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► To cite this version:

Fabien Cousin, Rozenn Le Guellec, Caroline Chagnot, Didier Goux, Marion Dalmasso, et al.. *Oenococcus siceræ* sp. nov., isolated from French cider. *Systematic and Applied Microbiology*, 2019, 42 (3), pp.302-308. <10.1016/j.syapm.2018.12.006>. <hal-02166854>

HAL Id: hal-02166854

<https://normandie-univ.hal.science/hal-02166854v1>

Submitted on 25 Oct 2021

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Oenococcus sicerae sp. nov., isolated from French cider

Authors:

Fabien J. COUSIN^a, Rozenn LE GUELLEC^a, Caroline CHAGNOT^a, Didier GOUX^b, Marion DALMASSO^a, Jean-Marie LAPLACE^a, Marina CRETENET^{¶ a,c}

^a Normandie Univ, UNICAEN, UNIROUEN, ABTE, 14000 Caen, France

^b Normandie Univ, UNICAEN, SF ICORE 4206, CMAbio3, F-14032 Caen, France

^c Normandie Univ, UNICAEN, SF ICORE 4206, CBM, F-14032 Caen, France

E-mail addresses:

fabien.cousin@unicaen.fr

rozenn.le.guellec@live.fr

caroline.chagnot@unicaen.fr

didier.goux@unicaen.fr

marion.dalmasso@unicaen.fr

jean-marie.laplace@unicaen.fr

marina.cretenet@unicaen.fr

¶ Corresponding author:

Mailing address: ER MALIM, EA 4651 ABTE, Esplanade de la paix, 14032 Caen cedex 05, France

Phone: +33 (0)2 31 56 57 85

Fax: +33 (0)2 31 56 61 79

E-mail: marina.cretenet@unicaen.fr

1 **ABSTRACT**

2 Two Gram-stain-positive, small ellipsoidal cocci, non-motile, oxidase- and catalase-negative, and
3 facultative anaerobic strains (UCMA15228^T and UCMA17102) were isolated in France, from
4 fermented apple juices (ciders). The 16S rRNA gene sequence was identical between the two
5 isolates and showed 97 % similarity with respect to the closest related species *Oenococcus oeni* and
6 *O. kitaharae*. Therefore, the two isolates were classified within the genus *Oenococcus*. The
7 phylogeny based on the *pheS* gene sequences also confirmed the position of the new taxon. DNA–
8 DNA hybridizations based on *in silico* genome-to-genome comparisons (GGDC) and Average
9 Nucleotide Identity (ANI) values, as well as species-specific PCR, validated the novelty of the
10 taxon. Various phenotypic characteristics such as the optimum temperature and pH for growth, the
11 ability to metabolise sugars, the aptitude to perform the malolactic fermentation, and the resistance
12 to ethanol and NaCl, revealed that the two strains are distinguishable from the other members of the
13 *Oenococcus* genus. The combined genotypic and phenotypic data support the classification of
14 strains UCMA15228^T and UCMA17102 into a novel species of *Oenococcus*, for which the name
15 *O. sicerae* sp. nov. is proposed. The type strain is UCMA15228^T (= DSM107163^T = CIRM-
16 BIA2288^T).

17

18 **KEY WORDS**

19 Lactic acid bacteria; *Oenococcus sicerae*; Cider; Apple; fermented beverage

20

21 **ABBREVIATIONS**

22

23 ANI: Average Nucleotide Identity

24 DDH: DNA–DNA Hybridization

25 GGDC: Genome-To-Genome Distance Calculator

26 LAB: Lactic Acid Bacteria

27 MLF: MaloLactic Fermentation

28 MLO: Medium for *Leuconostoc oenos*

29 RAPD: Randomly Amplified Polymorphic DNA

30 UCMA: Université de Caen Microbiologie Alimentaire

31

32

33 INTRODUCTION

34 French cider is produced from apple juice, which is usually fermented by indigenous yeasts and
35 bacteria, and is produced mainly in the Normandy and Brittany regions in France [4]. The
36 abundance and diversity of microorganisms during the fermentation processes are widely
37 recognised to contribute to the quality of the final product [4]. French ciders can be bottled for
38 direct consumption or distilled in order to produce spirit (i.e. calvados). *Saccharomyces* yeasts are
39 principally responsible for the alcoholic fermentation of apple juice, and predominate at the
40 beginning of the cider process [4]. Non-*Saccharomyces* yeasts and lactic acid bacteria (LAB) are
41 also present. The major LAB isolated from cider are part of the *Lactobacillus* sp., *Pediococcus* sp.,
42 *Oenococcus* sp. and *Leuconostoc* sp. genera [4]. They are particularly involved in the malolactic
43 fermentation (MLF) during the second step of the cider fermentation process, and especially the
44 *Oenococcus* genus.

45 The *Oenococcus* genus currently comprises three species, *O. oeni* [5], *O. kitaharae* [6] and
46 *O. alcoholitolerans* [1]. *Oenococcus oeni* is, by far, the most studied species in the genus, especially
47 for its ability to perform MLF during wine and other alcoholic-food related fermentation processes
48 [2,18]. Only *O. kitaharae* is not able to perform MLF due to a point mutation resulting in a
49 premature stop codon in the *mleA* gene encoding the malolactic enzyme [3].

