Draft Genome Sequence of the Heavy-Metal-Tolerant Marine Yeast *Debaryomyces hansenii* J6

Camille A. Berrocal, Ramon E. Rivera-Vicens, Govind S. Nadathur

Department of Marine Sciences, University of Puerto Rico, Mayagüez, Puerto Rico

C.A.B and R.E.R.-V. contributed equally to this article.

Debaryomyces hansenii J6 is a heavy-metal-tolerant, flavinogenic yeast isolated from a Swedish estuary. We present here the 11.63-Mb genome of this organism containing 5,717 open reading frames. Comparison with available *Debaryomyces* genomes demonstrated that J6 is closer to *D. hansenii* MTCC234 than *D. fabry* CBS789 and *D. hansenii* CBS767.

Address correspondence to Govind S. Nadathur, govind.nadathur@upr.edu.

*D*ebaryomyces hansenii is a unicellular, halotolerant, heavy-metal-resistant ascomycete yeast widely distributed in nature (1, 2). This organism has been taxonomically differentiated into *D. hansenii* and *D. fabryi* (3, 4). J6 is a flavinogenic *Debaryomyces* strain that grows between 15 and 37°C and tolerates heavy metals such as cobalt(II) (5).

Genomic DNA was extracted by the method of Cryer et al (6). A library was prepared utilizing the Illumina Nextera DNA sample prep kit, generating 500-bp fragments. Paired-end sequencing (2×300-bp) was performed using the Illumina MiSeq platform at Ciris Energy Inc. (Colorado, USA), generating 4,386,465 reads. Quality assessment and trimming of the reads were performed with FastQC (7) and the FASTX-Toolkit (http://hannonlab.cshl.edu/fastx_toolkit/index.html), respectively. *De novo* genome assembly was performed with ABySS version 1.9.0 (8) ($k = 155$), generating 444 contigs after filtering (minimum length 200 bp), for an 11.63-Mb total genome length. Assemblage quality was examined by QUAST (9) (N_{50} of 186,435 bp, GC content of 35.43%). Using tRNA-Scan_SE (10) and the WebMGA server (11), a total of 223 tRNAs and three rRNAs (5S, 18S, and 28S rRNAs) were found, respectively. Gene prediction and annotation were performed by the MAKER pipeline (12), which resulted in a total of 5,717 genes. Comparing these results to the transcriptome analysis under cobalt stress for J6 (13) demonstrated that only 998 genes were not expressed under those conditions.

J6 was compared to the MTCC234 (AHBE01000000) (14), CBS767 (NC_006043.2 to NC_006049.2) (15), and CBS789 (LMYN01000000) (16) genomes. Bowtie 2 (17), Burrows–Wheeler alignment (BWA) (18), BBMap (19), and CUSHAW2 (20) were used to align the sequenced reads to the previously mentioned species. Qualimap was used to calculate correctly mapped reads to the genomes (21). The mapping alignment percentages of J6 to the other genomes, depending on the program used, are as follows: (a) MTCC234—95.89% (Bowtie 2), 98.85% (BWA), 96.43% (BBMap), and 98.84% (CUSHAW2); (b) CBS767—13.87% (Bowtie 2), 73.12% (BWA), 48.31% (BBMap), and 80.4% (CUSHAW2); and (c) CBS789—53.08% (Bowtie 2), 88.92%

(BWA), 67.94% (BBMap), and 54.68% (CUSHAW2). These results place J6 closest to MTCC234, followed by CBS789 and CBS767.

Accession number(s). This whole-genome shotgun project has been deposited at GenBank under the accession number LZDI00000000. The version described in this paper is the first version, LZDI01000000.

REFERENCES

1. **Adler L.** 1986. Physiological and biochemical characterization of the yeast *Debaryomyces hansenii* in relation to salinity, p. 81–90. *In* Moss ST (ed), The biology of marine fungi. Cambridge University Press, New York, NY.

2. **Gadd GM, Edwards SW.** 1986. Heavy-metal-induced flavin production by Debaryomyces hansenii and possible connexions with iron metabolism. Trans British Mycolog Soc **87**:533–542. http://dx.doi.org/10.1016/S0007-1536(86)80094-8.

3. **Michán C, Martínez JL, Alvarez MC, Turk M, Sychrova H, Ramos J.** 2013. Salt and oxidative stress tolerance in *Debaryomyces hansenii* and *Debaryomyces fabryi*. FEMS Yeast Res **13**:180–188. http://dx.doi.org/10.1111/1567-1364.12020.

4. **Nguyen HV, Gaillardin C, Neuvéglise C.** 2009. Differentiation of *Debaryomyces hansenii* and *Candida famata* by rRNA gene intergenic spacer fingerprinting and reassessment of phylogenetic relationships among *D. Hansenii*, *C. famata*, *D. fabryi*, *C. flareri* (=*D. subglobosus*) and D. *prosopidis*: description of *D. vietnamensis* sp. nov. closely related to *D. nepalen-*

sis. FEMS Yeast Res **9**:641–662. http://dx.doi.org/10.1111/j.1567 -1364.2009.00510.x.

