Tenacibaculum dicentrarchi sp. nov., a marine bacterium of the family *Flavobacteriaceae* isolated from European sea bass

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A novel Gram-stain-negative rod-shaped gliding bacterial strain, designated 35/09^T, was isolated from diseased European sea bass (*Dicentrarchus labrax* L.) in Spain. Colonies were pale-yellow-pigmented with uneven edges and did not adhere to the agar. The DNA G + C content of the isolate was 31.3 mol%. 16S rRNA gene sequence analysis indicated affiliation to the genus *Tenacibaculum* (family *Flavobacteriaceae*, phylum 'Bacteroidetes'). Sequence similarities between the isolate and type strains of other members of the genus were 93.1–97.3 %. The major fatty acids (>5 % of the total fatty acids) were iso-C_{15:0} (24.8 %), iso-C_{15:0} 3-OH (18.0 %), anteiso-C_{15:0} (8.1 %), C_{15:1ω6c} (6.9 %) and iso-C_{15:1} (6.2 %). Genotypic and phenotypic data indicate that strain 35/09^T should be classified as a representative of a novel species in the genus *Tenacibaculum*, for which the name *Tenacibaculum dicentrarchi* sp. nov. is proposed; the type strain is 35/09^T (=CECT 7612^T=NCIMB 14598^T).

The genus *Tenacibaculum* proposed by Suzuki *et al.* (2001) belongs to the family *Flavobacteriaceae* (Reichenbach, 1992a, b; Bernardet *et al.*, 1996, 2002). It currently comprises 15 species isolated from a variety of marine sources: *Tenacibaculum maritimum* (type species) from diseased fish (Wakabayashi *et al.*, 1986); *T. ovolyticum* from fish eggs (Hansen *et al.*, 1992); *T. amylolyticum* from the surface of marine macroalgae and *T. mesophilum* from sponges (Suzuki *et al.*, 2001); *T. skagerrakense* from seawater (Frette *et al.*, 2004); *T. lutimaris*, *T. litoreum* and *T. aestuarii* from tidal flat sediment (Yoon *et al.*, 2005; Choi *et al.*, 2006; Jung *et al.*, 2006); *T. litopenaei* from shrimp mariculture pond (Sheu *et al.*, 2007); *T. discolor* and *T. soleae* from diseased sole and *T. gallaicum* from seawater of a turbot holding-tank (Piñeiro-Vidal *et al.*, 2008a, b); *T. adriaticum* from a bryozoan (Heindl *et al.*, 2008); *T. aiptasiae* from sea anemone (Wang *et al.*, 2008); and *T. crassostreae* from pacific oyster (Lee *et al.*, 2009). In this study, we report on the detailed taxonomic characterization of strain 35/09^T, a *Tenacibaculum*-like isolate. During the characterization of bacteria isolated from skin lesions of diseased European sea bass (*Dicentrarchus labrax* L.), strain 35/09^T was recovered on plates of *Flexibacter maritimus* medium (FMM; Pazos *et al.*, 1996). Subcultivation was done on FMM and marine agar (MA; Cultimed) at 25 °C for 48 h. The strain was preserved in Microbank tubes (Prolab Diagnostics) at –80 °C.

