UC Davis

UC Davis Previously Published Works

Title

Draft Genome Sequence of Tatumella sp. Strain UCD-D_suzukii (Phylum Proteobacteria) Isolated from Drosophila suzukii Larvae

Permalink

https://escholarship.org/uc/item/53f9t4j6

Journal

Microbiology Resource Announcements, 2(2)

ISSN

2576-098X

Authors

Dunitz, Madison I
James, Pamela M
Jospin, Guillaume
et al.

Publication Date

2014-05-01

DOI

10.1128/genomea.00349-14

Peer reviewed

eScholarship.org Powered by the California Digital Library
University of California

genomeA
Journals.ASM.org

Draft Genome Sequence of *Tatumella* sp. Strain UCD-D_suzukii (Phylum *Proteobacteria*) Isolated from *Drosophila suzukii* Larvae

Madison I. Dunitz,[a] Pamela M. James,[b] Guillaume Jospin,[a] Jonathan A. Eisen,[a,b,c] David A. Coil,[a] James Angus Chandler[b*]

University of California Davis Genome Center, Davis, California, USA[a]; Department of Evolution and Ecology, University of California Davis, Davis, California, USA[b]; Department of Medical Microbiology and Immunology, University of California Davis, Davis, California, USA[c]

* Present address: James Angus Chandler, Department of Microbiology, California Academy of Sciences, San Francisco, California, USA.

Here we present the draft genome of *Tatumella* sp. strain UCD-D_suzukii, the first member of this genus to be sequenced. The genome contains 3,602,931 bp in 72 scaffolds. This strain was isolated from *Drosophila suzukii* larvae as part of a larger project to study the microbiota of *D. suzukii*.

Received 3 April 2014 **Accepted** 9 April 2014 **Published** 24 April 2014

Citation Dunitz MI, James PM, Jospin G, Eisen JA, Coil DA, Chandler JA. 2014. Draft genome sequence of *Tatumella* sp. strain UCD-D_*suzukii* (phylum *Proteobacteria*) isolated from *Drosophila suzukii* larvae. Genome Announc. 2(2):e00349-14. doi:10.1128/genomeA.00349-14.

Copyright © 2014 Dunitz et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Jonathan A. Eisen, jaeisen@ucdavis.edu.

Tatumella sp. strain UCD-D_suzukii was isolated from *Drosophila suzukii* larvae collected at the Wolfskill Experimental Orchard near Winters, CA. On 28 June 2012 undamaged whole cherries were collected in sterile plastic bags for transport to the University of California, Davis. The cherries were macerated in the bags and the largest visible larvae were picked from the bags, externally washed in 70% ethanol, rinsed in sterile water, and then individually placed in yeast extract-peptone-dextrose (YEPD) plates (1% yeast extract, 2% peptone, and 2% glucose/dextrose) (methods adapted from [1]). The larvae were allowed to migrate for 30 to 60 s and then transferred to a vial containing Bloomington *Drosophila* medium. All eclosing adults were identified as *D. suzukii*.

The resulting colonies were double-dilution streaked onto YEPD plates and incubated for 5 days at 20°C. Single colonies were transferred and incubated for 48 h in liquid YEPD medium at 20°C. Genomic DNA was extracted using a Wizard genomic DNA purification kit (Promega) from fresh overnight cultures. Illumina paired-end libraries were then made from sonicated DNA using a TruSeq DNA sample prep v2 kit (Illumina).

A total of 4,503,930 paired-end reads were generated on an Illumina MiSeq, at a read length of 300 bp. Quality trimming and error correction resulted in 3,975,054 high-quality reads. All sequence processing and assembly were performed using the A5 assembly pipeline (2). The assembly produced 85 contigs, contained in 72 scaffolds (minimum, 598 bp; maximum, 441,247 bp; N_{50}, 329,990 bp). The final assembly contained 3,602,931 bp with a GC content of 51.44, and estimated overall coverage of 330×. Completeness of the genome was assessed using Phylosift (3), which searches for 37 highly conserved, single-copy marker genes (4), all of which were found in this assembly.