50 Two LAB strains, UCMA15228^T and UCMA17102, were isolated from fermenting ciders,
51 produced in Normandy (France). These strains differed from the currently documented *Oenococcus*
52 species based on the 16S rRNA gene sequences. *Oenococcus* members are usual inhabitants of
53 fermenting apple juice during cider production, which makes cider a potential source for revealing
54 new biochemical and genomic traits of the genus. The aim of this study was to perform the
55 taxonomic characterisation of these new *Oenococcus* strains. They were found to form a separate
56 genetic group from the other known *Oenococcus* species, which is here proposed as *Oenococcus*
57 *sicerae* sp. nov., with the type strain UCMA15228^T (= DSM107163^T = CIRM-BIA2288^T). In our

58 genomic taxonomic approach, we analysed a complete genome sequence of the type strain
59 UCMA15228^T in order to determine genomic and phenotypic features of the new species.

60

61 **MATERIAL AND METHODS**

62 **Bacterial strains and growth conditions**

63 The novel strains, UCMA15228^T and UCMA17102, were isolated from two distinct cider samples
64 during the fermentation process, originating from two separate localities in Normandy (France). The
65 UCMA15228^T strain has been isolated from a cider intended to be bottled whereas the
66 UCMA17102 strain has been isolated from a cider intended to be distilled for spirit production. The
67 isolation media used were modified medium for *Leuconostoc oenos* (MLO) supplemented with
68 10 g.L⁻¹ L-malic acid, and Rogosa SL agar (Rogosa SL agar, Conda) for UCMA15228^T and
69 UCMA17102 strains, respectively. The agar plates were supplemented with 7 mg.L⁻¹ cycloheximide
70 and 100 mg.L⁻¹ pimaricin, and incubated at 10°C under anaerobic conditions (Anaerogen, Thermo
71 Scientific) for a month. After isolation, bacteria were routinely cultured on MRS (Difco) at pH 5.5,
72 supplemented with 5 g.L⁻¹ fructose and 0.5 g.L⁻¹ cysteine, and incubated at 30°C with 5 % CO₂.

73 **Phenotypic characterization**

74 Physiological and biochemical characteristics were assessed by standard methods. Briefly, the
75 nitrate reductase test was performed in Nitrate Broth with inverted Durham tubes, and zinc and
76 Griess reagents (Biomérieux, France). The growth of the two strains was tested with 49 different
77 carbon sources using Api 50 CHL strips (Biomérieux, France) according to the manufacturer's
78 instructions. Isomers of lactic acid formed from D-glucose were determined with Enzytec™ D-/L-
79 Lactic Acid kit (r-biopharm), according to the manufacturer's instructions. Fatty acid and
80 peptidoglycan analyses were carried out by the Identification Service of the DSMZ, Braunschweig,
81 Germany.

82 Sugar and organic acid contents were determined by HPLC (Waters Alliance HPLC system) at
83 40°C at 0.6 ml/min on a C18 Carbomix H-NP 5 column with 5mM sulfuric acid as mobile phase.
84 Sugars and organic acids were monitored with the FID and the PAD (210 nm) detectors at 30°C,
85 respectively. HPLC data were also used to validate the heterofermentative metabolism of
86 UCMA15228^T and UCMA17102 strains.

87 The optimal pH and temperature ranges for growth were assessed at pH 2.0, 2.5, 3.0, 3.5, 4.0, 4.5,
88 5.0, 5.5, 6.0, 6.5 and 7.0, and at 5, 10, 15, 20, 22.5, 25, 27.5, 30 and 37°C, respectively. Tolerance
89 towards NaCl (1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0, 4.5 and 5.0 % w/v) and ethanol content (2, 4, 6, 8, 10,
90 12, 14, 16 and 18 % v/v) was also checked. All these tests were performed in tubes containing 3 ml
91 of MRS supplemented with 20 % apple juice and 0.05 % cysteine, and inoculated at 1% (v/v) with
92 fresh cultures for 72 h. For testing the temperature range, assays were performed under both aerobic
93 and anaerobic conditions. For all the other tests, they were performed at 30°C supplemented with
94 5% CO₂, with no NaCl and ethanol for testing pH, with no ethanol at pH 5.5 for testing NaCl, and
95 with no NaCl at pH 5.5 for testing ethanol.

96 **Phylogenetic and fingerprinting analyses**

97 DNA amplification of the 16S rRNA gene was performed directly on colonies in 30 µL containing
98 1X Phusion High Fidelity (Phusion High-Fidelity PCR Master Mix, Thermo Fisher, United States)
99 and 0.25 µM of both primers 16S_F (5'-AGAGTTTGATYMTGGCTC-3') and 16S_R (5'-
100 GGNTACCTTGTTACGACTT-3'). PCR was carried out as follows: an initial denaturation step at
101 98°C for 10 min, 35 cycles composed of a denaturation step at 98°C for 10 s, an annealing step at
102 54°C for 20 s and an amplification step at 72°C for 45 s, and final extension at 72°C for 5 min. The
103 *pheS* gene was also amplified using primers Oeno_PheS_F (5'-TGGGTGGTAACACGATAA-3',
104 targeting the upstream area of the *pheS* gene) and Oeno_PheS_R (5'-
105 CCMARACCAAARGCAAACC-3', slightly modified from [13]). The PCR conditions were the
106 same as described above except for an annealing temperature of 57°C and an amplification step

107 reduced to 30 s. PCR product purification and Sanger sequencing were carried out at GATC
108 Biotech (Germany). The closest recognized relatives of the isolates were determined by performing
109 BLAST and Sequence Match (RDP) searches, and the sequences of closely related species were
110 retrieved from the DDBJ database. Multiple alignments and manual cleaning (deletion of the extra
111 beginning and ending sequences to homogenize the alignment) of the sequences and maximum
112 likelihood (ML) phylogenetic trees were carried out with MEGA7 [9] with the appropriate
113 substitution model for the ML option selected [7] and 1,000 bootstrap replications. The 16S rRNA
114 and *pheS* gene sequences of the closest LAB type strains used for the phylogenetic analysis were
115 extracted from the genomes when available (using RNAmmer [10] for 16S rRNA gene sequences)
116 or obtained from the Genbank database.

