Winemaking is a complex process that involves two different fermentations, alcoholic fermentation and malolactic fermentation (MLF). MLF is an important stage impacting wine quality, in which lactic acid bacteria transform malic acid into lactic acid and CO₂, decreasing the overall acidity of a wine and proving microbiological stability. In most Chilean wineries, the MLF stage of winemaking largely occurs in a spontaneous manner; thus, autochthonous Oenococcus oeni species are involved in this process (1). Chilean isolates might be autochthonous starter cultures for performing MLF in Cabernet Sauvignon grapes in Maipo Valley, Chile. The genome analyses might help understand the adaptation of the strains to wine-hostile conditions and their contribution to the organoleptic properties of the final product.

Bacterial genomes were sequenced using the Ion Torrent PGM platform with mate-paired end of 3-kbp span library for each isolate. The data were quality trimmed using Prinseq with a Phred score of 15, sequencing errors were corrected using the software Pollux, and data were subsequently assembled with Celera Assembler version 8.3. The genomic analysis was performed using the RAST server (2). The assembled sequence was annotated by the National Center for Biotechnology Information (NCBI) Prokaryotic Genomes Annotation Pipeline (PGAP). The genome information for each strain is summarized in Table 1. The genome size, G+C content, number of predicted genes, and number of RNA coding genes are comparable to those of the other published O. oeni strains (3, 4). These Chilean isolates showed genes related to the transformation of malic acid to lactic acid and citric acid metabolism. Furthermore, genes involved in biogenic amine formation (histamine and arginine) were not found; hence, they could be used as a safety starter for wines of a specific terroir, as suggested previously (5).

### Nucleotide sequence accession numbers

These genome sequences were deposited in DDBJ/EMBL/GenBank under the accession numbers listed in Table 1. The versions described in this paper are the first versions of the assemblies.

### ACKNOWLEDGMENTS

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### REFERENCES


### TABLE 1 Information for the whole genomes of three Chilean O. oeni strains

<table>
<thead>
<tr>
<th>Strain</th>
<th>G+C content (%)</th>
<th>Genome size (bp)</th>
<th>No. of scaffolds</th>
<th>Accession no.</th>
<th>No. of tRNAs</th>
<th>No. of rRNAs (type)</th>
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</tbody>
</table>

Maipo Valley, Chile

Oenococcus oeni is part of the microbial terroir involved in wine production. Here, we present three genome sequences of O. oeni strains isolated from spontaneous malolactic fermentation of cultivar Cabernet Sauvignon Maipo Valley, Chile.