



# Genome Sequencing of *Kocuria varians* Strain 80, Isolated from Starter Culture for Dry Sausage

Evgenii A. Konorov,<sup>a,b</sup> Konstantin A. Kurbakov,<sup>a,b</sup> Mikhail Y. Minaev<sup>a</sup>

<sup>a</sup>V. M. Gorbato Federal Research Center for Food Systems, Russian Academy of Sciences, Moscow, Russia

<sup>b</sup>Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow, Russia

**ABSTRACT** The genome of the meat starter culture strain *Kocuria varians* 80 was sequenced and assembled into a single 2.82-Mb chromosome. Genome sequence comparison of *K. varians* strain 80 and previously sequenced strains revealed predicted proteomic differences that can impact its technological properties.

*Kocuria varians* is used as a starter culture for processed meat and dairy products. In combination with other starter cultures or by itself, it can participate in proteolysis, denitrification, and biogenic amine degradation (1–3), which leads to changes in the flavor and aroma of a processed product. Recent genome studies of starter cultures have succeeded in describing the biotechnological properties of starter cultures. Among them are the meat starter culture strains *Staphylococcus carnosus* TM300 (4), *Staphylococcus xylosus* (5), *Lactobacillus sakei* (6), and others. Here, we present the genomic characteristics of *Kocuria varians* strain 80 (SSCA-2165).

*Kocuria varians* strain 80 was received from State Scientific Center for Antibiotics Culture (SSCA; culture number 2165) and was originally isolated from dried fermented sausages in 1978 (7). The strain was grown in 1 ml of Trypticase soy broth (TSB) (Liofilchem, Roseto degli Abruzzi, Italy) at 30°C for 24 h. The culture was inoculated onto mannitol salt agar (MSA; Liofilchem) and incubated at 30°C for 48 h. Then, one colony was inoculated in a tube with 5 ml TSB and incubated at 30°C for 48 h.

Bacterial DNA was isolated with the GBD kit (Biosilica, Russia). We used the NEBNext Ultra DNA library prep kit (New England Biolabs, USA) for Illumina HiSeq 2500 sequencing. For PacBio RS II single-molecule real-time (SMRT) sequencing, we used the SMRTbell template prep kit v1.0 (Pacific Biosciences, USA) following the 20-kb template preparation protocol using the BluePippin size selection system. In total, there were 2.1 billion ( $2 \times 250$ -bp) Illumina reads and 158,304 PacBio reads (average read length, 7.6 kb).

After read and adapter trimming with Trimmomatic v0.36 (8) with the command line parameters ILLUMINACLIP:TruSeq3-PE.fa:2:30:10 LEADING:3 TRAILING:3 SLIDINGWINDOW:4:20 MINLEN:100, the genome sequence of *K. varians* was assembled with SPAdes v3.11 (9), with error correction using both PacBio and Illumina reads. Gene annotation was conducted with NCBI Prokaryotic Genome Annotation Pipeline v4.12 (10); every predicted gene product was subjected to a BLASTp v2.9.0 (11) search against the NCBI nonredundant (nr) database and an InterProScan v5.33-72.0 (12) search. Gene Ontology and KEGG pathway annotations were performed using Blast2GO v4 (13) for *K. varians* strain 80, *K. salsicia* G1 (GenBank accession number [GCA\\_001408335.1](https://.ncbi.nlm.nih.gov/nuccore/GCA_001408335.1)), and *K. varians* G6 ([GCA\\_900014985.1](https://.ncbi.nlm.nih.gov/nuccore/GCA_900014985.1)). After circularization using Simple Circularise v1.0 (<https://github.com/Kzra/Simple-Circularise>), the genome assembly consisted of a single contig with a 2,823,038-bp circular chromosome (assembly coverage, 47.9 $\times$ ). The genome has a 70.55% GC content. We found 2,465 protein-coding sequences, 48 tRNA genes, and 9 rRNA genes.

**Citation** Konorov EA, Kurbakov KA, Minaev MY. 2021. Genome sequencing of *Kocuria varians* strain 80, isolated from starter culture for dry sausage. *Microbiol Resour Announc* 10:e00086-21. <https://doi.org/10.1128/MRA.00086-21>.

