Draft Genome Sequence for a Urinary Isolate of Nosocomiicoccus Ampullae

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Recommended Citation
Hilt, Evann Elizabeth; Price, Travis Kyle; Diebel, Katherine; Putonti, Catherine; and Wolfe, Alan J.. Draft Genome Sequence for a Urinary Isolate of Nosocomiicoccus Ampullae. Genome Announcements, 4, 6: e01248-16, 2016. Retrieved from Loyola eCommons, Bioinformatics Faculty Publications, http://dx.doi.org/10.1128/genomeA.01248-16

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Draft Genome Sequence for a Urinary Isolate of Nosocomiicoccus ampullae

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A draft genome sequence for a urinary isolate of Nosocomiicoccus ampullae (UMB0853) was investigated. The size of the genome was 1,578,043 bp, with an observed G+C content of 36.1%. Annotation revealed 10 rRNA sequences, 40 tRNA genes, and 1,532 protein-coding sequences. Genome coverage was 727× and consisted of 32 contigs, with an N50 of 109,831 bp.

Received 17 September 2016 Accepted 26 September 2016 Published 17 November 2016


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As part of an attempt to characterize the newly discovered female urinary microbiota (1–9), we report here the genome sequence and annotation of a strain of Nosocomiicoccus ampullae isolated from a female pursuing urologynecologic clinical care. This is the first report of a human isolate of N. ampullae, a species that has not been associated with pathogenesis.

N. ampullae strain UMB0853 was isolated from urine obtained by transurethral catheterization of an adult woman with urinary symptoms, using the described enhanced quantitative urine culture protocol (4). Strain UMB0853 was subcultured to purity and analyzed by matrix-assisted laser desorption ionization—time of flight mass spectrometry (10), which could not provide an assignment. In contrast, 16S rRNA gene sequence analysis identified the isolate as N. ampullae. A pure culture was stored at -80°C in a 2-ml CryoSaver brucella broth with 10% glycerol, and no beads (Hardy Diagnostics). For genome extraction and sequencing, the preserved pure culture isolate was grown on 5% sheep blood agar (BD BBL prepared plated medium) under 5% CO2 at 35°C for 48 h.

To extract genomic DNA, cells were resuspended in 0.5 ml of DNA extraction buffer (20 mM Tris-HCl, 2 mM EDTA, 1.2% Triton X-100 [pH 8]), followed by the addition of 50 μl of lysozyme (20 mg/ml), 30 μl of mutanolysin, and 5 μl of RNase (10 mg/ml). After a 1-h incubation at 37°C, 80 μl of 10% SDS and 20 μl proteinase K were added, followed by a 2-h incubation at 55°C. Two hundred ten microliters of 6 M NaCl and 700 μl of phenol-chloroform were added. The two runs produced 11,221,884 reads in total. Assembly was performed using Velvet (11) (k = 99), followed by SSPACE (12) for scaffolding, producing 32 contigs, which varied in size from 2,642 bp to 337,531 bp (#50, 109,831 bp), with an average coverage of 727×. The NCBI Prokaryotic Genome Annotation Pipeline (13) detected 10 rRNA genes, 40 tRNA genes, 1,532 protein-coding sequences, and 35 pseudogenes. Six clustered regularly interspaced short palindromic repeat sequences (CRISPRs) were found (14). The genome size was 1,578,043 bp, with an observed G+C content of 36.1%.

Accession number(s). The draft whole-genome project for N. ampullae strain UMB0853 has been deposited at DDBJ/EMBL/GenBank under accession number MBFG0000000. Raw sequence reads are deposited at DDBJ/EMBL/GenBank under accession number SRR3828836.

ACKNOWLEDGMENTS We acknowledge Gina Kuffel and Michael Zilliox for sequencing this genome.

FUNDING INFORMATION This work, including the efforts of Alan J. Wolfe, was funded by HHS | National Institutes of Health (NIH) (RO1DK104718). This work, including the efforts of Catherine Putonti, was funded by National Science Foundation (NSF) (1149387). This work, including the efforts of Alan J. Wolfe and Catherine Putonti, was funded by Loyola University Chicago (LUC) (multidisciplinary research award). This work, including the efforts of Catherine Putonti, was funded by HHS | National Institutes of Health (NIH) (RO1DK104718). This work, including the efforts of Alan J. Wolfe and Catherine Putonti, was funded by Loyola University Chicago (LUC) (multidisciplinary research award).

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