117 Species-specific PCR primers *Osic_16S_F* (5'-TCTTCGGAGTGACGCCTAACT-3') and
118 *Osic_16S_R* (5'-GACCGACATGTGTCAGAC-3') for the novel species were designed based on
119 the 16S rRNA gene sequences. The specificity of the primers was confirmed by PCR using genomic
120 DNA from *Oenococcus* sp. strains (Table S1). Universal primers targeting the 23S rRNA gene of
121 all bacteria (500-bp PCR product) were also used as an internal PCR control (Cousin *et al.*,
122 submitted). PCR amplification was performed using 15 µl of a mixture containing 1× DreamTaq
123 Green PCR Master Mix (Thermo Fisher Scientific), 250 nM of each primer and 5 ng of template
124 DNA. The PCR cycling program consisted of one cycle of 95°C for 3 min; 35 cycles of 95°C for 15
125 s, 50°C for 15 s and 72°C for 15 s; and a final extension step at 72°C for 5 min.

126 In addition, genotypic differentiation was assessed by multiplex randomly amplified polymorphic
127 DNA (RAPD) using the *Coc* and *On2* primers as previously described [15], with an annealing
128 temperature of 29°C as previously described [21].

129 **Genome sequencing**

130 Genomic DNA was extracted from 10 mL stationary phase cultures using the PowerFood microbial
131 DNA kit (Mobio) with slight modifications from the manufacturer's instructions for the lysis step.

132 Briefly, the bacterial pellet was resuspended in 450 µl PF1 solution and transferred into a sterile
133 2ml microtube containing 0.1 mm diameter zirconium beads. Mechanical lysis was performed using
134 a MM200 mixer mill (Retsch) for 5 min at 25 Hz. The amount and quality of isolated genomic
135 DNA was verified using a NanoDrop spectrophotometer, Quant-it PicoGreen dsDNA assay kit and
136 gel electrophoresis.

137 The genome of strain UCMA15228^T was completely sequenced using a PacBio RSII single-
138 molecule real-time (SMRT) sequencing with a 10 kb library at Genoscreen (Lille, France). *De novo*
139 assembly of sequencing reads was performed through the HGAP (hierarchical genome assembly
140 process) protocol version 2.0 in SMRT Analysis version 2.3.0 (Pacific Biosciences, USA). The
141 genome was annotated by using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline
142 (PGAAP) version 4.5.

143 The average nucleotide identity (ANI) and DNA G + C content values were estimated with
144 orthologous average nucleotide identity (OrthoANI) and original ANI [11], digital DNA-DNA
145 hybridization (DDH) values were estimated using *in silico* genome-to-genome comparison
146 Genome-To-Genome Distance Calculator (GGDC) V.2.1 using the recommended BLAST+
147 alignment and formula 2 (identities/HSP length) [12]. These values were calculated for
148 UCMA15228^T against *O. oeni* PSU-1, and against the type strains *O. oeni* NCDO1674^T,
149 *O. kitaharae* NRIC0645^T and *O. alcoholitolerans* UFRJ-M7.2.18^T.

150 **Bacterial cell morphology**

151 The bacterial cells were rinsed with physiological water, and fixed with 1% glutaraldehyde in
152 phosphate buffer (0.1 M, pH 7.0) for 5 days at 4°C. During this fixation, the cells were sedimented
153 on Thermanox® coverslip coated with poly-L-lysine. The cells were rinsed in phosphate buffer (0.1
154 M, pH 7.0) again. The cells were then dehydrated through successive baths of ethanol (70 to 100%),
155 and critical point dried (CPD 030 LEICA Microsystem). The cells were sputtered with platinum and
156 observed with the scanning electron microscope JEOL 6400F. Images were processed with the

157 public-domain image processing and analysing program Fiji. The measures of bacterial cell size
158 were performed on 20 images of 20 cells each.

159 **Accession numbers**

160 The GenBank/EMBL/DDBJ sequence accession numbers are as follows: MH384882 and
161 MH384883 for the 16S rRNA gene sequences of strains UCMA15228^T and UCMA17102,
162 respectively; MH392191 and MH392192 for the *pheS* gene sequences of strains UCMA15228^T and
163 UCMA17102, respectively; and CP029684 for the complete genome of strain UCMA15228^T.

164

165 **RESULTS AND DISCUSSION**

166 **Phylogenetic analysis**

167 The 16S rRNA gene sequence analysis revealed that the designated type strain UCMA15228^T
168 formed a tight monophyletic branch affiliated to the genus *Oenococcus*, in a robust sub-cluster
169 separated from its closest neighbours (Fig. 1 and S1). UCMA15228^T strain showed 16S rRNA gene
170 sequence identities of 97.4 % and 97.0 % with *O. kitaharae* NRIC0645^T and *O. oeni* NCDO1674^T,
171 respectively (Table S2). The 16S rRNA sequence identity of UCMA15228^T strain with its two
172 closest phylogenetic neighbours was close to 97%, the conservative threshold established for a
173 bacterial species delineation [17,19]. The other phylogenetic analysis, based on the *pheS* gene
174 sequence, confirmed this new branch (Fig. 2 and S2). Strain UCMA15228^T shared 74.2 % and
175 76.5 % identity of the *pheS* gene sequence with *O. kitaharae* NRIC0645^T and *O. oeni* NCDO1674^T,
176 respectively (Table S2). These identity scores are comparable to those described for
177 *O. alcoholitolerans*, the last designated species of *Oenococcus* sp. [1]. The 16S rRNA gene
178 sequences of the two strains, UCMA15228^T and UCMA17102 shared 100 % identity. Nonetheless,
179 two SNPs were found between the *pheS* gene sequences of the two strains (Table S2), which also
180 displayed different RAPD (Fig. S3) patterns, suggesting a non-clonal origin of the strains (Fig. S3).
181 This assertion is confirmed by the fact that the two strains have been isolated from different cider

182 samples, at two distinct producers in Normandy about 50 km apart with no known history of
183 interactions.

