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GENOME SEQUENCES

Complete Genome Sequence of *Weissella cibaria* Strain BM2, Isolated from Korean Kimchi

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ABSTRACT *Weissella cibaria* appears to have broad-spectrum health benefits. Here, we report the genome sequence of *Weissella cibaria* strain BM2, which was isolated from homemade kimchi; it consists of one circular chromosome of 2,462,443 bp and one plasmid of 11,067 bp. A total of 2,337 coding sequences were predicted, including 2,117 protein-coding sequences and a G+C content of 45.06%.

Weissella cibaria is a Gram-positive, non-spore-forming, nonmotile, hetero-lactic acid-fermenting, and catalase-negative bacillus that cannot produce dextran from sucrose (1). Members of *Weissella* are lactic acid bacteria and have been isolated from various sources, including fermented foods, Spanish sausages, Greek salami, human gut, and insect gut (2–5). Recently, certain members of the *Weissella* genus, such as *W. cibaria*, *W. koreensis*, and *W. confusa*, were reported to dominate during the early stage of kimchi fermentation (6, 7). In particular, *W. cibaria* has been reported to have probiotic properties (6, 8, 9). Here, we report the complete genome sequence of *W. cibaria* strain BM2, isolated from homemade kimchi.

We isolated *W. cibaria* BM2 from homemade kimchi. To isolate *W. cibaria* BM2, the soup of kimchi was diluted 1,000-fold with buffered peptone water, and then 100 μl of diluted sample was spread onto MRS agar (Difco, USA) and incubated at 30°C for 48 h under aerobic conditions. Finally, morphologically distinct single colonies were purified by repeated streak culturing on the same medium. The genomic DNA of *W. cibaria* BM2 was extracted using the Wizard genomic DNA purification kit (Promega, USA), following the protocol recommended by the manufacturer. The quantity and quality of isolated DNA were determined using a NanoDrop spectrophotometer. The isolate was characterized as *W. cibaria* based on PCR amplification of the 16S rRNA gene using primers 27F (5′-AGAGTTTGATCCTGGCTCAG-3′) and 1492R (5′-GGTTACCTTGTTACGACTT-3′), as described previously (10). A BLAST search of the sequence obtained was conducted using NCBI BLASTn. The *W. cibaria* BM2 gene showed 100% identity with the *W. cibaria* 16S rRNA gene.

To sequence the whole genome of *W. cibaria* BM2, a SMRTbell library with a 20-kb insert size was constructed with the PacBio DNA template preparation kit v1.0. The genome was sequenced by Macrogen (Seoul, Republic of Korea) with the PacBio RS II sequencing platform (Pacific Biosciences, USA) using a single-molecule real-time (SMRT) cell 8Pac v3 and DNA polymerase binding kit P6 reagents (11). In total, 127,616 PacBio subreads (average subread length, 10,522 bp; subread N_{50}, 15,092 bp) of *W. cibaria* BM2

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were generated. PacBio reads were assembled using the RS Hierarchical Genome Assembly Process (HGAP) protocol v3.0. The process consists of preassembly, *de novo* assembly with the Celera Assembler, alignment with Basic Local Alignment with Successive Refinement (BLASR) v1, and assembly polishing with Quiver v1 in SMRT Portal v2.3 (12–14). Default parameters were used except where otherwise noted. When the contig ends overlapped, contigs were connected to form circular DNA. The result of the assembly was two contigs, including one closed circular chromosome of 2,462,443 bp (G+C content, 45.1%; coverage, 380× [GenBank accession number CP027427]) and a plasmid of 11,067 bp (G+C content, 37.7%; coverage, 36× [GenBank accession number CP027428]). The genomes were annotated with Prokka v1.12b software (15), which identified 2,436 genes, 2,319 coding DNA sequences (CDSs), 28 rRNAs, 88 tRNAs, and 1 transfer-messenger RNA on the chromosome and 8 genes and 8 CDSs on the plasmid.

Data availability. The complete genome sequence of *W. cibaria* strain BM2 was deposited in GenBank under the accession numbers CP027427 and CP027428. The associated BioProject, BioSample, and SRA accession numbers are PRJNA436626, SAMN08628864, and SRR11558354, respectively.