5. **Seda-Miró JM, Arroyo-González N, Pérez-Matos A, Govind NS**. 2007. Impairment of cobalt-induced riboflavin biosynthesis in a *Debaryomyces hansenii* mutant. Can J Microbiol **53**:1272–1277. http://dx.doi.org/ 10.1139/W07-098.

6. **Cryer DR, Eccleshall R, Marmur J**. 1975. Isolation of yeast DNA. Methods Cell Biol **12**:39–44. http://dx.doi.org/10.1016/S0091-679X(08)60950-4.

7. **Andrews S**. 2010. FastQC: a quality control tool for high throughput sequence data. http://www.bioinformatics.babraham.ac.uk/projects/fastqc.

8. **Simpson JT, Wong K, Jackman SD, Schein JE, Jones SJ, Birol I**. 2009. ABySS: a parallel assembler for short read sequence data. Genome Res **19**:1117–1123. http://dx.doi.org/10.1101/gr.089532.108.

9. **Gurevich A, Saveliev V, Vyahhi N, Tesler G**. 2013. QUAST: quality assessment tool for genome assemblies. Bioinformatics **29**:1072–1075. http://dx.doi.org/10.1093/bioinformatics/btt086.

10. **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. http://dx.doi.org/10.1093/nar/25.5.0955.

11. **Wu S, Zhu Z, Fu L, Niu B, Li W**. 2011. WebMGA: a customizable web server for fast metagenomic sequence analysis. BMC Genomics **12**: http:// dx.doi.org/10.1186/1471-2164-12-444.

12. **Cantarel BL, Korf I, Robb SM, Parra G, Ross E, Moore B, Holt C, Sánchez Alvarado A, Yandell M**. 2008. MAKER: an easy-to-use annotation pipeline designed for emerging model organism genomes. Genome Res **18**:188–196. http://dx.doi.org/10.1101/gr.6743907.

13. **Gumá-Cintrón Y, Bandyopadhyay A, Rosado W, Shu-Hu W, Nadathur GS**. 2015. Transcriptomic analysis of cobalt stress in the marine yeast *Debaryomyces hansenii*. FEMS Yeast Res **15**:fov099. http://dx.doi.org/ 10.1093/femsyr/fov099.

14. **Kumar S, Randhawa A, Ganesan K, Raghava GP, Mondal AK**. 2012. Draft genome sequence of salt-tolerant yeast *Debaryomyces hansenii* var.

hansenii MTCC 234. Eukaryot Cell **11**:961–962. http://dx.doi.org/ 10.1128/EC.00137-12.

15. **Dujon B, Sherman D, Fischer G, Durrens P, Casaregola S, Lafontaine I, De Montigny J, Marck C, Neuvéglise C, Talla E, Goffard N, Frangeul L, Aigle M, Anthouard V, Babour A, Barbe V, Barnay S, Blanchin S, Beckerich JM, Beyne E, Bleykasten C, Boisramé A, Boyer J, Cattolico L, Confanioleri F, De Daruvar A, Despons L, Fabre E, Fairhead C, Ferry-Dumazet H, Groppi A, Hantraye F, Hennequin C, Jauniaux N, Joyet P, Kachouri R, Kerrest A, Koszul R, Lemaire M, Lesur I, Ma L, Muller H, Nicaud JM, Nikolski M, Oztas S, Ozier-Kalogeropoulos O, Pellenz S, Potier S, Richard GF, Straub ML, Suleau A, Swennen D, Tekaia F, Wésolowski-Louvel M, Westhof E, Wirth B, Zeniou-Meyer M, Zivanovic I, Bolotin-Fukuhara M, Thierry A, Bouchier C, Caudron B, Scarpelli C, Gaillardin C, Weissenbach J, Wincker P, Souciet JL**. 2004. Genome evolution in yeasts. Nature **430**:35–44. http://dx.doi.org/ 10.1038/nature02579.

16. **Tafer H, Sterflinger K, Lopandic K**. 2016. Draft genome of *Debaryomyces fabryi* CBS 789T, isolated from a human interdigital mycotic lesion. Genome Announc **4**(1):. http://dx.doi.org/10.1128/genomeA.01580-15.

17. **Langmead B, Salzberg SL**. 2012. Fast gapped-read alignment with Bowtie 2. Nat Methods **9**:357–359. http://dx.doi.org/10.1038/nmeth.1923.

18. **Li H, Durbin R**. 2010. Fast and accurate long-read alignment with Burrows–Wheeler transform. Bioinformatics **26**:589–595. http:// dx.doi.org/10.1093/bioinformatics/btp698.

19. **Bushnell B**. 2014. BBMap: a fast, accurate, splice-aware aligner (no. LBNL-7065E). https://sourceforge.net/projects/bbmap.

20. **Liu Y, Schmidt B**. 2012. Long read alignment based on maximal exact match seeds. BioInformatics **28**:i318–i324. http://dx.doi.org/10.1093/ bioinformatics/bts414.

21. **Okonechnikov K, Conesa A, García-Alcalde F**. 2016. Qualimap 2: advanced multi-sample quality control for high-throughput sequencing data. Bioinformatics **32**:292–294. http://dx.doi.org/10.1093/ bioinformatics/btv566.