

1 ***Wickerhamiella verensis* f.a. sp. nov., a novel yeast species isolated from**
2 **subsoil groundwater contaminated with hydrocarbons and from a human**
3 **infection**

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25 **Keywords:** *Wickerhamiella*, *verensis*, hydrocarbon, clinical

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27 **Running title:** *Wickerhamiella verensis* isolated from hydrocarbon
28 contaminated samples and clinical environment.

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30 **Repositories:** The GenBank accession numbers for the D1/D2 LSU rRNA gene
31 and ITS-5.8S rDNA region sequences of strain YEALI 107^T (=CECT 12028^T)
32 are EF141077 and EU818715, respectively.

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35 **Abstract**

36 Yeast strains belonging to a novel anamorphic yeast species were isolated
37 from subsoil groundwater contaminated with hydrocarbons in a metal working
38 factory located in Northern Spain, and from a human infection in the USA.
39 Comparison of ITS sequences between the isolates revealed 0.2% divergence
40 between the Spanish isolates and 0.46% divergence between those and the
41 USA isolate. Phylogenetic analysis based on the D1/D2 domains of the LSU
42 rRNA gene showed that these isolates belong to the *Wickerhamiella* clade and
43 *W. sorbophila* and *W. infanticola* are their closest relatives. Sequence
44 divergence between the new isolates and *W. sorbophila* and *W. infanticola* is
45 1.97 and 1.79 %, respectively. The isolates in the new species are not
46 fermentative and pseudohyphae were not produced. Sexual reproduction was
47 not observed for individual isolates or in mixtures of isolates. Conjugation
48 between the isolates in the new species and close relatives *W. sorbophila* and
49 *W. infanticola* was not observed. These data support the proposal of
50 *Wickerhamiella verensis* as a novel species, with CECT 12028^T as the holotype.

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69 **Main text**

70 The genus *Wickerhamiella* was erected in 1973 (1) to accommodate yeast
71 strains forming very small vegetative cells and showing conjugation and
72 ascospore formation. Based on these characteristics four new species *W.*
73 *australiensis*, *W. occidentalis*, *W. lipophila* and *W. cacticola* were later
74 described (2, 3). Phylogenetic analysis of D1/D2 LSU rRNA gene sequences
75 placed *W. domercqiae*, the type species in the genus *Wickerhamiella*, in a clade
76 together with several *Candida* species but separated from the other four
77 species of the genus (4). Later, based on D1/D2 LSU rRNA gene sequences,
78 18 new species transferred from the genus *Candida* were described (5). The
79 genus *Wickerhamiella* comprises now more than 40 species
80 (www.Mycobank.org). The ecology of the genus is not well established, most
81 species have been isolated from flowers and associated insects, fruit, wineries
82 or distilleries, but some have been recovered from human sources. Most
83 species appear to be endemic to tropical regions and Asia, but other species
84 have a cosmopolitan distribution.

85 During a survey of the microorganisms present in a hydrocarbon-
86 contaminated factory in Northern Spain, 78 yeasts were isolated and identified.
87 After the identification process, two strains YEALI 107 (=CECT 12028) and
88 YEALI 108 (CECT 12036) could not be assigned to a known yeast species. In
89 addition, a strain (CDC 11278) isolated in Atlanta, Georgia USA from an infant
90 with a blood infection also proved to be a member of the new species. In this
91 study, we present the phenotypic characterization and phylogenetic analyses of
92 the strains representing the novel asexual species, which we propose as
93 *Wickerhamiella verensis*, a new species in the *Wickerhamiella* clade.

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95 **Collection site and isolation of yeasts**

96 Norther Spain samples

97 Samples collection site were subsoil groundwater of an old metal working
98 factory in Vera de Bidasoa (Spain) (Longitude -1.6830042, Latitude
99 43.2808504) polluted by different mixtures of hydrocarbons released over
100 several decades of industrial activity. Vera de Bidasoa is located in Northern
101 Spain, and the weather is oceanic temperate, strongly influenced by the
102 Cantabrian Sea (Bay of Biscay) with abundant rains, mist and drizzle but

