

# Complete Genome Sequence of Halophilic Yeast *Meyerozyma caribbica* MG20W Isolated from Rhizosphere Soil

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***Meyerozyma caribbica* MG20W was originally isolated from rhizosphere soil on reclaimed land in the Republic of Korea. We describe herein the 10.64-Mbp-long genome sequence of *M. caribbica* MG20W, which exhibits high salt resistance.**

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*Meyerozyma caribbica* MG20W is a yeast strain isolated from plant rhizosphere soil of Saemangeum reclaimed land on the west coast of the Republic of Korea. Analysis using a Genome Sequencer FLX system (Titanium; 454 Life Sciences, Branford, CT, USA) resulted in 651,521 high-quality reads assembled using Newbler2.5.3 software (1) into 52 contigs of >500 bp. Paired-end sequencing produced 93,485 reads (mean read length, 2,758 bp).

The genome sequence of *M. caribbica* MG20W was determined at Macrogen, Inc. (Seoul, Korea) with 454 technology, and was paired read and gapped using Phred 0.990310. The genome size is 10.64 Mbps, and 9 contigs are represented. A total of 227,896,009 bp of raw data was sequenced, representing approximately 20-fold coverage of the *M. guilliermondii* ATCC 6260 genome. The average G+C content and quinone (high-performance liquid chromatography) were 45.14% and Q-9, respectively.

Gene prediction analysis using the software program Glimmer (2) identified 7,472 open reading frames (ORFs) in the genome, 226 ORFs of tRNA, 9 ORFs of 18S rRNA, 113 ORFs of 8S rRNA, 49 ORFs of lipase, 512 ORFs of transporter, and 8 ORFs of pump.

Comparative genomic analysis revealed that the genome of *M. caribbica* MG20W is most closely related to that of *M. guilliermondii* ATCC 6260 (3, 4), sharing 45% of homologous proteins. We found the following gene ontology terms after mapping: biological process, 2,040; cellular component, 1,969; molecular function, 1,207; no hits, 2,256.

**Nucleotide sequence accession numbers.** The sequence data reported in this paper were deposited in the DNA Data Bank of

Japan/EMBL/GenBank nucleotide sequence databases with the accession numbers [BADS01000001](https://www.ncbi.nlm.nih.gov/nuccore/BADS01000001) to [BADS01000009](https://www.ncbi.nlm.nih.gov/nuccore/BADS01000009).

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