

Complete Genome Sequences of *Aerococcus christensenii* CCUG 28831^T, *Aerococcus sanguinicola* CCUG 43001^T, *Aerococcus urinae* CCUG 36881^T, *Aerococcus urinaeequi* CCUG 28094^T, *Aerococcus urinaehominis* CCUG 42038 B^T, and *Aerococcus viridans* CCUG 4311^T

Derya Carkaci,^{a,b,c} Rintas Dargis,^a Xiaohui Chen Nielsen,^a Ole Skovgaard,^b Kurt Fuursted,^c Jens Jørgen Christensen^{a,d}

Department of Clinical Microbiology, Slagelse Hospital, Slagelse, Denmark^a; Department of Science and Environment, Roskilde University, Roskilde, Denmark^b; Department of Microbiology and Infection Control, Statens Serum Institut, Copenhagen, Denmark^c; Department of Clinical Medicine, University of Copenhagen, Copenhagen, Denmark^d

Strains belonging to the genus *Aerococcus* are causative agents of human and animal infections, including urogenital infections, bacteremia/septicemia, and infective endocarditis. This study reports the first fully closed and complete genome sequences of six type strains belonging to the genus *Aerococcus* using a combination of Illumina HiSeq and PacBio sequencing technologies.

Received 3 March 2016 Accepted 7 March 2016 Published 21 April 2016

Citation Carkaci D, Dargis R, Nielsen XC, Skovgaard O, Fuursted K, Christensen JJ. 2016. Complete genome sequences of *Aerococcus christensenii* CCUG 28831^T, *Aerococcus sanguinicola* CCUG 43001^T, *Aerococcus urinae* CCUG 36881^T, *Aerococcus urinaeequi* CCUG 28094^T, *Aerococcus urinaehominis* CCUG 42038 B^T, and *Aerococcus viridans* CCUG 4311^T. *Genome Announc* 4(2):e00302-16. doi:10.1128/genomeA.00302-16.

Copyright © 2016 Carkaci 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 Xiaohui Chen Nielsen, xcn@regionsjaelland.dk, or Jens Jørgen Christensen, jejc@regionsjaelland.dk.

The genus *Aerococcus* encompasses eight species, which are Gram-positive cocci. For a long time, *Aerococcus viridans* (1953) (1) was the only known species. An additional seven species were described: *A. urinae* (1992) (2), *A. christensenii* (1999) (3), *A. urinaehominis* (2001) (4), *A. sanguinicola* (2001) (5), *A. urinaeequi* (2005) (6), *A. suis* (2007) (7), and *A. vaginalis* (2014) (8). *Aerococcus* spp. have been reported as human pathogens and associated with urogenital infections, bacteremia/septicemia, and infective endocarditis (1–5, 7–9). *A. suis* (from pig farms), *A. urinaeequi* (from horses and cattle), and *A. vaginalis* (from cow) have only been described as pathogens in animals (6–8).

In fact, little is known about *Aerococcus* pathogenicity and virulence mechanisms for causing infections in human and animals (10–13). One explanation for this has been stated as underestimated incidence in clinical settings, partly due to misidentification with closely related Gram-positive cocci (10, 14–16).

To date, six *Aerococcus* strains (*A. christensenii*, *A. urinae*, two *A. urinaeequi*, and two *A. viridans*) have been whole-genome sequenced and published in NCBI (National Center for Biotechnology Information), but these strains were either nontype strains or incomplete genome sequences.

Here, we announce the complete genome sequences of six

TABLE 1 *Aerococcus* type strain information, genome sequence data, and GenBank accession numbers

Type strain	Sequence depth		PacBio sequence statistic			NCBI prokaryotic genome annotation pipeline			General strain information			
	PacBio	HiSeq	No. of contigs	Genome size (bp) and N_{50} (bp)	G+C content (%)	No. of coding genes	No. of 5S, 16S, and 23S rRNAs	No. of tRNAs	Yr of strain announcement	Source of isolation	Host disease	Accession no. ^a
<i>A. christensenii</i> CCUG 28831 ^T	467×	290×	1	1,634,920	39.2	1,428	4, 4, 4	60	1988/1999 ^b	Human vagina	Vaginosis	CP014159
<i>A. sanguinicola</i> CCUG 43001 ^T	515×	210×	1	2,033,849	47.6	1,733	4, 4, 4	62	2001	Human blood	Septicemia	CP014160
<i>A. urinae</i> CCUG 36881 ^T	594×	190×	1	1,974,262	42.6	1,712	4, 4, 4	60	1989/1992 ^c	Human urine	Urinary tract infection	CP014161
<i>A. urinaeequi</i> CCUG 28094 ^T	348×	220×	1	2,013,339	39.4	1,761	5, 5, 5	54	1934/1988/2005 ^d	Horse urine	ND ^e	CP014162
<i>A. urinaehominis</i> CCUG 42038 B ^T	592×	170×	1	1,831,400	42.8	1,605	4, 4, 4	57	2001	Human urine	Urinary tract infection	CP014163
<i>A. viridans</i> CCUG 4311 ^T	486×	250×	1	2,199,877	39.4	1,914	7, 7, 7	55	1953	Air sample	ND	CP014164

^a Bioproject accession number PRJNA308559.