103 relatively warm. The annual average temperature lies between 8.5°C and
104 14.5°C and annual average precipitation ranges from 1,100 to 2,500 mm. In the
105 metal working factory, four zones of contamination were identified: Z1, fuel oil
106 spilled from heating systems; Z2, lubricant-oil leaked from metal working units;
107 Z3, diesel fuel spilled from underground tanks; and Z4, perimeter with mixtures
108 of the three contaminants. The hydrocarbon-polluted areas were initially treated
109 using physico-chemical techniques followed by a bioremediation approach
110 based on the injection of an oleophilic fertilizer (S200, IEP
111 www.iepeurope.com), diluted hydrogen peroxide, and a surfactant (Bioversal
112 HC, IEP). Yeasts were isolated before, during and after the bioremediation
113 process using a synthetic medium for hydrocarbon degradation (DM medium
114 0.3% NH₄NO₃; 0.05% MgSO₄·7H₂O; 2% CaCl₂·2H₂O; 0.007% K₂HPO₄; 0.05%
115 KH₂PO₄; 2% agar) supplemented with 2% fuel oil, 2% lubricant oil or 2% diesel
116 (Repsol, S.A., Spain) as sole carbon source. Information about bacterial counts
117 and hydrocarbon degradation along the bioremediation process are found in
118 Menendez-Vega *et al.* (6). Seventy-eight yeast strains were isolated from three
119 contaminated areas Z1, Z2 and Z4 before, during and after the bioremediation
120 process (Table 1).

121 USA samples

122 An unidentified strain (CDC 11278) was received from the U.S. Center for
123 Disease Control and Prevention, Atlanta, Georgia USA. The strain had been
124 isolated from an infant suffering from a blood infection.

125

126 **Ecology of yeast species found in subsoil groundwater samples from** 127 **Vera de Bidasoa, Spain**

128 During this study, 78 yeast strains pertaining to species different from *W.*
129 *verensis* were isolated and identified from a hydrocarbon contaminated factory
130 in Vera de Bidasoa, Spain. Most of the strains pertained to the species *Candida*
131 *viswanathii*, and 6 other yeast species (Table 1) were represented with less
132 strains. Most of these yeast species contain strains isolated from clinical or
133 human environment. The most represented species *C. viswanathii*, isolated
134 from a fatal case of meningitis in India and subsequently isolated in 1962 from
135 sputum, is considered an opportunistic pathogen (7). Moreover, strains in
136 species *C. parapsilosis*, *Rhodotorula mucilaginosa*, *Meyerozyma guilliermondii*

137 and *Lodderomyces elongisporus* are commonly associated with fungemia (8).
138 The new species *W. verensis* also includes environmental and clinical strains.

139

140 **Sequencing and phylogenetic analysis**

141 D1 and D2 domains of the nuclear LSU rRNA gene were amplified by PCR
142 using the primers NL-1 and NL-4 (9). PCR products were cleaned and
143 sequenced. Sequences were edited and assembled using MEGA X (10) and
144 then subjected to a sequence similarity search using the BLASTN tool in NCBI
145 to identify them by sequence homology of described taxa (Table 1). The D1/D2
146 LSU rRNA gene sequence of CECT 12028^T as the holotype was included in a
147 multiple alignment generated using MEGA X, which included described species
148 of the *Wickerhamiella* clade and selected reference species (11). A
149 phylogenetic tree was inferred using the Maximum Likelihood method in MEGA
150 X. Sequence HQ111062 representing the D1/D2 LSU rRNA gene of *Starmerella*
151 *bombicola* was used as outgroup (11). Additionally, the ITS1-5.8S-ITS2 rRNA
152 region of the new isolates and closely related species was amplified and
153 sequenced using primers ITS1 and ITS4 (12). Sequences were aligned using
154 MEGA X and nucleotide substitutions were determined.

155

156 **Species delimitation**

157 *Wickerhamiella verensis* strains CECT 12028^T and CECT 12036 had the
158 same D1/D2 nucleotide sequence. The clinical isolate, CDC 11278, differed
159 from the type of *W. verensis* by 3 substitutions and 1 deletion for D1/D2. BLAST
160 alignment of the D1/D2 LSU rRNA sequences showed 11 substitutions between
161 neighbouring species *W. verensis* and *W. sorbophila*, and 10 substitutions
162 between *W. verensis* and *W. infanticola* in the 577 nucleotide positions
163 examined.

164 The ITS1-5.8S-ITS2 rRNA sequences alignment showed 1 substitution
165 between the Spanish strains (433 bp, including PCR primers) and by 2
166 substitutions in case of the USA clinical isolate. The ITS1-5.8S-ITS2 rRNA
167 sequences alignment of *W. verensis* CECT 12028^T with closely related
168 *Wickerhamiella* species (446 positions) showed 12 substitutions between *W.*
169 *verensis* and *W. sorbophila* and 9 substitutions between *W. verensis* and *W.*
170 *infanticola*. The nucleotide substitutions found between *W. verensis* and *W.*

171 *infanticola* or *W. sorbophila* indicate that *W. verensis* is a new species different
172 from its closest relatives.

