in Kuala Selangor which is located on the west coast of Peninsular Malaysia. In order to obtain better understanding of the strain, the genome sequence of MUM 116 was acquired through Illumina MiSeq sequencing platform and yielded 5,720,395 bp along with 165 tRNA and 25 rRNA genes. Based on antiSMASH and RAST annotation, there was one cluster associated with production of bacteriocin. A deeper analysis into the genome sequence of MUM 116 would be essential to exploit the strain for production of bioactive compounds, which could potentially be developed as potent antibacterial agent.

**Keywords:** *Bacillus*; antibiotics; mangrove; secondary metabolite; genome

***Correspondence:** Vengadesh Letchumanan, Jeffrey Cheah School of Medicine and Health Sciences, Monash University Malaysia, 47500, Bandar Sunway, Selangor Darul Ehsan, Malaysia; Vengadesh.Letchumanan1@monash.edu

**Received:** 26th November 2019
**Accepted:** 26th December 2019
**Published Online:** 20th January 2020

**Citation:** Ser H-L, Tan W-S, Yin W-F, *et al*. Whole genome sequence of MUM116, a *Bacillus* species isolated from intertidal soil. Prog Microbes Mol Biol 2020; 3(1): a0000052. https://doi.org/10.36877/pmmb.a0000052

## Short Introduction

As a unique ecosystem, the mangrove forest are habitat for many plants as well as microbial populations that highly capable of adapting to fluctuations in temperatures, organic matter content, salinities and oxygen conditions[1,2]. Owing to these factors, some strains came up with adaptation strategies to survive and persist in the environment; one of which is by modifying metabolic pathway by scavenging nutrients available in the environment before converting them into useful, bioactive compounds that improve their survivability (i.e. antibacterials and antifungal)[3–5]. With reference to mangrove forest, Asia represents an ideal "hunting zone" for bioactive microbial strains as this continent has got the largest coverage of mangrove forests, contributing 42 % of the global total[6,7].

Several studies have shown that *Bacillus* sp. derived from mangrove forest have great potential in producing bioactive compounds[8–13]. *Bacillus* sp. MUM 116 was isolated from the west coast of Peninsular Malaysia during a screening program for bioactive microbes[14–19]. 16S rRNA analysis showed that MUM116 showed high similarities (<90%) to some bioactive type strains including *Bacillus ginsengisoli*, *Bacillus niacini* and *Bacillus mesonae*[20]. Given that mangrove-derived *Bacillus* sp. have been demonstrated to possess potential bioactive potential and MUM 116 displayed high 16S rRNA gene similarities with bioactive type strains, the strain was subjected to genome sequencing to uncover its genomic potential.

## Data description

The genomic DNA of MUM 116 was extracted using Masterpure™ DNA purification kit (Epicentre, Illumina Inc., Madison, WI, USA) before subjected to RNase

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(Qiagen, USA) treatment[21,22]. Genomic DNA quality was evaluated using NanoDrop spectrophotometer (Thermo Scientific, Waltham, MA, USA) and a Qubit version 2.0 fluorometer (Life Technologies, Carlsbad, CA, USA)[23,24]. Nextera™ DNA Sample Preparation kit (Nextera, USA) was used to generate DNA library and its quality was examined with Bioanalyzer 2100 high sensitivity DNA kit (Agilent Technologies, Palo Alto, CA) prior to sequencing[25,26]. Whole genome sequence of MUM 116 was obtained via paired-end sequencing on Illumina MiSeq platform with MiSeq Reagent Kit 2 (2 × 250 bp; Illumina Inc., Madison, WI, USA)[27]. The assembly of trimmed seqeuence was done with CLC Genomic Workbench version 5.1 (CLC Bio, Denmark), resulting in 208 contigs and an $N_{50}$ contig size of approximately 52,003 bp. The assembled genome size of MUM 116 consists 5,720,395 bp, with an average coverage of 74.0-fold and G + C content of 38.4%. The genome sequence of *Bacillus* sp. MUM 116 has been deposited at DDBJ/EMBL/GenBank under accession of MLYR00000000.