Automated annotation was performed using the RAST server (5). *Tatumella* sp. strain UCD-D_suzukii contains 3,725 predicted coding sequences and 110 predicted RNAs. A full-length (1,499 bp) 16S sequence was obtained from this annotation and was used to attempt to identify the species of *Tatumella*. This sequence is 100% identical to the representative sequence of the most common *Tatumella* operational taxonomic unit (OTU) found with *D. suzukii* larvae (J. A. Chandler, P. James, G. Jospin, and J. Lang, submitted for publication). Due to the recent transfer of select *Pantoea* into the *Tatumella* genus (6), the 16 s sequence was aligned with sequences from both genera in RDP (7), this alignment was then used to construct a phylogenetic tree in RAxML (8). *Tatumella* sp. strain UCD-D_suzukii is most closely related to *Tatumella ptyseos*, but is more than 99% identical to at least one other *Tatumella* species; therefore, we are unable to assign a species name to this isolate. Multiple *Pantoea* genomes have been published; however, none belong to the three species that were transferred to the *Tatumella* genus, making *Tatumella* sp. strain UCD-D_suzukii the first *Tatumella* genome to be sequenced.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number JFJX00000000. The version described in this paper is version JFJX01000000. The raw Illumina reads are available at ENA/SRA under accession number PRJEB5959 (ERP005406).

ACKNOWLEDGMENTS

We thank the University of California Wolfskill Experimental Orchard for access and Kelly Hamby for assisting with specimen collections. Olga Barmina provided technical assistance. Illumina sequencing was performed at the DNA Technologies Core facility in the Genome Center at the University of California Davis, Davis, California (UCD).

This work was funded by a grant to J.A.E. from the Alfred P. Sloan Foundation as part of their "Microbiology of the Built Environment" program. Further support was provided by a UCD Center for Population Biology Graduate Student Research Award to J.A.C., a UCD Dean's Mentorship Award to J.A.C., a UCD Provost's Undergraduate Fellowship to P.M.J., and NSF grant IOS-0815141 and REU supplement to Artyom Kopp (UCD).

REFERENCES

1. **Hamby KA, Hernández A, Boundy-Mills K, Zalom FG.** 2012. Associations of yeasts with spotted-wing *Drosophila* (*Drosophila suzukii*; *Diptera*: *Drosophilidae*) in cherries and raspberries. Appl. Environ. Microbiol. **78:** 4869–4873. http://dx.doi.org/10.1128/AEM.00841-12.
2. **Tritt A, Eisen JA, Facciotti MT, Darling AE.** 2012. An integrated pipeline for *de novo* assembly of microbial genomes. PLoS One **7:**e42304. http://dx.doi.org/10.1371/journal.pone.0042304.
3. **Darling AE, Jospin G, Lowe E, Matsen FA, Bik HM, Eisen JA.** 2014. PhyloSift: phylogenetic analysis of genomes and metagenomes. PeerJ 2:e243. http://dx.doi.org/10.7717/peerj.243.
4. **Wu D, Jospin G, Eisen JA.** 2013. Systematic identification of gene families for use as "markers" for phylogenetic and phylogeny-driven ecological studies of bacteria and archaea and their major subgroups. PLoS One **8:**e77033. http://dx.doi.org/10.1371/journal.pone.0077033.
5. **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.
6. **Brady CL, Venter SN, Cleenwerck I, Vandemeulebroecke K, De Vos P, Coutinho TA.** 2010. Transfer of *Pantoea citrea*, *Pantoea punctata* and *Pantoea terrea* to the genus *Tatumella* emend. as *Tatumella citrea* comb. nov., *Tatumella punctata* comb. nov. and *Tatumella terrea* comb. nov. and description of *Tatumella morbirosei* sp. nov. Int. J. Syst. Evol. Microbiol. **60:** 484–494. http://dx.doi.org/10.1099/ijs.0.012070-0.
7. **Cole JR, Wang Q, Fish JA, Chai B, McGarrell DM, Sun Y, Brown CT, Porras-Alfaro A, Kuske CR, Tiedje JM.** 2014. Ribosomal Database project: data and tools for high throughput rRNA analysis. Nucleic Acids Res. **42:** D633–D642. http://dx.doi.org/10.1093/nar/gkt1244.
8. **Stamatakis A Hoover P, Rougemont J.** 2008. A rapid bootstrap algorithm for the RAxML Web servers. Syst. Biol. **57:**758–771. http://dx.doi.org/10.1080/10635150802429642.