Rhodotorula glutinis ATCC 204091 is an oleaginous oxidative red yeast that can accumulate lipids to >50% of its biomass when grown with appropriate carbon and nitrogen ratios. It produces a red pigment consisting of useful antioxidants, such as carotenoids, torulene, and torularhodin, when cultivated under carbon-deficient conditions.

R. glutinis was used to identify a yeast pathway for L-lysine biosynthesis via L-pipecolic acid (4). Rhodotorula secretes α-1-arabinofuranosidase, which is important to the wine industry for aroma of the wine. R. glutinis is nonfastidious, making it attractive for the production of phenylalanine ammonia lyase (PAL) (EC 4.3.1.5), which is a nonhydrolytic enzyme produced in high quantities by R. glutinis (5). Here, we report the R. glutinis genome sequence, which can be used to study the regulation of these important pathways and to explore genes encoding other useful products.

Genomic DNA was isolated using the Wizard genomic DNA purification kit (Promega) with overnight lyticase treatment (20 mg/ml lyticase [catalog no. L.2524; Sigma]) to lyse the cells. The purity and the concentration of DNA were measured by NanoDrop (Thermo Scientific). Genome sequencing was conducted using a 454 GS-FLX Titanium platform. One standard run and one paired-end run were completed, resulting in a genome size of 20,476,699 bp that was organized in 384 large contigs and one paired-end run were completed, resulting in a genome size of 20,476,699 bp that was organized in 384 large contigs and 176 gaps, resulting in an assembly with 208 contigs. An Illumina sequencing run was also conducted on genomic DNA from R. glutinis, which was amplified by PCR, and subsequent Sanger sequencing closed 521 is 19,742,445 nucleotides (nt) in length and has a 54% G+C content of 61.9%. The length of putative genic regions is 17,229,291 bp, and there are 3,359 putative genes coding for 2,817 proteins. By comparison, the genome of the systematically similar yeast Ustilago maydis 521 is 19,742,445 nucleotides (nt) in length and has a 54% G+C content with 6,631 genes. The R. glutinis genome sequence will enable pathway analysis and functional genomics investigations, which will allow for the identification of regulatory mechanisms controlling lipid accumulation. By improving the efficiency of carotenoid/lipid accumulation in R. glutinis, this yeast has the potential to produce useful antioxidants and biodiesel.

Nucleotide sequence accession numbers. The R. glutinis whole-genome shotgun (WGS) project (PID-59971) has been deposited at DDBJ/EMBL/GenBank under the accession no. AEVR00000000 and consists of (WGS) sequences AEVR02000001 to AEVR02000029. The version described in this paper is AEVR02000000.

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