**Table 1.** General genomic features of *Bacillus sp*. strain MUM 116.

| | *Bacillus* sp. MUM116 |
|---|---|
| Genome size (bp) | 5,720,395 |
| Contigs | 208 |
| Contigs $N_{50}$ (bp) | 52,003 |
| G + C content % | 38.4 |
| Protein coding genes | 5,273 |
| tRNA | 165 |
| rRNA | 25 |

Annotation of MUM 116 genome was carried out using Rapid Annotation using Subsystem Technology (RAST) [28] while gene prediction was performed using Prodigal version 2.6. The detection of ribosomal RNA (rRNA) and transfer RNA (tRNA) was done using RNAmmer and tRNAscan SE version 1.21, respectively[29–31]. Based on RAST analysis, more than one-quarter of the protein-coding genes were associated with primary metabolism and highest number of genes were related with metabolism of amino acid and derivatives (12%). Furthermore, both RAST and another bioinformatics tools, antibiotics & Secondary Metabolite Analysis SHell (antiSMASH) revealed potential of MUM 116 in producing bacteriocin under the thiazole/oxazole-modified microcins (TOMMs) class[32,33]. Several *Bacillus* sp. have been described to have the potential of synthesizing TOMMs[34,35]. For instance, *Bacillus amyloliquefaciens* FZB42 isolated from plant-pathogen-infested soil was capable of compounds producing not just plant-promoting activity, the strain produced a novel TOMMs — plantazolicin which can suppress growth of bacterial and fungal plant pathogens[35]. Even though *Bacillus* sp. isolated from terrestrial region showed great potential in producing bioactive compounds, several studies have hinted that genomes of *Bacillus* sp. from special environment like mangrove area are generally more "enriched" than those from terrestrial area, as the dynamic environment imposes selective pressure on genomic region associated with adaptation which then promotes production of unique secondary metabolites[36,37]. Altogether, the availability of MUM 116 genome sequences enabled further investigation into its genomic potential, particularly for the production of bacteriocin(s). In future work, more experimental testing is required to optimize production medium and culture conditions for *Bacillus* sp. before exhaustively examine all potential antimicrobials.

## Conflict of Interest

The authors declare that there is no conflict of interest in this work.

## Acknowledgement

This work was supported by the University of Malaya for High Impact Research Grant (UM-MOHE HIR Nature Microbiome Grant No. H-50001-A000027 and No. A000001-5001) and PPP Grant (PG090-2015B) awarded to K.-G. C.

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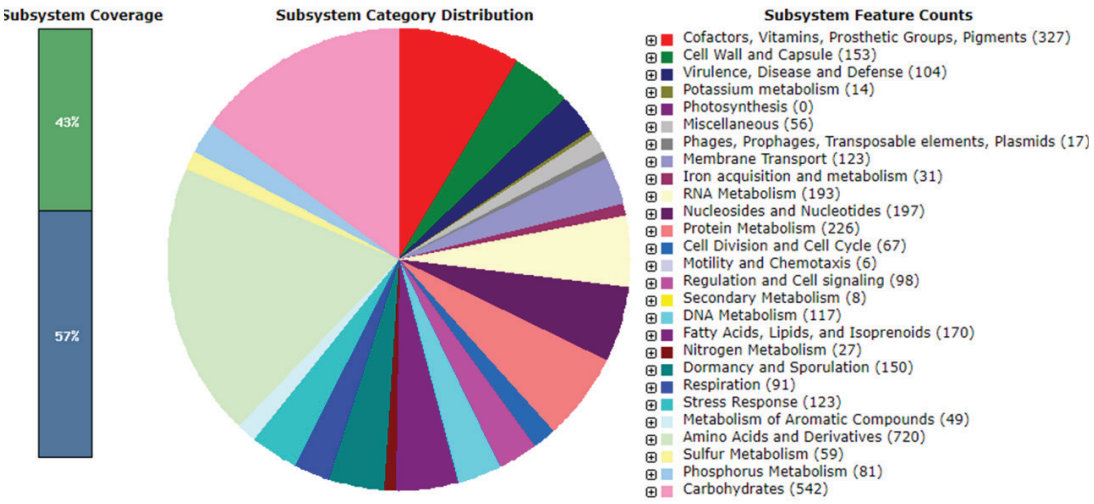


**Figure 1.** Subsystem category distribution of *Bacillus* sp. MUM 116 (based on RAST annotation server).

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