The 16S rRNA gene sequence of strain 35/09^T was determined by the identification service of the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ, Braunschweig, Germany). The 1507 bp sequence of strain 35/09^T was automatically aligned using CLUSTAL W (Thompson *et al.*, 1994) with those of the type strains of the 15 *Tenacibaculum* species and of other representative members of the family *Flavobacteriaceae* obtained from EMBL. Phylogenetic trees were constructed by the neighbour-joining (Saitou & Nei, 1987) and maximum-parsimony (Fitch, 1971) methods (Fig. 1). The evolutionary distance matrix for the neighbour-joining method was generated according to Kimura's two-parameter model (Kimura, 1980). To evaluate phylogenetic trees, a bootstrap analysis with 1000 sample replications was performed with the SEQBOOT and CONSENSE programs in the PHYLIP package (Felsenstein, 2007). The identification of phylogenetic neighbours and calculation of pairwise 16S rRNA gene sequence similarity values were achieved using the EzTaxon server (<http://www.eztaxon.org/>; Chun *et al.*, 2007). Strain 35/09^T formed a robust cluster with the 15 *Tenacibaculum* species in the phylogenetic tree based on 16S rRNA gene sequences (Fig. 1). The closest relatives of strain 35/09^T were *T. ovolyticum* IAM 14318^T (97.3 % similarity) and *T. soleae* CECT 7292^T (96.4 % similarity). Sequence similarities with the type strains of other *Tenacibaculum* species were: *T. aiptasiae*, 96.3 %; *T. adriaticum* and *T. gallaicum*, 95.3 %; *T. mesophilum* and *T. lutimaris*, 95.2 %; *T. litoreum*, 95.1 %; and *T. discolor*, 95.0 %.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain 35/09^T is FN545354.

Fig. 1. Neighbour-joining phylogenetic tree showing relationships between strain 35/09^T, members of the genus *Tenacibaculum* and representatives of other related genera belonging to the family *Flavobacteriaceae*. The sequence of *Flexibacter flexilis* ATCC 23079^T was used as an outgroup. Bootstrap values >70% based on 1000 replications are listed as percentages at the branching points. Solid circles indicate that the corresponding nodes were also recovered in the maximum-parsimony tree. Bars, 0.02 nt substitutions per site.

Morphological, physiological and biochemical tests were performed as described by Bernardet *et al.* (2002). The type strains of the two closest phylogenetic neighbours (*T. ovolyticum* DSM 18103^T and *T. soleae* CECT 7292^T) were obtained from culture collections, grown under the same conditions as the isolate and used as reference strains in all phenotypic tests. The Gram reaction was tested by using the bioMérieux Gram stain kit according to the manufacturer's instructions and the non-staining KOH method (Buck, 1982). Gliding motility was determined by phase-contrast microscopic examination of a fresh marine broth (MB; Cultimed) culture by the hanging drop technique as recommended by Bernardet *et al.* (2002). The presence of flexirubin-type pigments was determined as described by Reichenbach (1989). Catalase and oxidase activities were determined as described by Cowan & Steel (1965). Growth under anaerobic conditions was tested on MA using the GasPak anaerobic system (BBL). Growth at pH 4–10 (at unit intervals) was assessed in FMM broth; pH was adjusted using 1 M NaOH and 1 M HCl. The temperature range for growth was determined on MA plates incubated

at 4, 8, 15, 18, 22, 25, 30, 37 and 44 °C for 7 days. Salinity tolerance was tested in FMM broth containing 10, 20, 30, 50, 70 and 100% strength seawater or 0.8, 1.0, 3.0, 5.0, 7.0 and 10.0% (w/v) NaCl. Production of indole was tested in FMM broth supplemented with 1% (w/v) tryptone as a source of tryptophan (MacFaddin, 1976). H₂S production was determined with lead acetate strips suspended above FMM broth supplemented with 5% (w/v) peptone (MacFaddin, 1976). The Voges–Proskauer reaction was performed in seawater supplemented with 0.7% (w/v) peptone and 0.5% (w/v) D-glucose. Degradation of casein (1%), gelatin (1%), starch (1%) and Tween 80 (1%), and reduction of potassium nitrate (0.1%) were evaluated on FMM agar (Suzuki *et al.*, 2001). Utilization of carbon sources was tested on basal agar medium [0.2 g NaNO₃, 0.2 g NH₄Cl, 0.05 g yeast extract, 15 g agar in 1 l synthetic seawater (Sigma)] containing 0.4% carbon source [D(+)–sucrose, D(–)–ribose, D(+)–galactose, D-glucose, L-proline, L-glutamate, L-tyrosine] as described by Suzuki *et al.* (2001). The absence of growth after 1 month of incubation was scored as a negative result. Other enzymic activities

Table 1. Differential characteristics of strain 35/09^T, *T. ovolyticum* DSM 18103^T and *T. soleae* CECT 7292^T

Strains: 1, 35/09^T; 2, *T. ovolyticum* DSM 18103^T; 3, *T. soleae* CECT 7292^T. All data are from this study, except the DNA G+C contents of the two reference strains taken from Suzuki *et al.* (2001) and Piñeiro-Vidal *et al.* (2008b). All strains are susceptible to O/129, ampicillin and novobiocin. All strains are negative for trypsin and α -chymotrysin (API ZYM).