173 Figure 1 shows the phylogenetic position of CECT 12028^T and related
174 species based on LSU D1/D2 sequences. *W. verensis* is closely related to
175 isolate SJ-1. D1/D2 LSU alignment (598 positions) shows that they differ in one
176 nucleotide substitution and 2 gaps, indicating that they probably pertain to the
177 same species. The subclade constituted by *W. verensis*, *W. sorbophila* and *W.*
178 *infanticola* is related to isolate *Candida* sp. SN-102 and *W. siamensis*. Strains
179 SJ-1 and SN-102 have been isolated from sea surface microlayer in Taiwan,
180 two isolates from *W. verensis* and *W. sorbophila* were isolated from industrial
181 waste water, and one isolate from *W. verensis* and *W. infanticola* were from
182 human source.

183

184 **Phenotypic characterization of the yeasts**

185 Yeast strains were maintained for short periods on GPYA (2% glucose,
186 0.5% peptone, 0.5% yeast extract and 2% agar). For long-term storage, yeasts
187 were frozen at -80°C in 15% glycerol or maintained as lyophilized preparations.
188 Morphological and physiological characterization of *W. verensis* CECT 12028^T
189 and closely related strains *W. sorbophila* NRRL Y-7921 and *W. infanticola*
190 NRRL Y-17858, was performed according to standard methods (13). Hydrolysis
191 of Tween 80 was tested on media devised by Sierra *et al.* (14). Cell morphology
192 was examined in cultures grown on malt extract agar (Difco) using a light
193 microscope (Nikon Eclipse E800). Media tested to detect sporulation in the
194 isolates included glucose-yeast extract-malt extract-peptone (YM) agar, potato
195 dextrose agar (PDA), restricted growth (RG) agar and yeast carbon base-
196 ammonium sulphate (YCBAS) agar (13). Strains were examined
197 microscopically for ascospore formation individually and as a group on the four
198 media at 15 °C and 25 °C.

199 The ability of the strains to mate was tested by mixing equal amounts of
200 young actively growing cells (2 d, 25 °C) from *W. verensis* CECT 12028^T, CECT
201 12036, CDC 11278, *W. sorbophila* NRRL Y-9721, *W. infanticola* NRRL Y-17858
202 onto slants of YM, 5% malt extract, RG and YCBAS agar media. Incubation was
203 at 15 °C and 25 °C for 6 weeks.

204 Table 2 shows the ability of Spanish yeast isolates to grow on different
205 hydrocarbons. All yeasts isolated from Spain were able to grow on lubricant oil
206 (isolation medium). The new species *W. verensis* was not able to grow on any
207 hydrocarbon tested. Table 3 shows the physiological differences between the
208 Spanish isolates of *W. verensis* and closest relatives *W. sorbophila* NRRL Y-
209 7921 and *W. infanticola* NRRL Y-17858. Sporulation media were observed for
210 two months, but neither asci nor ascospores were found. Mating experiments
211 revealed that neither conjugation nor ascospores were observed.

212

213 **Description of *Wickerhamiella verensis* f.a., sp. nov. Belloch, Pelaez,**
214 **Menendez-Vega, Sanchez & Kurtzman**

215 *Wickerhamiella verensis* (ve.ren'sis. N.L. fem. adj. *verensis* of Vera de Bidasoa,
216 a town in Navarra (Northern Spain).

217 In malt extract medium after 3 days at 25°C, cells are globose to ellipsoidal (1-2
218 x 1.5-3.5 µm), occur singly or in parent-bud pairs (Figure 1). After one month at
219 25 ° C, sediment is present. After one month on GPY agar at 25 ° C, colonies
220 are cream coloured, smooth and the margin is entire. No true hyphae or
221 pseudohyphae develop in Dalmau plate cultures. Conjugation and ascospore
222 formation is absent. Fermentation is absent. Assimilates D-glucose, D-
223 galactose, L-sorbose, sucrose, inulin, D-glucitol, D-mannitol, ethanol, succinate
224 and hexadecane. Does not assimilate cellobiose, lactose, maltose, melibiose,
225 trehalose, melezitose, raffinose, soluble starch, D-arabinose, L-arabinose, D-
226 ribose, L-rhamnose, D-xylose, methanol, glycerol, meso-erythritol, inositol,
227 ribitol, xylitol, galactitol, citrate, DL-lactate, D-gluconate, methyl-α-D-glucoside,
228 salicin, D-glucosamine, N-acetyl-D-glucosamine, saccharate, D-glucuronate
229 and L-arabinitol. Assimilates ethylamine and L-lysine but not nitrate, nitrite,
230 imidazole and glucosamine. No starch-like substance is produced. Urease
231 reaction is negative. Hydrolysis of Tween 80 is positive. Growth on vitamin free
232 medium is negative. Optimal growth temperature is 25°C, but growth at 37°C is
233 weak. Growth on 0.01% cycloheximide is positive, whereas growth on 0.1%
234 cycloheximide is negative. Acid formation on chalk agar is negative. Growth on
235 50% D-glucose and 10% NaCl / 5% glucose media is positive and growth on
236 1% acetic acid is negative.