184 **Species-specific PCR for *Oenococcus sicerae* sp. nov.**

185 A species-specific primer pair (Osic_16S_F/R) was designed from r16S sequence multiple
186 alignments of *Oenococcus* spp. Genomic DNA of several oenococci were used as templates for
187 PCR amplification using universal and species-specific primer pairs (Table S1). The universal
188 primers, used as an internal PCR control, gave a 500 bp positive signal for all the tested bacteria
189 (Fig. S4), as expected. A single species-specific band of 134 bp was observed for *O. sicerae* sp.
190 nov. (Fig. S4), with no cross-reaction against the other species of *Oenococcus* spp. (Fig. S4 and
191 Table S1). This result confirms the divergence of these new members of the genus *Oenococcus*.
192 This PCR method may constitute an efficient tool for their rapid identification in future works.

193 **General taxonomic genome features of *Oenococcus sicerae* sp. nov. UCMA15228^T**

194 The complete genome sequence of strain UCMA15228^T was obtained using the PacBio RSII. A
195 library, with inserts of 10 kb, was sequenced, and 110,082 polymerase reads were generated.
196 Sequence processing and *de novo* assembly were performed using 205,930 postfiltered subreads
197 with an average read length of 9,560.8 bp, resulting in a unique contig. The complete genome
198 sequence of UCMA15228^T consisted of 1,684,519 bp with an average coverage of 880× and a G+C
199 mol% of 40.35. It contains 1,663 coding genes and 53 predicted RNA genes.

200 We compared the genome characteristics and sequence of strain UCMA15228^T to other related
201 species (Tables 1 and S3). The orthoANI and original values between *O. sicerae* sp. nov.
202 UCMA15228^T and *O. oeni* NCDO1674^T were of 73.72 % and 73.35 %, respectively (Table 1),
203 which is far below the proposed threshold of 95–96% for species delineation [11,16]. The GGDC
204 value (isDDH) between these strains obtained by the recommended formula 2 (identities/HSP
205 length) was of 17.7 % [15.6–20.0 %], which is also clearly below the boundary of 70 % for species
206 circumscriptions [20]. The calculated probability that isDDH is >70 % was of 0 %. An isDDH

207 value of 22.6 % was obtained with formula 1 (HSP length/total length) and of 20.8 % with formula
208 3 (identities/total length), supporting the affiliation of strain UCMA15228^T to a single species. The
209 OrthoANI, original ANI and isDDH values between strain UCMA15228^T and the other *Oenococcus*
210 sp. strains varied from 70.08 to 73.72 %, 69.62 to 73.35 %, and 17.5 to 19.5 % respectively (Table
211 1), which is clearly lower than the generally accepted cut-off threshold values of 95–96% and 70%
212 for delineation of bacterial species, confirming the authenticity of the novel species.

213 **Phenotypic and chemotaxonomic characteristics of *O. sicerae* sp. nov.**

214 Strains are heterofermentative, produce lactic acid, carbon dioxide and ethanol or acetic acid from
215 D-glucose. D- and L-lactic acid are produced in the ratio 9:1. Nitrate is not reduced. The major
216 cellular fatty acids (>10% of the total fatty acids) of UCMA15228^T strain were C 16:0 (39.52%),
217 C 18:1 ω 9c (40.21%) and C 19:0 cyclo ω 10c (12.46%). The overall fatty acid profile of
218 UCMA15228^T strain is presented in Table S4. The total hydrolysate (100 °C, 4N HCl, 16 h) of
219 UCMA15228^T strain contained the amino acids alanine, serine, glutamic acid and lysine, while the
220 analysis of partial hydrolysates (100 °C, 4N HCl, 45 min) revealed the presence of the
221 peptidoglycan type A3 α (L-Lys – L-Ser – L-Ala), corresponding to type A11.13 (
222 www.peptidoglycan-types.info). Growth profiles and phenotypic features of the novel species and
223 its phylogenetically related species are listed in Table 2. In addition, the decarboxylation of L-
224 malate into L-lactate (malolactic fermentation) was investigated by using HPLC. Both *O. sicerae*
225 strains were able to convert L-malate into L-lactate when inoculated in apple juice at pH 4
226 (Fig. S5). The genes responsible for this malolactic conversion have been found in the genome of
227 UCMA15228^T and are organised in an operon similar to that of *O. oeni* [2]. This operon is
228 composed of three genes involved in the malolactic reaction: *mleA*, encoding the malolactic enzyme
229 (responsible for the conversion of malic acid into lactic acid), *mleP*, encoding the malate permease
230 (responsible for the transport of malate into the cell) and *mleR*, encoding the LysR-type regulatory
231 protein for these two downstream genes.