REFERENCES

1. Kang MS, Kim BG, Chung J, Lee HC, Oh JS. 2006. Inhibitory effect of *Weissella cibaria* isolates on the production of volatile sulphur compounds. J Clin Periodontol 33:226–232. https://doi.org/10.1111/j.1600-051X.2006.00893.x.
2. Kwak SH, Cho YM, Noh GM, Om AS. 2014. Cancer preventive potential of kimchi lactic acid bacteria (*Weissella cibaria*, *Lactobacillus plantarum*). J Cancer Prev 19:253–258. https://doi.org/10.15430/JCP.2014.19.4.253.
3. Lee SH, Ku HJ, Ahn MJ, Hong JS, Lee SH, Shin H, Lee KC, Lee JS, Ryu S, Jeon CO, Lee JH. 2015. *Weissella jogaejeotgali* sp. nov., isolated from jogae jeotgal, a traditional Korean fermented seafood. Int J Syst Evol Microbiol 65:4674–4681. https://doi.org/10.1099/ijsem.0.000631.
4. Praet J, Meeus I, Cnockaert M, Houf K, Smagghe G, Vandamme P. 2015. Novel lactic acid bacteria isolated from the bumble bee gut: *Convivina intestini* gen. nov., sp. nov., *Lactobacillus bombicola* sp. nov., and *Weissella bombi* sp. nov. Antonie Van Leeuwenhoek 107:1337–1349. https://doi.org/10.1007/s10482-015-0429-z.
5. Collins MD, Samelis J, Metaxopoulos J, Wallbanks S. 1993. Taxonomic studies on some leuconostoc-like organisms from fermented sausages: description of a new genus *Weissella* for the *Leuconostoc paramesenteroides* group of species. J Appl Bacteriol 75:595–603. https://doi.org/10.1111/j.1365-2672.1993.tb01600.x.
6. Yu HS, Lee NK, Choi AJ, Choe JS, Bae CH, Paik HD. 2019. Anti-inflammatory potential of probiotic strain *Weissella cibaria* JW15 isolated from kimchi through regulation of NF-κB and MAPKs pathways in LPS-induced RAW 264.7 cells. J Microbiol Biotechnol 29:1022–1032. https://doi.org/10.4014/jmb.1903.03014.
7. Jeong SE, Chun BH, Kim KH, Park D, Roh SW, Lee SH, Jeon CO. 2018. Genomic and metatranscriptomic analyses of *Weissella koreensis* reveal its metabolic and fermentative features during kimchi fermentation. Food Microbiol 76:1–10. https://doi.org/10.1016/j.fm.2018.04.003.
8. Sun HY, Kim KP, Bae CH, Choi AJ, Paik HD, Kim IH. 2019. Evaluation of *Weissella cibaria* JW15 probiotic derived from fermented Korean vegetable product supplementation in diet on performance characteristics in adult beagle dog. Animals (Basel) 9:581. https://doi.org/10.3390/ani9080581.
9. Yu HS, Lee NK, Choi AJ, Choe JS, Bae CH, Paik HD. 2019. Antagonistic and antioxidant effect of probiotic *Weissella cibaria* JW15. Food Sci Biotechnol 28:851–855. https://doi.org/10.1007/s10068-018-0519-6.
10. Bao R, Liu S, Ji C, Liang H, Yang S, Yan X, Zhou Y, Lin X, Zhu B. 2018. Shortening fermentation period and quality improvement of fermented fish, Chouguiyu, by co-inoculation of *Lactococcus lactis* M10 and *Weissella cibaria* M3. Front Microbiol 9:3003. https://doi.org/10.3389/fmicb.2018.03003.
11. Tombácz D, Csabai Z, Oláh P, Balázs Z, Likó I, Zsigmond L, Sharon D, Snyder M, Boldogkői Z. 2016. Full-length isoform sequencing reveals novel transcripts and substantial transcriptional overlaps in a herpesvirus. PLoS One 11:e0162868. https://doi.org/10.1371/journal.pone.0162868.
12. Zhao H, Kang XL, Chen XL, Wang JX, Le Y, Shen ZG, Chen JF. 2009. Antibacterial activities of amorphous cefuroxime axetil ultrafine particles prepared by high gravity antisolvent precipitation (HGAP). Pharm Dev Technol 14:485–491. https://doi.org/10.1080/10837450902762991.
13. Liao YC, Lin SH, Lin HH. 2015. Completing bacterial genome assemblies: strategy and performance comparisons. Sci Rep 5:8747. https://doi.org/10.1038/srep08747.
14. Chin CS, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. Nat Methods 10:563–569. https://doi.org/10.1038/nmeth.2474.
15. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. https://doi.org/10.1093/bioinformatics/btu153.