^b Reclassification of *Streptococcus acidominimus* (1988) as *Aerococcus christensenii* in 1999.

^c Characterization of *Aerococcus*-like organisms (1989) as *Aerococcus urinae* in 1992.

^d Reclassification of *Pediococcus urinaeequi* ([ex Mees 1934] Garvie 1988) as *Aerococcus urinaeequi* in 2005.

^e ND, not defined.

Aerococcus type strains: *A. christensenii* CCUG 28831^T, *A. sanguinicola* CCUG 43001^T, *A. urinae* CCUG 36881^T, *A. urinaeequi* CCUG 28094^T, *A. urinaehominis* CCUG 42038 B^T, and *A. viridans* CCUG 4311^T.

The type strains were cultivated at 35 to 37°C for 9 to 10 h in Todd-Hewitt media with shaking in 5% CO₂ atmosphere. Isolation and purification of high-quality genomic DNA was achieved using the Qiagen Genomic-tip 500/G system and the corresponding Genomic DNA buffer set with additional lysozyme and mutanolysin to improve bacterial cell lysis.

Illumina HiSeq (Illumina, USA) and PacBio (Pacific Biosciences, USA) sequence reads were generated at BGI (BGI, Shenzhen, China) and used in combination to obtain complete genome sequences. The HiSeq library sizes of 500-bp and 2-kb (500-bp and 6-kb for *A. urinaehominis* CCUG 42038 B^T) were prepared using a BGI in-house method and were sequenced using the Illumina HiSeq2000 platform. The 20-kb PacBio Template Prep Kit was used to generate the PacBio libraries, followed by PacBio RS II sequencing. SOAPdenovo version 2.04 (17) was used to assemble preprocessed HiSeq sequence reads, whereas PacBio sequence reads were assembled using the Celera Assembler version 8.1 from the SMRT Analysis version 2.3.0 (<http://www.pacb.com/products-and-services/analytical-software/smrt-analysis/>). The combined HiSeq and PacBio assemblies generated one single contig of 1.6 to 2.2 Mb with 100% HiSeq coverages of the PacBio assemblies (Table 1). The NCBI Prokaryotic Genome Annotation pipeline version 3.1 (18) was used to annotate 1,428 to 1,914 coding genes, and plasmids were not detected in any of the genomes.

Genome sequences were in silico NCBI BLAST (19) confirmed by rRNAmmr version 1.2 (20) predicted 16S rRNA gene sequences achieving 99 to 100% sequence identities with corresponding NCBI deposited 16S rRNA gene sequences. Additional analysis of 16S-23S rRNA gene sequences distinguished *A. viridans* from *A. urinaeequi*.

The availability of these six *Aerococcus* type strain complete genome sequences will provide important information concerning the genetic content of the genus *Aerococcus*. These genomes will act as reference strains in terms of comparative genomics in relation to pathogenicity, which will improve the understanding of *Aerococcus*-associated infections in the future.

Nucleotide sequence accession numbers. The complete genome sequences of the six *Aerococcus* type strains were deposited in GenBank under the accession numbers stated in Table 1.

ACKNOWLEDGMENTS

We thank the staff of BGI, Shenzhen, China, for providing expert technical assistance and bioinformatic knowledge during the sequencing process.

FUNDING INFORMATION

This study was supported by the Research Foundation at Region Zealand (Denmark), the Common Funds for Research between Roskilde University (Denmark) and Region Zealand (Denmark), and The Danish Heart Foundation (Denmark).