232 **SEM morphology of the new species *O. sicerae***

233 Strains UCMA15228^T and UCMA17102 cells were ellipsoidal cocci, in couples, chains or piles
234 (Figs. 3 and S6). In comparison, *O. oeni* NCDO1674^T appeared almost exclusively in pairs in our
235 study. The “pile” phenotype of *O. sicerae* was also visible at a macroscopic scale where cellular
236 mass were observable in broth cultures, especially for strain UCMA17102.

237

238 Based on the phenotypic, genomic and phylogenetic data obtained in this study we propose the new
239 species *Oenococcus sicerae* for which the type strain UCMA15228^T (= DSM107163^T, = CIRM-
240 BIA2288^T) is designated.

241 The formal proposal of the species *Oenococcus sicerae* is given in Table 3 with the taxonumber
242 TA00560.

243

244 **Acknowledgments**

245 This work was supported by the region Basse-Normandie through the grant "Retour Jeune
246 Chercheur" 14P06493. The authors also thank all the cider producers for providing the cider
247 samples during the sample collection in Normandy, France, 2016.

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- 310

311 **FIGURE LEGENDS**

312

313 **Fig. 1.** Phylogenetic tree showing the position of the *Oenococcus sicerae* sp. nov. strains based on
314 the 16S rRNA gene sequences (1,463 bp). The tree was inferred by using the Maximum Likelihood
315 method based on the Kimura 2-parameter model [8] with MEGA7 [9]. Bootstrap values (>70 %)
316 based on 1,000 repetitions are shown. The sequence of *Lactococcus lactis* DSM 20481^T was used as
317 outgroup. Bar 5 % estimated sequence divergence.

318

319 **Fig. 2.** Phylogenetic tree showing the position of the *Oenococcus sicerae* sp. nov. strains based on
320 the *PheS* gene sequences (1,069 bp). The tree was inferred by using the Maximum Likelihood
321 method based on the General Time Reversible model [14] with MEGA7 [9]. Bootstrap values
322 (>70 %) based on 1,000 repetitions are shown. The sequence of *Lactococcus lactis* DSM 20481^T
323 was used as outgroup. Bar 20 % estimated sequence divergence.

324

325 **Fig. 3.** Photograph taken by SEM of *O. sicerae* sp. nov. UCMA15228^T cultured in MRS
326 supplemented with 20 % apple juice, pH 5.

327 **Table 1.** Ortho Average Nucleotide Identity (OrthoANI), original ANI and GGDC values (%) between *Oenococcus sicerae* sp. nov. and the
 328 other *Oenococcus* species

Species	Strain	<i>O. sicerae</i> sp. nov.	<i>O. oeni</i>	<i>O. oeni</i>	<i>O. kitaharae</i>	<i>O. alcoholitolerans</i>
		UCMA15228 ^T	NCDO1674 ^T	PSU-1	NRIC0645 ^T	UFRJ-M7.2.18 ^T
<i>O. sicerae</i> sp. nov.	UCMA15228 ^T	100				
		73.72 ^a				
<i>O. oeni</i>	NCDO1674 ^T	73.35 ^b	100			
		17.7 ^c				
		73.56	99.66			
<i>O. oeni</i>	PSU-1	73.34	99.63	100		
		17.8	97.9			
		72.62	72.15	71.88		
<i>O. kitaharae</i>	NRIC0645 ^T	71.99	71.61	71.51	100	
		17.5	17.6	17.6		
		70.08	69.79	69.99	70.08	
<i>O. alcoholitolerans</i>	UFRJ-M7.2.18 ^T	69.62	69.59	69.81	69.73	100
		19.5	20.6	21.9	20.3	

329 ^a OrthoANI values; ^b Original ANI values; ^c GGDC values.

330 **Table 2.** Differential phenotypic characteristics of the *O. sicerae* sp. nov. strains and the other *Oenococcus* species

Characteristics	<i>Oenococcus oeni</i>	<i>O. kitaharae</i>	<i>O. alcoholitolerans</i>	<i>O. sicerae</i> sp. nov.	
	[5]	[6]	[1]	UCMA15228 ^T	UCMA17102
Growth					
T °C range	15-30 ^b	20-30	20 - 40	5 - 30	5 - 30
Optimum growth T °C	22	30	30	25	25
pH range	3.0 - 6.5 ^b	5.0 - 7.5	4.0 - 7.5	4.0 - 7.0	4.0 - 7.0
Optimum growth pH	4.8	6.0 - 6.8	6.0 - 6.5	5.5 - 6.0	5.5 - 6.0
Max ethanol (%)	10.0	5.0	12.0	6.0	6.0
Max NaCl (%)	3.5 ^b	1.0	2.5	2.0	2.5
Malolactic fermentation	+	-	+	+	+
Acid production^a from:					
L-arabinose	+/-	-	+/-	-	-
D-ribose	ND	+	+/-	+	+
D-xylose	+/-	-	+/-	+	+
D-galactose	+/-	+	+/-	-	-
D-glucose *	+	+	+	+	+
D-fructose	+	+	+	+	+
D-mannose	+/-	+	+/-	+	-
Salicin	+/-	+/-	+/-	-	-
D-cellobiose	+/-	+/-	+/-	-	-

D-maltose	-	+	+/-	-	-
D-lactose	-	-	+/-	-	-
D-melibiose	+/-	+	+	+	-
Sucrose	-	-	+	+	+
D-trehalose	+	+	-	+	-
D-raffinose	-	+	+	+	-
Gluconate potassium	+	+	-	+	+

