

Draft Genome Sequence of *Staphylococcus carnosus* subsp. *utilis* LTH 7013, Isolated from South Tyrolean Ham

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***Staphylococcus carnosus* is used as a starter culture in meat fermentation, where it contributes to color formation and produces aromatic compounds. Here, we report the first draft genome sequence of an *S. carnosus* subsp. *utilis* strain, LTH 7013, isolated from South Tyrolean ham, with potential application as a starter culture.**

Received 1 April 2015 Accepted 14 April 2015 Published 14 May 2015

Citation Müller A, Huptas C, Wenning M, Schmidt H, Weiss A. 2015. Draft genome sequence of *Staphylococcus carnosus* subsp. *utilis* LTH 7013, isolated from South Tyrolean ham. *Genome Announc* 3(3):e00456-15. doi:10.1128/genomeA.00456-15.

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Strains of the species *Staphylococcus carnosus* are used as bacterial starter cultures for the fermentation of meat products, such as sausage. They contribute to the development and stabilization of a typically red color (1) and to the formation of aromatic compounds (2). This species consists of two subspecies, namely, *S. carnosus* subsp. *carnosus* and *S. carnosus* subsp. *utilis*. The complete genome sequence of *S. carnosus* subsp. *carnosus* strain TM300 has been published (3), but no insights into the genome sequence of *S. carnosus* subsp. *utilis* have been reported so far.

Strain LTH 7013 was isolated from South Tyrolean ham, and genomic DNA was extracted with CTAB (4). Sequencing was performed in the 250-nucleotide (nt) paired-end mode on an Illumina MiSeq platform using the TruSeq DNA PCR-free sample prep kit (Illumina) for library preparation. Sequenced read pairs were trimmed by 10 nt from the 5' end and 1 nt from the 3' end prior to read filtering (parameter setting, $-l\ 70 -s\ 20$) with the NGS QC toolkit version 2.2.3 (5). Then, high-quality read pairs were assembled with SPAdes version 2.5.1 (6) using default parameter settings.

The draft genome sequence of *S. carnosus* subsp. *utilis* LTH 7013 comprises 34 contigs with a total length of 2,632,443 bp. The contigs were compared to the genome sequence of strain TM300 (3) with GGDC version 2.0 (7), which confirmed the classification to the subspecies *utilis*. The annotation with RAST (8) predicted 2,607 coding sequences (CDSs) and 68 RNAs. The phage search tool PHAST (9) revealed one intact prophage region with a size of 32.1 kb and a GC content of 34%.

The draft genome of LTH 7013 reveals a multitude of functions necessary for a starter culture. For example, the pathway for reduction of nitrate to nitrite and further to ammonia is complete. Nitrate reductase activity contributes to the formation of red color in meat products and is therefore a welcome characteristic for a starter culture. Also, pathways for the degradation of different amino acids like isoleucine and valine are complete. Degradation products of both amino acids are described to have a sensory effect

(10). Similar to *S. carnosus* subsp. *carnosus*, *S. carnosus* subsp. *utilis* has different possibilities to respond to osmotic, cold, and oxidative stress, for example, the glycine betaine transporter OpuD, the cold shock protein CspA, or genes encoding for superoxide dismutase and catalase. No genes encoding for staphylococcal toxins and superantigens were predicted. One gene, which encodes for a beta-lactamase, was found in the genome but not on the intact prophage.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in GenBank under the accession number LAIU00000000. The version described in this paper is the version LAIU00000000.1.

ACKNOWLEDGMENTS

This work was supported by the German Ministry of Economics and Technology (via AiF) and the FEI (Forschungskreis der Ernährungsindustrie e.V., Bonn), Project AiF 17687 N.

We thank Claudia Lis, University of Hohenheim, for isolating strain LTH 7013 from South Tyrolean ham.

REFERENCES

- Götterup J, Olsen K, Knöchel S, Tjener K, Stahnke LH, Møller JK. 2008. Colour formation in fermented sausages by meat-associated staphylococci with different nitrite- and nitrate-reductase activities. *Meat Sci* 78: 492–501. <http://dx.doi.org/10.1016/j.meatsci.2007.07.023>.
- Søndergaard AK, Stahnke LH. 2002. Growth and aroma production by *Staphylococcus xylosum*, *S. carnosus* and *S. equorum*—a comparative study in model systems. *Int J Food Microbiol* 75:99–109. [http://dx.doi.org/10.1016/S0168-1605\(01\)00729-2](http://dx.doi.org/10.1016/S0168-1605(01)00729-2).
- 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. <http://dx.doi.org/10.1128/AEM.01982-08>.
- Wilson K. 2001. Preparation of genomic DNA from bacteria. *Curr Protoc Mol Biol* 2001:1. <http://dx.doi.org/10.1002/0471142727.mb0204s56>.
- Patel RK, Jain M. 2012. NGS QC toolkit: a toolkit for quality control of next generation sequencing data. *PLoS One* 7:e30619. <http://dx.doi.org/10.1371/journal.pone.0030619>.

6. 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. <http://dx.doi.org/10.1089/cmb.2012.0021>.
7. Meier-Kolthoff JP, Auch AF, Klenk HP, Göker M. 2013. Genome sequence-based species delimitation with confidence intervals and improved distance functions. *BMC Bioinformatics* 14:60. <http://dx.doi.org/10.1186/1471-2105-14-60>.
8. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
9. Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res* 39:W347–W352. <http://dx.doi.org/10.1093/nar/gkr485>.
10. Montel M-, Reitz J, Talon R, Berdagué J-L, Rousset-Akrim S. 1996. Biochemical activities of *Micrococccaceae* and their effects on the aromatic profiles and odours of a dry sausage model. *Food Microbiol* 13:489–499. <http://dx.doi.org/10.1006/fmic.1996.0056>.