Genome Sequences of 12 Spore-Forming Bacillus Species, Comprising Bacillus coagulans, Bacillus licheniformis, Bacillus amyloliquefaciens, Bacillus sporothermodurans, and Bacillus vallismortis, Isolated from Foods
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Bacillus species have the ability to form endospores (spores). Bacillus species are ubiquitously present in soil, and transmission to food products can take place (1). Spores are highly resistant to environmental stresses and can form food processing conditions. Germination of spores followed by growth may result in food spoilage (2). Here, we report the draft genome sequences of twelve isolates belonging to five different Bacillus species that were isolated from foods: Four strains of Bacillus coagulans, four strains of Bacillus licheniformis, one strain of Bacillus amyloliquefaciens, one strain of Bacillus sporothermodurans, and one strain of Bacillus vallismortis. Comparison of the sequenced genomes with those described previously (5) can provide insight into the genomic potential of Bacillus species, all spore-forming, Gram-positive bacteria.

Twelve strains of different isolation sources (Table 1), were grown overnight in 10 ml of brain heart infusion (BHI) broth (Difco) at 37°C. The overnight cultures were diluted 100-fold in fresh medium and incubated at 37°C until the culture reached an optical density (at 660 nm) of approximately 0.5, and cells were then harvested by centrifugation at 5000 rcf. DNA was isolated as described previously (5). The isolated DNA was sheared to 500-bp fragments in a Covaris (KBioscience) ultrasonic device for preparation of the Next-Generation Sequencing (NGS) library preps using the paired-end NEB NExtGen library preparation kit. The prepared libraries were 101 bases paired-end sequenced on an Illumina HiSeq2000 by multiplexing 12 samples per flow cell. De novo paired-end assembly of the genomes was performed using Velvet (6). The genomes were annotated using RAST (7), and scaffolds were mapped on the closest neighbor according to RAST using CONTIGuator (8). Protein annotations were extended using Interproscan (9) and BAGEL3 (10) was used for identification of putative bacteriocin gene clusters.

TABLE 1 Genome features and GenBank accession numbers of the strains

<table>
<thead>
<tr>
<th>Strain</th>
<th>Species</th>
<th>Source of isolation</th>
<th>Bioproject no.</th>
<th>Accession no.</th>
</tr>
</thead>
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<tr>
<td>B4098</td>
<td>Bacillus coagulans</td>
<td>Chinese tomato</td>
<td>PRINA270593</td>
<td>LQYG00000000</td>
</tr>
<tr>
<td>B4100</td>
<td>Bacillus coagulans</td>
<td>Low pH sauce</td>
<td>PRINA270593</td>
<td>LQYH00000000</td>
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<td>B4099</td>
<td>Bacillus coagulans</td>
<td>Indian curry</td>
<td>PRINA270593</td>
<td>LQYI00000000</td>
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<td>B4096</td>
<td>Bacillus coagulans</td>
<td>Tomato supreme</td>
<td>PRINA270593</td>
<td>LQYO00000000</td>
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<td>B4092</td>
<td>Bacillus licheniformis</td>
<td>Buttermilk powder</td>
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<td>LQYK00000000</td>
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<td>B4090</td>
<td>Bacillus licheniformis</td>
<td>Pea soup</td>
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<td>B4091</td>
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<td>Mushroom soup</td>
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<td>LQYM00000000</td>
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<td>B4102</td>
<td>Bacillus sporothermodurans</td>
<td>Indian curry</td>
<td>PRINA270602</td>
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<td>B4140</td>
<td>Bacillus amyloliquefaciens</td>
<td>Pizza</td>
<td>PRINA270600</td>
<td>LQYP00000000</td>
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<td>B425</td>
<td>Bacillus amyloliquefaciens</td>
<td>Sterilized milk</td>
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<td>B4164</td>
<td>Bacillus licheniformis</td>
<td>Unknown food</td>
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<td>B4144</td>
<td>Bacillus vallismortis</td>
<td>Quiche</td>
<td>PRINA270602</td>
<td>LQYR00000000</td>
</tr>
</tbody>
</table>
Nucleotide sequence accession numbers. The genome sequences of the twelve Bacillus sp. strains have been deposited as whole-genome shotgun projects at DDBJ/EMBL/GenBank under the accession numbers listed in Table 1.

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REFERENCES