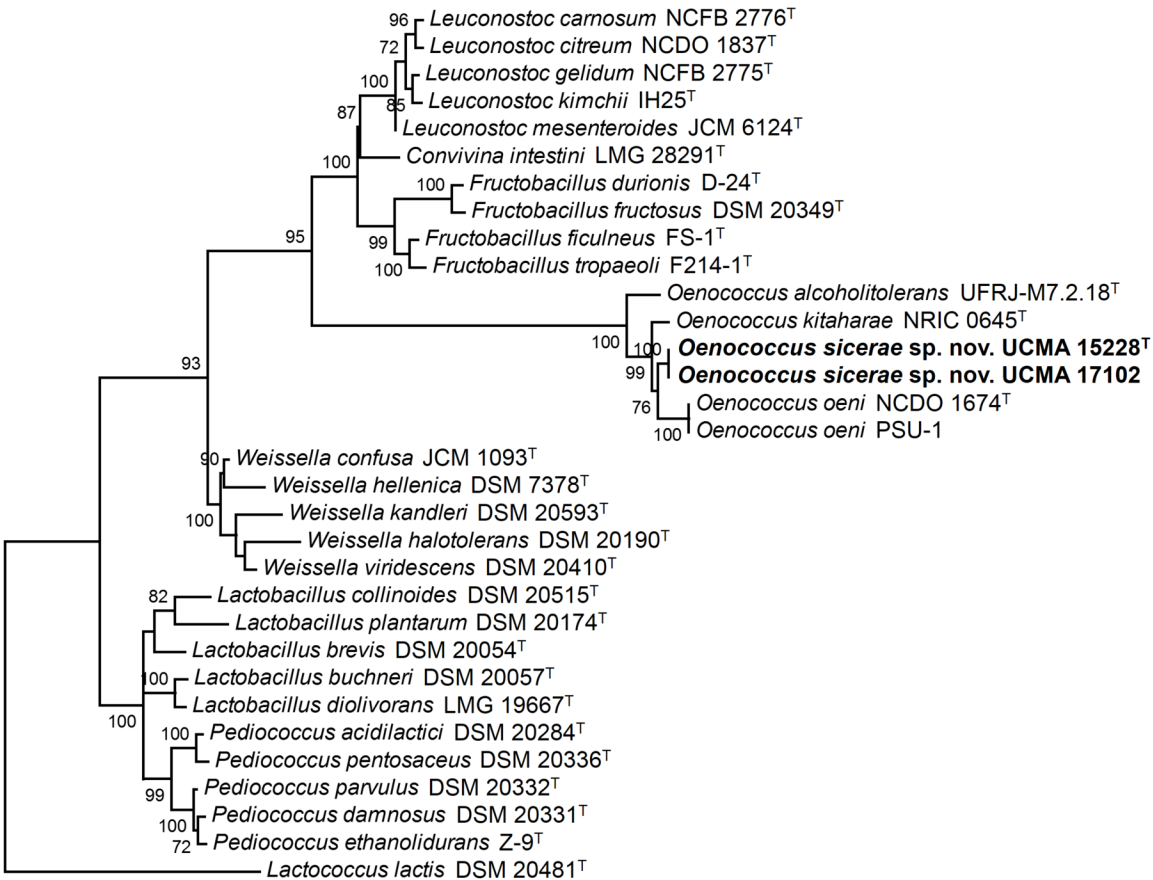
331 ^a + Acid production, - no acid production, +/- strain dependent, ND not determined. ^b Data obtained in this study. * D-glucose was negative for
332 strain UCMA17102 with API50CHL test but D-glucose was shown to be used by this strain by HPLC analysis.

Table 3. Description of *Oenococcus sicerae* sp. nov. according to Digital Protologue TA00560 assigned by the www.imedea.uib.es/dprotologue website.

