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. uropathemnonis* (2001) (4), *A. sanguinicola* (2001) (5), *A. urinaeaequi* (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. urinaeaequi* (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. urinaeaequi*, 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

<table>
<thead>
<tr>
<th>Type strain</th>
<th>Sequence depth</th>
<th>PacBio sequence statistic</th>
<th>NCBI prokaryotic genome annotation pipeline</th>
<th>General strain information</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>A. christensenii CCUG 28831T</em></td>
<td>467×290×1</td>
<td>1,634,920,39.2</td>
<td>4,4,4,60</td>
<td>1988/1999* Human vagina Vaginosis CP014159</td>
</tr>
<tr>
<td><em>A. sanguinicola CCUG 43001T</em></td>
<td>515×210×1</td>
<td>2,033,849,47.6</td>
<td>4,4,4,62</td>
<td>2001 Human blood Septicemia CP014160</td>
</tr>
<tr>
<td><em>A. urinaeaequi CCUG 36881T</em></td>
<td>594×190×1</td>
<td>1,974,262,42.6</td>
<td>4,4,4,60</td>
<td>1989/1992* Human urine Urinary tract infection CP014161</td>
</tr>
<tr>
<td><em>A. urinaeaequi CCUG 28094T</em></td>
<td>348×220×1</td>
<td>2,013,339,39.4</td>
<td>5,5,5,54</td>
<td>1934/1988/2005d Horse urine ND* CP014162</td>
</tr>
<tr>
<td><em>A. urinaeaequi CCUG 42038 B</em></td>
<td>592×170×1</td>
<td>1,831,400,42.8</td>
<td>4,4,4,57</td>
<td>2001 Human urine Urinary tract infection CP014163</td>
</tr>
<tr>
<td><em>A. viridans CCUG 4311T</em></td>
<td>486×250×1</td>
<td>2,199,877,39.4</td>
<td>7,7,7,55</td>
<td>1953 Air sample ND CP014164</td>
</tr>
</tbody>
</table>

* Bioproject accession number PRJNA308559.
* ND, not defined.

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 42038B) 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 the paired reads, and the assembled genome sequences were used as the reference genomes in comparison with the PacBio assemblies generated one single contig of 1.6 to 3.4 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.

Sequence accession numbers. 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.

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