237 The designated holotype of *Wickerhamiella verensis* sp. nov. is strain CECT
238 12028^T and the ex-type is CBS 10548^T. The holotype is preserved in a
239 metabolically inactive state (frozen in 15% glycerol at -80°C and lyophilised) in
240 the CECT collection of the University of Valencia, Spain. It was isolated from
241 subsoil water polluted with heavy lubricating oil in Vera de Bidasoa (Spain). The
242 MycoBank number is MB 833012.

243

244 **Funding information**

245 This work was supported by a grant from the Consejería de Educación y
246 Ciencia, Principado de Asturias, Spain (FC-05-IB-130).

247

248 **Acknowledgements**

249 We wish to thank Dr. José L. Rodríguez Gallego for providing the water
250 samples and for his useful suggestions. C.P.K thanks Mary E. Brandt, Shawn
251 Lockhart and Jeffrey O'Kelley, Mycology Branch, Centers for Disease Control
252 and Prevention, for providing the clinical isolate of *W. verensis*, and Christie J.
253 Robnett and Eleanor Basehoar for sequence determinations. Mention of trade
254 names or commercial products in this publication is solely for the purpose of
255 providing specific information and does not imply recommendation or
256 endorsement by USDA. The USDA is an equal opportunity provider and
257 employer.

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259 **Conflict of interest**

260 The authors declare that there are no conflicts of interest

261

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- 315
- 316

317 **Figure legends**

318 **Figure 1.** Phylogenetic placement of *Wickerhamiella verensis* among species of
319 the *Wickerhamiella* clade based on LSU rRNA gene D1/D2 sequences. The
320 tree was inferred using Maximum Likelihood analysis of 598 aligned positions
321 using the general Time Reversible model and a discrete Gamma distribution to
322 model evolutionary rate differences among sites. Bootstrap values are based on
323 1000 replicates and the outgroup species is *Starmerella bombicola*.

324

325 **Figure 2.** Budding cells of *Wickerhamiella verensis* CECT 12028 grown on malt
326 extract agar for 3 days at 25°C. Bar represents 5µm.

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328

Table 1.- Yeasts isolated from collection sites Z1, Z2, and Z4, before (A), during (D) and after (F) the bioremediation process. SN: number of samples taken from each area and YN: number of yeasts isolated in the different areas.

Species	collection site	bioremediation	SN	YN	BLAST
<i>Candida viswanathii</i>	Z1, Z2, Z4	A, D	6, 2, -2	27, 4, 3	100% U45752
<i>C. parapsilosis</i>	Z1, Z2, Z4	A, D	1, 2, 3	6, 7, 3	100% U45754
<i>Wickerhamiella verensis</i> sp. nov.	Z2	D	1	2	new <i>W. verensis</i>
<i>Rhodotorula mucilaginosa</i>	Z1, Z2, Z4	A, D, F	4, 1, 2	5, 1, 1	99% AF070432
<i>Yarrowia lipolytica</i>	Z2, Z4	A, D	1, 2	5, 2	100% AJ508570
<i>Rhodospidium toruloides</i>	Z1	D	1	2	99% AF444746
<i>Meyerozyma guilliermondii</i>	Z2	D	2	7	100% U45709
<i>Lodderomyces elongisporus</i>	Z1	D	1	3	99% U45763

Z1, fuel oil; Z2, lubricant-oil; Z3, diesel; Z4, mixture of Z1, Z2 and Z3

Table 2.- Hydrocarbon utilization spectrum for different yeast species isolated from the same collection sites.

Yeast species	Utilization of hydrocarbons ^a					
	naphthalene	fluorene	tetradecane	kerosene	diesel	octane
<i>Candida viswanathii</i>	v	+	+	-	v	v
<i>Candida parapsilosis</i>	v	+	+	-	v	v
<i>Lodderomyces elongisporus</i>	-	+	+	-	+	-
<i>Wickerhamiella verensis</i> sp. nov.	-	-	-	-	-	-
<i>Meyerozyma guilliermondii</i>	+	+	+	-	v	-
<i>Rhodospiridium toruloides</i>	+	+	+	-	+	-
<i>Rhodotorula mucilaginosa</i>	+	+	-	-	-	+
<i>Yarrowia lipolytica</i>	v	-	+	-	+	-

^a Results are presented as follows: +, positive; -, negative; v, variable: some isolates are positive, others negative.

