Whole-Genome Sequencing of Four Campylobacter Strains Isolated from Gull Excreta Collected from Hobie Beach (Oxnard, CA, USA)

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ABSTRACT Campylobacter spp. are commensal organisms in avian species and are one of the leading causes of bacterial foodborne human diarrheal disease worldwide. We report the draft genome sequences of Campylobacter volucris, C. lari, and C. jejuni strains isolated from California gull (Larus californicus) excreta collected from a California beach.

Campylobacter species are Gram-negative spiral rods, non-spore-forming chemooorganotrophs, and members of the Epsilonproteobacteria class, which grow under microaerobic conditions (1). Several Campylobacter species are recognized as a leading cause of bacterial foodborne infection diseases worldwide and are common inhabitants of the intestine of many wild and domestic avian species (2–4). A previous study documented the presence of a diverse and abundant population of campylobacters in the excreta of California gulls (Larus californicus) from California beaches (5). Although the risk from water impacted by California gulls is low for the community, advances in genomic analysis of potentially human infectious Campylobacter spp. in gull excreta may provide additional information for estimating the risks posed by nonsewage fecal sources (6).

Four strains (CaG_5A, CaG_58BB, CaG_63A, and CaG_70BB) were isolated from gull excreta collected in the summer of 2012 from Hobie Beach (Oxnard, CA, USA) following Waldenström et al. (7). The four colonies were transferred to individual Bolton enrichment agar plates (without antibiotics) and incubated at 42°C under microaerophilic conditions (10% CO₂, 5% O₂, and 85% N₂) for 24 h. All colonies were isolated separately, and their genomic DNA was extracted from a single colony using the MasterPure DNA extraction kit (Epicentre, Madison, WI) and purified with the DNA Clean & Concentrator kit (Zymo Research, Irvine, CA) following the manufacturer’s instructions. Genomic libraries were prepared using the TruSeq library kit followed by rapid mode sequencing (2 × 100 bp) on the HiSeq 2000 platform (Illumina, Inc., San Diego, CA).

A total of 39,770,374 reads were generated. Prior to assembly, the libraries were cleaned of adapters and phiX artifacts, error corrected, normalized, and filtered to a minimum length of 80 nucleotides using the software package BBMap v38.22 (with the following settings: ktrim=r k=23 mink=11 hdist=1 tbo tpe maxns=0 trimq=10 qtrim=r maq=12 minlength=100 ecco=t eccc=t ect=t target=100) (8). A reference-assisted de novo assembly approach was used to assemble the processed reads using Unicycler v0.4.7 (9). Average nucleotide identity (ANI), an index of similarity between two genomes (10), was calculated using FastANI v1.1 (11). The in silico multilocus sequence type (MLST) based on seven alleles (aspA, glnA, gitA, glyA, pgm, tkt, and uncA) was obtained using mlst v2.16.1 (12, 13), genes were assessed for antibiotic resistance with ResFinder v3.1 (14), and chromosomal point mutations were deter-


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Table 1: Summary statistics of whole-genome assemblies

<table>
<thead>
<tr>
<th>Strain</th>
<th>Coverage N₅₀ (contigs)</th>
<th>No. of contigs</th>
<th>Assembly size (bp)</th>
<th>Contig N₅₀ (bp)</th>
<th>G+C content (%)</th>
<th>Taxonomic affiliation</th>
<th>Reference accession no.</th>
</tr>
</thead>
<tbody>
<tr>
<td>CaG_5A</td>
<td>238</td>
<td>28</td>
<td>1,547,878</td>
<td>313,244</td>
<td>28.45</td>
<td>NA</td>
<td>Campylobacter volucris</td>
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<tr>
<td>CaG_5BB</td>
<td>231</td>
<td>50</td>
<td>1,537,596</td>
<td>170,866</td>
<td>29.50</td>
<td>NA</td>
<td>Campylobacter lari</td>
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<tr>
<td>CaG_63A</td>
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<td>45</td>
<td>1,687,991</td>
<td>219,579</td>
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<td>Campylobacter jejuni</td>
</tr>
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<td>CaG_70BB</td>
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<td>19</td>
<td>1,569,087</td>
<td>436,706</td>
<td>28.41</td>
<td>NA</td>
<td>Campylobacter coli</td>
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</tbody>
</table>

**REFERENCES**


