Multiple Genome Sequences of Important Beer-Spoiling Lactic Acid Bacteria

Andreas J. Geissler, a Jürgen Behr, b Rudi F. Vogel a

Technische Universität München, Lehrstuhl für Technische Mikrobiologie, Freising, Germany; Technische Universität München, Bavarian Center for Biomolecular Mass Spectrometry, Freising, Germany

Seven strains of important beer-spoiling lactic acid bacteria were sequenced using single-molecule real-time sequencing. Complete genomes were obtained for strains of Lactobacillus paracollinoides, Lactobacillus lindneri, and Pediococcus claussenii. The analysis of these genomes emphasizes the role of plasmids as the genomic foundation of beer-spoiling ability.

TABLE 1 Strain characteristics, sequencing statistics, genome information, and accession numbers

<table>
<thead>
<tr>
<th>Species</th>
<th>Strain</th>
<th>Beer</th>
<th>Beer spoilage ability</th>
<th>Biosample no.</th>
<th>Accession no.</th>
<th>Avg coverage of HGAP assembly (×)</th>
<th>Size (Mbp)</th>
<th>No. of contigs</th>
<th>G+C content (%)</th>
<th>PEG</th>
<th>CDSs</th>
</tr>
</thead>
<tbody>
<tr>
<td>L. paracollinoides</td>
<td>TMW 1.1979</td>
<td>Beer</td>
<td>NB</td>
<td>SAMN04505735</td>
<td>CP014912–CP014914</td>
<td>107</td>
<td>3.32</td>
<td>3</td>
<td>47.0</td>
<td>2,953</td>
<td>2,872</td>
</tr>
<tr>
<td>L. paracollinoides</td>
<td>TMW 1.1994</td>
<td>Brewery environment</td>
<td>B</td>
<td>SAMN04505736</td>
<td>CP014915–CP014923</td>
<td>102</td>
<td>3.66</td>
<td>9</td>
<td>46.8</td>
<td>3,363</td>
<td>3,219</td>
</tr>
<tr>
<td>L. paracollinoides</td>
<td>TMW 1.1995</td>
<td>Pilsner beer</td>
<td>B</td>
<td>SAMN04505737</td>
<td>CP014924–CP014932</td>
<td>88</td>
<td>3.75</td>
<td>9</td>
<td>46.6</td>
<td>3,378</td>
<td>3,286</td>
</tr>
<tr>
<td>L. lindneri</td>
<td>TMW 1.481</td>
<td>Brewery environment</td>
<td>B</td>
<td>SAMN04505733</td>
<td>CP014907–CP014911</td>
<td>143</td>
<td>1.39</td>
<td>1</td>
<td>34.3</td>
<td>1,429</td>
<td>1,387</td>
</tr>
<tr>
<td>L. lindneri</td>
<td>TMW 1.1993</td>
<td>Beer</td>
<td>B</td>
<td>SAMN04505734</td>
<td>CP014872</td>
<td>262</td>
<td>1.39</td>
<td>1</td>
<td>34.3</td>
<td>1,429</td>
<td>1,387</td>
</tr>
<tr>
<td>P. claussenii</td>
<td>TMW 2.53</td>
<td>Brewery environment</td>
<td>B</td>
<td>SAMN04505734</td>
<td>CP014933–CP014935</td>
<td>192</td>
<td>1.95</td>
<td>3</td>
<td>37.1</td>
<td>1,895</td>
<td>1,849</td>
</tr>
<tr>
<td>P. claussenii</td>
<td>TMW 2.54</td>
<td>Brewery environment</td>
<td>B</td>
<td>SAMN04505732</td>
<td>CP014936–CP014939</td>
<td>146</td>
<td>1.99</td>
<td>4</td>
<td>37.1</td>
<td>1,940</td>
<td>1,884</td>
</tr>
</tbody>
</table>

a NB, nonspoiler; B, spoiler; NB-B, unstable, mostly B.
All BioSamples are part of BioProject PRJNA290141.
Accession numbers are listed for all contigs of each whole genome (as range).
In chromosome plus plasmids and partial plasmids.
PEG, number of protein-encoding genes based on RAST annotation.
CDSs, number of coding sequences (total) based on NCBI PGAP.
ber of proteins, G+C content, coding density, codon usage, amino acid usage, proteome similarity, chromosome (DNA) similarity, functional pattern (SEED/COG), and subcellular localization of proteins. Regarding chromosomal properties, beer-spoiling LAB species cover the whole diversity within the genus Lactobacillus. In contrast, brewery isolates of the abovementioned species, although to a different extent, share a number of highly homologous plasmid-carried genes, including the important lifestyle markers horA, horC, and fabZ (3, 17, 18). This emphasizes the role of plasmids in beer-spoiling ability (3, 19, 20).

Accession number(s). The seven complete genomes have been deposited in DDBJ/EMBL/GenBank under the accession numbers listed in Table 1.

FUNDING INFORMATION
This work, including the efforts of Rudi F. Vogel, was funded by Allianz Industrie Forschung (AiF) (AiF 17576N). This research project was funded by the German Ministry of Economics and Technology (via AiF) and the Wifo (Wissenschaftsförderung der Deutschen Brauwirtschaft e.V., Berlin), project AiF 17576N. None of the funding sources had any influence on the study design, the collection, analysis, and interpretation of data, the writing of the report, or the decision to submit the article for publication.

REFERENCES