**Editor** Julia A. Maresca, University of Delaware

**Copyright** © 2021 Konorov et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Evgenii A. Konorov, [casq@yandex.ru](mailto:casq@yandex.ru).

**Received** 29 January 2021

**Accepted** 5 February 2021

**Published** 25 February 2021

Unlike *K. varians* C6, both *K. varians* 80 and *K. salsicia* G1 contain the *xykB* gene, according to KEGG pathway analysis. Also unlike *K. varians* G6 and *K. salsicia* G1, strain 80 has a complete metabolic pathway from D-glucose-1P to L-rhamnose, which is potentially important to its properties as a meat-fermenting starter culture.

**Data availability.** The PacBio and Illumina reads were submitted to the SRA under accession numbers [SRR13177364](https://www.ncbi.nlm.nih.gov/sra/SRR13177364) and [SRR13177365](https://www.ncbi.nlm.nih.gov/sra/SRR13177365), respectively. The genome sequence of *K. varians* strain 80 (SSCA-2165) has been deposited at GenBank under accession number [GCF\\_002250745.2](https://www.ncbi.nlm.nih.gov/genbank/GCF_002250745.2).

## ACKNOWLEDGMENT

The work was supported by the Ministry of Science and Higher Education of the Russian Federation (agreement number 0437.19.001).

## REFERENCES

1. Tremonte P, Succi M, Reale A, Di Renzo T, Sorrentino E, Coppola R. 2007. Interactions between strains of *Staphylococcus xylosum* and *Kocuria varians* isolated from fermented meats. *J Appl Microbiol* 103:743–751. <https://doi.org/10.1111/j.1365-2672.2007.03315.x>.
2. Scannell AGM, Kenneally PM, Arendt EK. 2004. Contribution of starter cultures to the proteolytic process of a fermented non-dried whole muscle ham product. *Int J Food Microbiol* 93:219–230. <https://doi.org/10.1016/j.jfoodmicro.2003.11.007>.
3. Fadda S, Vignolo G, Oliver G. 2001. Tyramine degradation and tyramine/histamine production by lactic acid bacteria and *Kocuria* strains. *Biotechnol Lett* 23:2015–2019. <https://doi.org/10.1023/A:1013783030276>.
4. Rosenstein R, Nerz C, Biswas L, Resch A, Raddatz G, Schuster SC, Götz F. 2009. Genome analysis of the meat starter culture bacterium *Staphylococcus carnosus* TM300. *Appl Environ Microbiol* 75:811–822. <https://doi.org/10.1128/AEM.01982-08>.
5. Labrie SJ, El Haddad L, Tremblay DM, Plante P-L, Wasserscheid J, Dumaresq J, Dewar K, Corbeil J, Moineau S. 2014. First complete genome sequence of *Staphylococcus xylosum*, a meat starter culture and a host to propagate *Staphylococcus aureus* phages. *Genome Announc* 2:e00671-14. <https://doi.org/10.1128/genomeA.00671-14>.
6. McLeod A, Brede DA, Rud I, Axelsson L. 2013. Genome sequence of *Lactobacillus sakei* subsp. *sakei* LS25, a commercial starter culture strain for fermented sausage. *Genome Announc* 1:e00475-13. <https://doi.org/10.1128/genomeA.00475-13>.
7. Kostenko JG, Solodovnikova GI, Kuznetsova GA, Spitsyna DN. September 1997. Strain *Micrococcus varians* 80 used for meatstuffs production. Russian patent RU2091486C1.
8. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>.
9. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski 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>.
10. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.
11. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. *J Mol Biol* 215:403–410. [https://doi.org/10.1016/S0022-2836\(05\)80360-2](https://doi.org/10.1016/S0022-2836(05)80360-2).
12. Quevillon E, Silventoinen V, Pillai S, Harte N, Mulder N, Apweiler R, Lopez R. 2005. InterProScan: protein domains identifier. *Nucleic Acids Res* 33:W116–W120. <https://doi.org/10.1093/nar/gki442>.
13. Conesa A, Götz S, García-Gómez JM, Terol J, Talón M, Robles M. 2005. Blast2GO: a universal tool for annotation, visualization and analysis in functional genomics research. *Bioinformatics* 21:3674–3676. <https://doi.org/10.1093/bioinformatics/bti610>.