



# Draft Genome Sequence of a Multistress-Tolerant Yeast, *Pichia kudriavzevii* NG7

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**ABSTRACT** *Pichia kudriavzevii* NG7 is a multistress-tolerant yeast, isolated from grape skins. Here, we report the draft genome sequence of *P. kudriavzevii* NG7, to understand its biochemical regulation and metabolic pathways.

*Pichia kudriavzevii* (syn. *Issatchenkia orientalis*) has been isolated from various environments and reported to metabolize a variety of complex substrates (1, 2). This indicates that *P. kudriavzevii* is a robust yeast strain tolerant to multistress conditions (low pH, high salt and sugar concentrations, and temperature up to 45°C) (3). In particular, due to its ability to grow at extremely low pH conditions, *P. kudriavzevii* has been applied in ethanol fermentation at pH 2 and in the saccharification of lignocellulosic biomasses hydrolyzed by sulfuric acid (4–7). It also has been used in the production of succinic acid in unbuffered culture conditions (8). The use of yeast species tolerant to acid is of industrial importance for several bioproduction processes (9). Therefore, we present here the draft genome sequence of *P. kudriavzevii* NG7 as a good model yeast for multistress-tolerant species in order to understand its biochemical properties and metabolic pathways.

*P. kudriavzevii* NG7 is a multistress-tolerant yeast isolated from grape skins. Genomic DNA of NG7 was sequenced on an Illumina HiSeq 2500 platform using paired-end libraries at the Core Facility Management Center of the Korea Research Institute of Bioscience and Biotechnology (KRIBB). We used the HTQC program to eliminate low-quality ( $Q$  value  $<30$ ) reads, generating a total of 2.5 million paired-end reads (58.7-fold coverage), before genome assembly with the SPAdes version 3.9.0 pipeline (10, 11). The genome assembly totaled 10,643,833 bp, consisting of 350 scaffolds with 39 gaps. The draft genome sequence of NG7 exhibited an overall GC content of 38.27%. The  $N_{50}$  value is 136,929 bp, and the length of the longest contig is 319,187 bp. Gene prediction of the genomic sequence was performed using AUGUSTUS (12). A total of 4,001 protein-encoding genes and 192 tRNA coding sequences were identified by tRNAscan-SE (13).

**Accession number(s).** The nucleotide sequence of *P. kudriavzevii* NG7 has been deposited in GenBank under the accession number **NWTR00000000**.

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## REFERENCES

1. Radecka D, Mukherjee V, Mateo RQ, Stojiljkovic M, Foulquié-Moreno MR, Thevelein JM. 2015. Looking beyond *Saccharomyces*: the potential of non-conventional yeast species for desirable traits in bioethanol fermentation. *FEMS Yeast Res* 15:fov053. <https://doi.org/10.1093/femsyr/fov053>.
2. Oberoi HS, Babbar N, Sandhu SK, Dhaliwal SS, Kaur U, Chadha BS, Bhargav VK. 2012. Ethanol production from alkali-treated rice straw via simultaneous saccharification and fermentation using newly isolated thermotolerant *Pichia kudriavzevii* HOP-1. *J Ind Microbiol Biotechnol* 39:557–566. <https://doi.org/10.1007/s10295-011-1060-2>.
3. Toivari M, Vehkomäki ML, Nygård Y, Penttilä M, Ruohonen L, Wiebe MG. 2013. Low pH D-xylonate production with *Pichia kudriavzevii*. *Bioresour Technol* 133:555–562. <https://doi.org/10.1016/j.biortech.2013.01.157>.
4. Gallardo JC, Souza CS, Cicarelli RM, Oliveira KF, Morais MR, Laluec C. 2011. Enrichment of a continuous culture of *Saccharomyces cerevisiae* with the yeast *Issatchenkia orientalis* in the production of ethanol at increasing temperatures. *J Ind Microbiol Biotechnol* 38:405–414. <https://doi.org/10.1007/s10295-010-0783-9>.
5. Isono N, Hayakawa H, Usami A, Mishima T, Hisamatsu M. 2012. A comparative study of ethanol production by *Issatchenkia orientalis* strains under stress conditions. *J Biosci Bioeng* 113:76–78. <https://doi.org/10.1016/j.jbiosc.2011.09.004>.
6. Kitagawa T, Tokuhiro K, Sugiyama H, Kohda K, Isono N, Hisamatsu M, Takahashi H, Imaeda T. 2010. Construction of a beta-glucosidase expression system using the multistress-tolerant yeast *Issatchenkia orientalis*. *Appl Microbiol Biotechnol* 87:1841–1853. <https://doi.org/10.1007/s00253-010-2629-9>.
7. Kwon YJ, Ma AZ, Li Q, Wang F, Zhuang GQ, Liu CZ. 2011. Effect of lignocellulosic inhibitory compounds on growth and ethanol fermentation of newly-isolated thermotolerant *Issatchenkia orientalis*. *Bioresour Technol* 102:8099–8104. <https://doi.org/10.1016/j.biortech.2011.06.035>.
8. Xiao H, Shao Z, Jiang Y, Dole S, Zhao H. 2014. Exploiting *Issatchenkia orientalis* SD108 for succinic acid production. *Microb Cell Fact* 13:121. <https://doi.org/10.1186/s12934-014-0121-4>.
9. Steensels J, Snoek T, Meersman E, Picca Nicolino M, Voordeckers K, Verstrepen KJ. 2014. Improving industrial yeast strains: exploiting natural and artificial diversity. *FEMS Microbiol Rev* 38:947–995. <https://doi.org/10.1111/1574-6976.12073>.
10. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
11. Yang X, Liu D, Liu F, Wu J, Zou J, Xiao X, Zhao F, Zhu B. 2013. HTQC: a fast quality control toolkit for Illumina sequencing data. *BMC Bioinformatics* 14:33. <https://doi.org/10.1186/1471-2105-14-33>.
12. Hoff KJ, Stanke M. 2013. WebAUGUSTUS—a web service for training AUGUSTUS and predicting genes in eukaryotes. *Nucleic Acids Res* 41:W123–W128. <https://doi.org/10.1093/nar/gkt418>.
13. Lowe TM, Chan PP. 2016. tRNAscan-SE On-line: integrating search and context for analysis of transfer RNA genes. *Nucleic Acids Res* 44:W54–W57. <https://doi.org/10.1093/nar/gkw413>.