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ORIGINAL ARTICLE

Whole genome sequencing analysis of *Komagataeibacter nataicola* reveals its potential in food waste valorisation for cellulose production

Muhammad Irhamni Haziqi Nasharudin[1] · Shing-Wei Siew[1] · Hajar Fauzan Ahmad[1,2] · Nazira Mahmud[1,2]

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Abstract

Background *Komagataeibacter nataicola* (*K. nataicola*) is a gram-negative acetic acid bacterium that produces natural bacterial cellulose (BC) as a fermentation product under acidic conditions. The goal of this work was to study the complete genome of *K. nataicola* and gain insight into the functional genes in *K. nataicola* that are responsible for BC synthesis in acidic environments.

Methods and result The pure culture of *K. nataicola* was obtained from yeast-glucose-calcium carbonate (YGC) agar, followed by genomic DNA extraction, and subjected to whole genome sequencing on a Nanopore flongle flow cell. The genome of *K. nataicola* consists of a 3,767,936 bp chromosome with six contigs and 4,557 protein coding sequences. The maximum likelihood phylogenetic tree and average nucleotide identity analysis confirmed that the bacterial isolate was *K. nataicola*. The gene annotation via RAST server discovered the presence of cellulose synthase, along with three genes associated with lactate utilization and eight genes involved in lactate fermentation that could potentially contribute to the increase in acid concentration during BC synthesis.

Conclusion A more comprehensive genome study of *K. nataicola* may shed light into biological pathway in BC productivity as well as benefit the analysis of metabolites generated and understanding of biological and chemical interactions in BC production later.

Keywords Bacterial cellulose · Bioconversion · Food waste · *K. nataicola* · Whole genome sequencing

Introduction

Bacterial cellulose (BC) is increasingly used and acceptable as important cellulose source due to its benefit of pure cellulose produced, potentially produced from various waste materials and better overall environmental footprint. For various applications, BC might design adaptable matrixes and internal structures used in biomedicine, food production, cosmetics, food packaging, and many more [1]. Implementing BC to replace conventional plant-based cellulose is crucial for reducing the number of needless trees chopped down and protecting numerous plant species [2]. This is because BC does not require the use of plants to produce quality cellulose, instead it only require growing bacteria in suitable media, such as Hestrin-Schramm (HS), Yeast-glucose-calcium carbonate (YGC), and Luria–Bertani (LB) [3–5]. Plant cellulose has the same organic compound, which is $(C_6H_{10}O_5)_n$, and BC has more advantages than plant cellulose, such as non-toxic, higher purity, higher crystallinity, and also strong tensile strength [6, 7]. BC is produced

✉ Nazira Mahmud
nazira@umpsa.edu.my

Muhammad Irhamni Haziqi Nasharudin
irhamnihaziqi@gmail.com

Shing-Wei Siew
shingwei999@gmail.com

Hajar Fauzan Ahmad
fauzanahmad@umpsa.edu.my

[1] Faculty of Industrial Sciences and Technology, Universiti Malaysia Pahang Al-Sultan Abdullah, Lebuh Persiaran Tun Khalil Yaakob, 26300 Kuantan, Pahang, Malaysia

[2] Group of Environment, Microbiology and Bioprocessing (GERMS), Faculty of Industrial Sciences and Technology, Universiti Malaysia Pahang Al-Sultan Abdullah, Lebuh Persiaran Tun Khalil Yaakob, 26300 Kuantan, Pahang, Malaysia

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