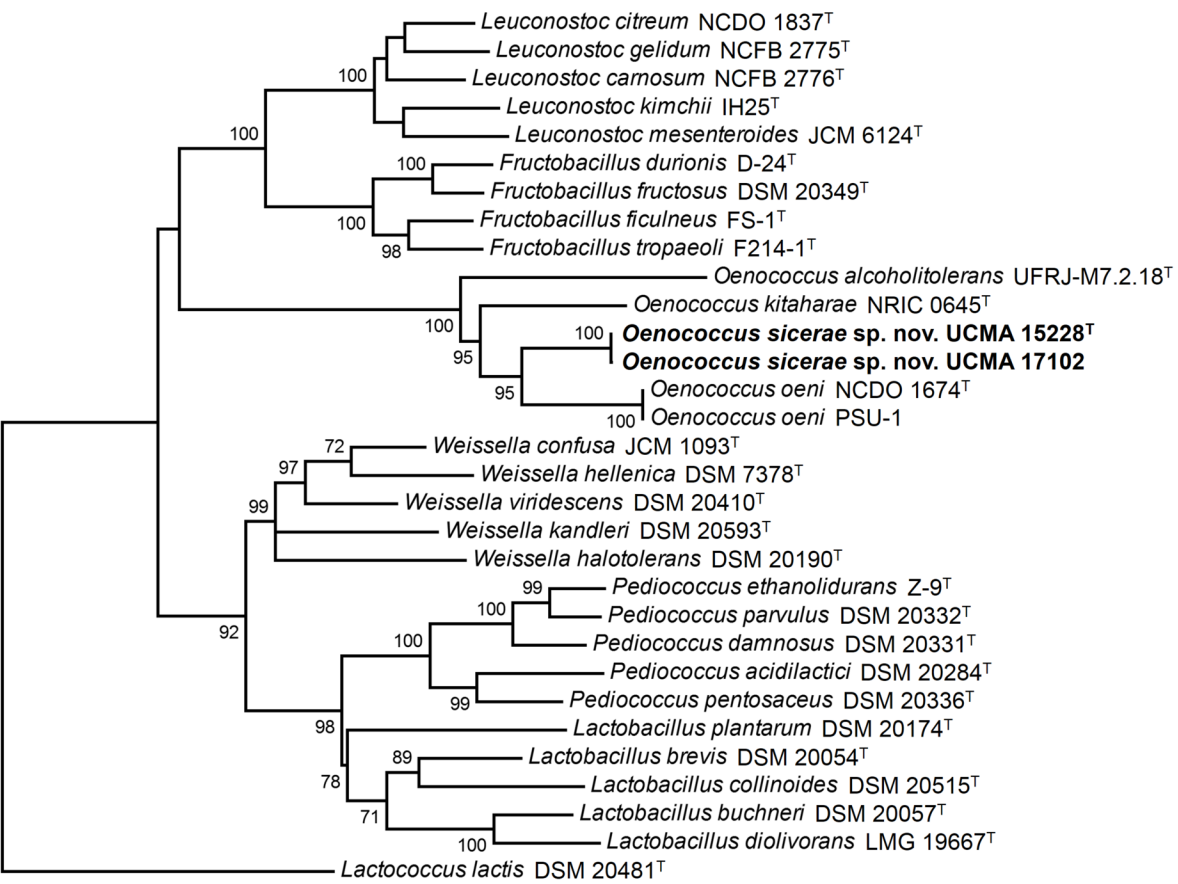
TAXONUMBER	TA00560
SPECIES NAME (Give the binomial species name)	<i>Oenococcus sicerae</i>
GENUS NAME	<i>Oenococcus</i>
SPECIFIC EPITHET	sicerae
SPECIES STATUS	sp. nov.
SPECIES ETYMOLOGY	si'ce.rae. L. fem. gen. n. sicerae of cider
DESIGNATION OF THE TYPE STRAIN	UCMA15228
STRAIN COLLECTION NUMBERS	DSM107163 = CIRM-BIA2288
16S rRNA GENE ACCESSION NUMBER	MH384882
ALTERNATIVE HOUSEKEEPING GENES:GENE [ACCESSION NUMBER]	pheS [MH392191]
GENOME ACCESSION NUMBER [RefSeq]	CP029684
GENOME STATUS	Complete
GENOME SIZE	1,684,519
GC mol %	40.35
DATA ON THE ORIGIN OF THE SAMPLE FROM WHICH THE STRAIN HAD BEEN ISOLATED	
COUNTRY OF ORIGIN	France
REGION OF ORIGIN	Normandie, Calvados
DATE OF ISOLATION	17/02/2016
SOURCE OF ISOLATION	Apple juice in fermentation (cider)
SAMPLING DATE	11/02/2016
GEOGRAPHIC LOCATION	Calvados
pH OF THE SAMPLE	4.05
NUMBER OF STRAINS IN STUDY	2
SOURCE OF ISOLATION OF NON-TYPE STRAINS	Apple juice in fermentation (cider)
GROWTH MEDIUM, INCUBATION CONDITIONS [Temperature, pH, and further information] USED FOR STANDARD CULTIVATION	- MRS (55 g/L, difco BD™ 288130) supplemented with 5 g/L D-Fructose and 0.5 g/L cysteine-HCl - pH 5.5 - 30°C in air with 5% CO ₂ - Growth on agar medium is enhanced under anaerobic conditions
ALTERNATIVE MEDIUM 1	MRS supplemented with 0.5 g/L cysteine-HCl
CONDITIONS OF PRESERVATION	Liquid medium mixed with 15% (v/v) glycerol and stored at -80°C Freeze-dried
GRAM STAIN	Positive
CELL SHAPE	Coccus
CELL SIZE (length or diameter)	0.5-0.8 by 0.3-0.6 µm
MOTILITY	Nonmotile
SPORULATION (resting)	None

cells)	
TEMPERATURE RANGE	5-30
LOWEST TEMPERATURE FOR GROWTH	5
HIGHEST TEMPERATURE FOR GROWTH	30
TEMPERATURE OPTIMUM	25
LOWEST pH FOR GROWTH	4
HIGHEST pH FOR GROWTH	7
pH OPTIMUM	5.5 - 6.0
pH CATEGORY	Acidophile (optimum < 6)
LOWEST NaCl CONCENTRATION FOR GROWTH	0
HIGHEST NaCl CONCENTRATION FOR GROWTH	2.5
SALINITY OPTIMUM	0-1.5
RELATIONSHIP TO O₂	Facultative aerobe
O₂ CONDITIONS FOR STRAIN TESTING	Air supplemented with 5% CO ₂ or anaerobiosis
CARBON SOURCE USED [class of compounds]	Carbohydrates, organic acids
CARBON SOURCE USED [specific compounds]	D-glucose, D-fructose, D-ribose, sucrose, D-xylose, L-xylose, D-lyxose, potassium gluconate and 5-ketogluconate potassium
CARBON SOURCE NOT USED [specific compounds]	glycerol, erythritol, D-arabinose, L-arabinose, D-adonitol, methyl-βD-xylopyranoside, D-galactose, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl-αD-mannopyranoside, N-acetylglucosamine, amygdalin, arbutin, salicin, D-cellobiose, D-maltose, D-lactose, inulin, D-melezitose, starch, glycogen, xylitol, gentiobiose, D-turanose, D-tagatose, D-fucose, L-fucose, D-arabitol, L-arabitol and 2-ketogluconate potassium
CARBON SOURCE VARIABLE [specific compounds]	D-mannose, D-melibiose, D-trehalose, D-raffinose and methyl-αD-glucopyranoside
Positive tests with API	D-fructose, D-ribose, sucrose, D-xylose, L-xylose, D-lyxose, potassium gluconate and 5-ketogluconate potassium
Negative tests with API	glycerol, erythritol, D-arabinose, L-arabinose, D-adonitol, methyl-βD-xylopyranoside, D-galactose, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl-αD-mannopyranoside, N-acetylglucosamine, amygdalin, arbutin, salicin, D-cellobiose, D-maltose, D-lactose, inulin, D-melezitose, starch, glycogen, xylitol, gentiobiose, D-turanose, D-tagatose, D-fucose, L-fucose, D-arabitol, L-arabitol and 2-ketogluconate potassium
Variable tests with API	D-glucose, D-mannose, D-melibiose, D-trehalose, D-raffinose and methyl-αD-glucopyranoside
COMMERCIAL KITS USED?	API50CHL
ENERGY METABOLISM	Heterofermentative
OXIDASE	Negative
CATALASE	Negative
POSITIVE TESTS	Gas production, malolactic fermentation, hydrolysis of esculin
NEGATIVE TESTS	Gas formation with nitrate, reduction of nitrate
MAJOR FATTY ACIDS	C 16:0, C 18:1ω9c, C 19:0 cyclo ω10c
PEPTIDOGLYCAN TYPE	A3α (L-Lys – L-Ala – L-Ser)

