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Draft Genome Sequence of a Lipolytic Yeast, *Candida aaseri* SH-14

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ABSTRACT We report here the draft genome sequence of the lipolytic yeast *Candida aaseri* SH-14, isolated from the compost of oil palm empty fruit bunches, and the identification of eight putative lipase genes. This genome information will provide the opportunity to produce potential lipases for a variety of industrial applications.

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Extracellular microbial lipases (triacylglycerol hydrolase, EC 3.1.1.3) catalyze the hydrolysis of ester bonds between alcohols and carboxylic acids at the lipid-water interface (1). Lipases have been widely used for a broad range of biotechnological and industrial processes (2, 3) and have recently been utilized as an important biocatalyst for the production of biodiesel in the field of bioenergy (4). Although lipases are widely distributed in nature, yeast and fungi have the most commercial potential of the primary sources of lipases used in industrial applications (5). There are various yeasts with lipase-producing capacities; however, only a few have been commercially employed for bulk production (6, 7). Therefore, it is important to isolate and exploit lipolytic yeast species when finding novel lipases for the development of biotechnological and industrial processes. Herein, we present the draft genome sequence of *Candida aaseri* SH-14 as a potential lipase producer.

Candida aaseri (syn. *Candida butyri*) SH-14 is a lipolytic yeast isolated from the compost of oil palm empty fruit bunches. We conducted a genome sequencing of *Candida aaseri* SH-14 using the Illumina HiSeq 2500 platform at the Core Facility Management Center at the Korea Research Institute of Bioscience and Biotechnology (KRIBB). We obtained 42.8 million paired-end reads (approximately 400-fold coverage) and assembled them *de novo* using Velvet version 1.2.10, which was facilitated using VelvetOptimiser version 2.2.5 (8). The total size of the draft genome of *C. aaseri* SH-14 was 10,491,190 bp (62 scaffolds including 630 gaps). The N_{50} value and the length of the longest contig were 450,417 bp and 1,399,148 bp, respectively. The G+C content was 34.2%, and 126 tRNA-coding sequences were identified using tRNAscan-SE version 2.0 (9). Structural annotation was carried out using the Yeast Genome Annotation Pipeline (YGAP) (10), and Blast2GO was utilized for a functional prediction of the protein-coding sequences (11). As a result, a total of 5,380 proteins were predicted, and we confirmed that 5,037 of them have at least one Gene Ontology (GO) term.

Some *Candida* species, particularly *Candida albicans*, translate the CUG codon as serine instead of leucine; therefore, we have used the Bagheera server (http://www.motorprotein.de/bagheera) to analyze the CUG codon translation of the genes from *C. aaseri* SH-14 (12). The prediction suggested that *C. aaseri* SH-14 belongs to the CUG:Ser group of *Candida* species. We identified eight putative lipase genes from the genome of *C. aaseri* SH-14. Information on putative lipase genes is available from http://genoglobe.kr/kribb/candida_aaseri_2017, where the classification of the putative

lipases was based on the oxyanion hole and conserved pentapeptide found in the Lipase Engineering Database (LED) (13, 14).

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. LKAN00000000. The version described in this paper is version LKAN01000000.

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REFERENCES

1. Jaeger KE, Dijkstra BW, Reetz MT. 1999. Bacterial biocatalysts: molecular biology, three-dimensional structures, and biotechnological applications of lipases. Annu Rev Microbiol 53:315–351. https://doi.org/10.1146/annurev.micro.53.1.315.
2. Jaeger KE, Eggert T. 2002. Lipases for biotechnology. Curr Opin Biotechnol 13:390–397. https://doi.org/10.1016/S0958-1669(02)00341-5.
3. Sharma D, Sharma B, Shukla AK. 2011. Biotechnological approach of microbial lipase: a review. Biotechnology 10:23–40. https://doi.org/10.3923/biotech.2011.23.40.
4. Ribeiro BD, de Castro AMd, Coelho MAZ, Freire DMG. 2011. Production and use of lipases in bioenergy: a review from the feedstocks to biodiesel production. Enzyme Res 2011:615803. https://doi.org/10.4061/2011/615803.
5. Sharma S, Kanwar SS. 2014. Organic solvent tolerant lipases and applications. ScientificWorldJournal 2014:625258. https://doi.org/10.1155/2014/625258.
6. Treichel H, de Oliveira D, Mazutti MA, Di Luccio M, Oliveira JV. 2010. A review on microbial lipases production. Food Bioprocess Technol 3:182–196. https://doi.org/10.1007/s11947-009-0202-2.
7. Gurung N, Ray S, Bose S, Rai V. 2013. A broader view: microbial enzymes and their relevance in industries, medicine, and beyond. Biomed Res Int 2013:1–18. https://doi.org/10.1155/2013/329121.
8. Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. Genome Res 18:821–829. https://doi.org/10.1101/gr.074492.107.
9. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res 25:955–964. https://doi.org/10.1093/nar/25.5.0955.
10. Proux-Wéra E, Armisén D, Byrne KP, Wolfe KH. 2012. A pipeline for automated annotation of yeast genome sequences by a conserved-synteny approach. BMC Bioinformatics 13:237. https://doi.org/10.1186/1471-2105-13-237.
11. Conesa A, Gotz S, Garcia-Gomez JM, Terol J, Talon M, Robles M. 2005. Blast2GO: a universal tool for annotation, visualization and analysis in functional genomics research. Bioinformatics 21:3674–3676. https://doi.org/10.1093/bioinformatics/bti610.
12. Mühlhausen S, Kollmar M. 2014. Predicting the fungal CUG codon translation with Bagheera. BMC Genomics 15:411. https://doi.org/10.1186/1471-2164-15-411.
13. Fischer M, Pleiss J. 2003. The Lipase Engineering Database: a navigation and analysis tool for protein families. Nucleic Acids Res 31:319–321. https://doi.org/10.1093/nar/gkg015.
14. Gupta R, Kumari A, Syal P, Singh Y. 2015. Molecular and functional diversity of yeast and fungal lipases: their role in biotechnology and cellular physiology. Prog Lipid Res 57:40–54. https://doi.org/10.1016/j.plipres.2014.12.001.