Table 3.- Physiological properties differentiating *W. verensis* sp. nov. CECT 12028^T from phylogenetically related species *W. sorbophila* NRRL Y-7921^T and *W. infanticola* NRRL Y-17858^T.

Assimilation of	Strains		
	CECT 12028	NRRL Y-7921	NRRL Y-17858
inulin	+	-	-
sucrose	+	-	-
ethanol	+	-	-
glycerol	-	+	+
xylitol	-	+	+

Figure 1

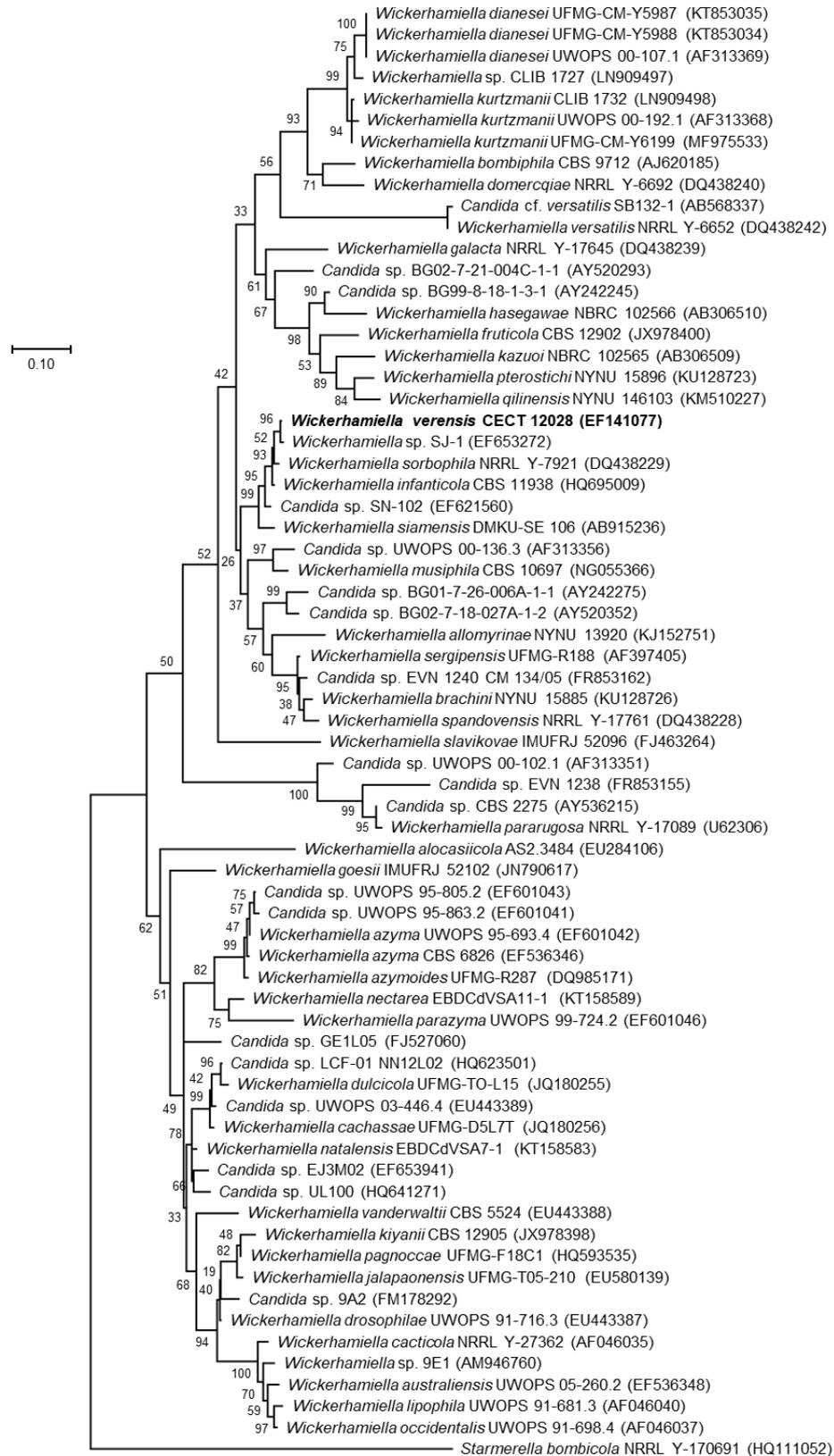


Figure 2