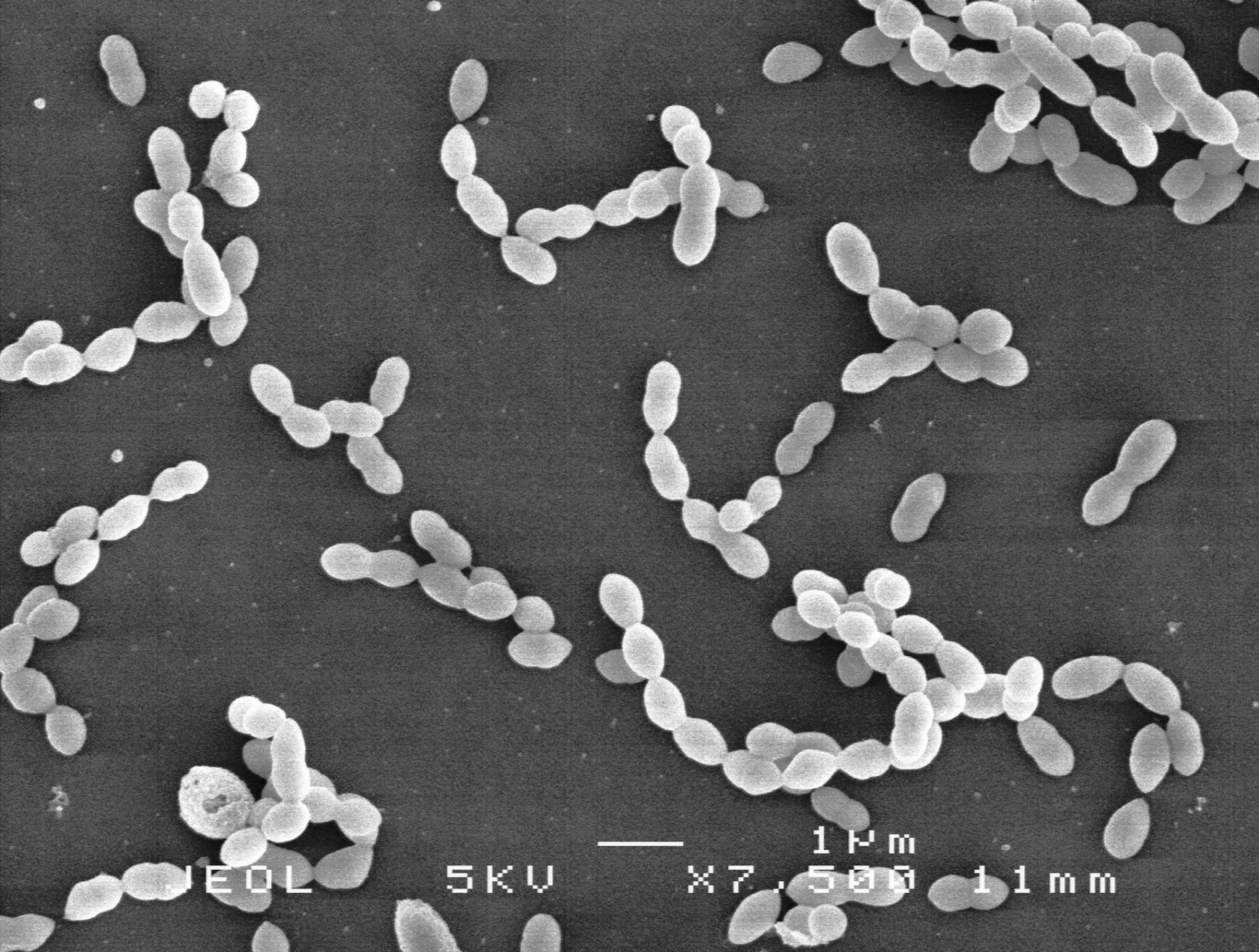
BIOSAFETY LEVEL	1
BIOTIC RELATIONSHIP	Free-living
KNOWN PATHOGENICITY	None



0.05



0.2



JEOL

5KV



1 μ m

X7,500

11mm