Oenococcus oeni is the principal lactic acid bacterium responsible for malolactic fermentation in wine. Here, we announce the genome sequences of five O. oeni strains isolated from Nero di Troia wine undergoing spontaneous malolactic fermentation, and we report, for the first time, several genome sequences of isolates from the same terroir.

O. oeni is the main species of lactic acid bacteria (LAB) responsible of driving malolactic fermentation (MLF) in wine. The key biochemical stage of MLF is the microbial decarboxylation of L-malic acid that leads to the production of L-lactic acid. MLF leads to a decrease in wine acidity and an improved microbial stability and sensory quality (1–3). Increasing attention to the selection of autochthonous microbes from spontaneous fermentation is warranted to aid the design of specific starter cultures used in fermented foods and beverages with a geographical indication status (4–6). This is particularly true for the grape/wine environment, in which a relationship exists among cultivars, vintages, climates, and wine grape microbial biogeography, suggesting a possible dimension of the so-called microbial terroir (7, 8).

While the only fully complete genome sequence is available for the O. oeni PSU-1 strain (9), an increasing number of O. oeni assembled genome sequences have also been deposited in the GenBank database (10–12). Moreover, for O. oeni strain ATCC BAA-1163, a proteome reference map is also available, which is useful for the validation of annotated genes (13).

Here, we present the genome sequences of five O. oeni strains (OM22, OT25, OT4, OT5, and OT3) isolated from Nero di Troia wine (a typical Apulian red wine obtained from uva di Troia, an autochthonous Apulian black grape variety) undergoing spontaneous malolactic fermentation (Table 1) (14).

These new assembled complete genomes represent an important opportunity for assessing the molecular basis of (i) some safety aspects (15–17), (ii) tolerance to the harsh wine conditions (18, 19), and (iii) the contribution to wine sensorial quality (2, 3, 20, 21). To the best of our knowledge, it is the first time that five strains isolated from the same terroir are sequenced.

Two micrographs of genomic DNA was subjected to library preparation using the TruSeq DNA sample prep kit FC-121-1001, according to the manufacturer’s instructions. Whole-genome sequencing was performed using the Illumina GAIIx platform. Prior to assembly, raw reads were filtered using the PrinSeq version 0.20.3 software (22) to remove low-quality 3' ends (Q < 25), reads containing a percentage of uncalled bases (Ns) of ≥10%, and duplicated sequences. The genome sequences of O. oeni OM22 were de novo assembled using the Ray version 2.2.0 assembly program (23), with a k-mer size of 71. The genome sequences of O. oeni OT25, O. oeni OT4, O. oeni OT5, and O. oeni OT3 were de novo assembled using CLC Genomics Workbench 7.0, with a k-mer size of 64. The sequence was annotated by the National Center for Biotechnology Information (NCBI) Prokaryotic Genomes Annotation Pipeline. The genome information for each strain is summarized in Table 1.

Nucleotide sequence accession numbers. The draft genome sequences of the O. oeni strains sequenced in this study have been deposited as whole-genome shotgun projects at DDBJ/EMBL/GenBank under the accession numbers JPEK00000000 (O. oeni OM22), JPEM00000000 (O. oeni OT25), JPEL00000000 (O. oeni OT4), JPEJ00000000 (O. oeni OT5), and JOOH00000000 (O. oeni OT3).

### Table 1

<table>
<thead>
<tr>
<th>O. oeni strain</th>
<th>G+C content (%)</th>
<th>Genome size (bp)</th>
<th>No. of genes</th>
<th>No. of proteins</th>
<th>Accession no.</th>
<th>No. of contigs</th>
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REFERENCES