REFERENCES

- Williams REO, Hirsch A, Cowan ST. 1953. *Aerococcus*, a New bacterial genus. J Gen Microbiol 8:475–480. <http://dx.doi.org/10.1099/00221287-8-3-475>.
- Aguirre M, Collins MD. 1992. Phylogenetic analysis of some *Aerococcus*-like organisms from urinary tract infections: description of *Aerococcus urinae* sp. nov. J Gen Microbiol 138:401–405. <http://dx.doi.org/10.1099/00221287-138-2-401>.
- Collins MD, Jovita MR, Hutson RA, Ohlén M, Falsen E. 1999. *Aerococcus christensenii* sp. nov., from the human vagina. Int J Syst Bacteriol 49:1125–1128. <http://dx.doi.org/10.1099/00207713-49-3-1125>.
- Lawson PA, Falsen E, Ohlén M, Collins MD. 2001. *Aerococcus urinaehominis* sp. nov., isolated from human urine. Int J Syst Evol Microbiol 51:683–686. <http://dx.doi.org/10.1099/00207713-51-2-683>.
- Lawson PA, Falsen E, Truberg-Jensen K, Collins MD. 2001. *Aerococcus sanguinicola* sp. nov., isolated from a human clinical source. Int J Syst Evol Microbiol 51:475–479. <http://dx.doi.org/10.1099/00207713-51-2-475>.
- Felis GE, Torriani S, Dellaglio F. 2005. Reclassification of *Pediococcus urinaeequi* (ex Mees 1934) Garvie 1988 as *Aerococcus urinaeequi* comb. nov. Int J Syst Evol Microbiol 55:1325–1327. <http://dx.doi.org/10.1099/ijs.0.63324-0>.
- Vela AI, García N, Latre MV, Casamayor A, Sánchez-Porro C, Briones V, Ventosa A, Domínguez L, Fernández-Garayzábal JF. 2007. *Aerococcus suis* sp. nov., isolated from clinical specimens from swine. Int J Syst Evol Microbiol 57:1291–1294. <http://dx.doi.org/10.1099/ijs.0.64537-0>.
- Tohno M, Kitahara M, Matsuyama S, Kimura K, Ohkuma M, Tajima K. 2014. *Aerococcus vaginalis* sp. nov., isolated from the vaginal mucosa of a beef cow, and emended descriptions of *Aerococcus suis*, *Aerococcus viridans*, *Aerococcus urinaeequi*, *Aerococcus urinaehominis*, *Aerococcus urinae*, *Aerococcus christensenii* and *Aerococcus sanguinicola*. Int J Syst Evol Microbiol 64:1229–1236. <http://dx.doi.org/10.1099/ijs.0.058081-0>.
- Kass M, Tøye B, Veinot JP. 2008. Fatal infective endocarditis due to *Aerococcus urinae*—case report and review of literature. Cardiovasc Pathol 17:410–412. <http://dx.doi.org/10.1016/j.carpath.2008.06.001>.
- Rasmussen M. 2013. Aerococci and aerococcal infections. J Infect 66:467–474. <http://dx.doi.org/10.1016/j.jinf.2012.12.006>.
- Shannon O, Mörgelin M, Rasmussen M. 2010. Platelet activation and biofilm formation by *Aerococcus urinae*, an endocarditis-causing pathogen. Infect Immun 78:4268–4275. <http://dx.doi.org/10.1128/IAI.00469-10>.
- Schuur PMH, Sabbe L, Van Der Wouw AJ, Montagne GJ, Buiting AGM. 1999. Three cases of serious infection caused by *Aerococcus urinae*. Eur J Clin Microbiol Infect Dis 18:368–371. <http://dx.doi.org/10.1007/PL00015022>.
- De Jong MFC, Soetekouw R, Ten Kate RW, Veenendaal D. 2010. *Aerococcus urinae*: severe and fatal bloodstream infections and endocarditis. J Clin Microbiol 48:3445–3447. <http://dx.doi.org/10.1128/JCM.00835-10>.
- Cattoir V, Kobal A, Legrand P. 2010. *Aerococcus urinae* and *Aerococcus sanguinicola*, two frequently misidentified uropathogens. Scand J Infect Dis 42:775–780. <http://dx.doi.org/10.3109/00365548.2010.485576>.
- Cone LA, Hirschberg J, Lopez C, Kanna PK, Goldstein EJC, Kazi A, Gade-Andavolu R, Younes B. 2008. Infective endocarditis associated with spondylodiscitis and frequent secondary epidural abscess. Surg Neurol 69:121–125. <http://dx.doi.org/10.1016/j.surneu.2007.03.024>.
- Christensen JJ, Kilian M, Fussing V, Andresen K, Blom J, Korner B, Steigerwald AG. 2005. *Aerococcus urinae*: polyphasic characterization of the species. APMIS 113:517–525. http://dx.doi.org/10.1111/j.1600-0463.2005.apm_183.x.
- Li R, Li Y, Kristiansen K, Wang J. 2008. SOAP: short oligonucleotide alignment program. Bioinformatics 24:713–714. <http://dx.doi.org/10.1093/bioinformatics/btn025>.
- Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Ciufu S, Li W. 2013. Prokaryotic genome annotation pipeline. In Beck J, Benson D, Coleman J, Hoepfner M, Johnson M, Maglott D, Mizrahi I, Morris R, Ostell J, Pruitt K, Rubinstein W, Sayers E, Sirotkin K, Tatusova T (ed), The NCBI handbook, 2nd ed. National Center for Biotechnology Information, Bethesda, MD.
- Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. J Mol Biol 215:403–410. [http://dx.doi.org/10.1016/S0022-2836\(05\)80360-2](http://dx.doi.org/10.1016/S0022-2836(05)80360-2).
- Lagesen K, Hallin P, Rødland EA, Staerfeldt H-H, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res 35:3100–3108. <http://dx.doi.org/10.1093/nar/gkm160>.