Characteristic	1	2	3
Colony morphology			
Shape	Uneven edge	Irregular spreading edge	Uneven edge
Colour	Pale yellow	Yellow	Yellow
Cell size (μ m)	2–150 $\times$ 0.7	1.5–20 $\times$ 0.6	2–35 $\times$ 0.5
Growth with 50 % seawater	+	+	–
pH range	6–8	6–10	5–10
Nitrate reduction	–	–	+
α -Glucosidase (API ZYM)	–	+	–
DNA G+C content (mol%)	31.3	30.3	29.8

were evaluated in the API ZYM system (bioMérieux) following the manufacturer's instructions, except that sterile seawater was used as the suspension medium.

Sensitivity to antimicrobials was evaluated by the disc diffusion method following the procedures of the Clinical and Laboratory Standards Institute (CLSI, 2006), on FMM plates using commercial discs (Oxoid) containing ampicillin (10 μ g), O/129 (pteridine; 150 μ g), and novobiocin (30 μ g).

The results of the morphological, physiological and biochemical tests are given in the species description and in Table 1.

For fatty acid analysis, strain 35/09^T and the two reference strains were grown on MA for 48 h at 25 °C. Extraction of fatty acid methyl esters, washing of extracts and GC analysis were performed according to the standard procedures of the Microbial Identification System (MIDI; Microbial ID) (Sasser, 1990) using the MIDI Sherlock version 4.5 and TSBA40 database.

The fatty acid compositions of strain 35/09^T and of its two closest phylogenetic neighbours are compared in Table 2. The cellular fatty acid profile of strain 35/09^T was dominated by iso-C_{15:0} (24.8 %), iso-C_{15:0} 3-OH (18.0 %), anteiso-C_{15:0} (8.1 %), C_{15:1} ω 6c (6.9 %) and iso-C_{15:1} (6.2 %) (Table 2). Overall, the fatty acid profiles of the three strains grown under the same conditions were very similar with only limited differences in the respective proportions of some components.

Determination of the DNA G+C content was carried out by the identification service of the DSMZ using the method described by Cashion *et al.* (1977). The DNA G+C content of strain 35/09^T was 31.3 mol%, a value within the range reported for *Tenacibaculum* strains (29.8–35.2 %) (Suzuki, 2011). DNA–DNA hybridization experiments were performed using the methods described by De Ley *et al.* (1970), as

Table 2. Cellular fatty acid composition (%) of strain 35/09^T, *T. ovolyticum* DSM 18103^T and *T. soleae* CECT 7292^T

Strains: 1, 35/09^T; 2, *T. ovolyticum* DSM 18103^T; 3, *T. soleae* CECT 7292^T. All data are from this study. Fatty acids amounting to <1 % of the total fatty acids in all strains are not shown. TR, Trace (<1 %); –, not detected.

Fatty acid	1	2	3
Straight chain			
C _{14:0}	1.9	–	TR
C _{15:0}	3.6	5.6	4.8
Branched chain			
iso-C _{13:0}	2.7	6.9	TR
iso-C _{14:0}	3.9	8.0	2.4
iso-C _{15:0}	24.8	11.0	23.1
anteiso-C _{15:0}	8.1	3.5	TR
iso-C _{15:1}	6.2	7.9	5.7
iso-C _{16:0}	TR	–	1.7
iso-C _{16:1}	TR	TR	2.4
Unsaturated			
C _{15:1} ω 6c	6.9	8.2	12.2
C _{17:1} ω 6c	TR	1.3	1.7
Hydroxylated			
iso-C _{15:0} 3-OH	18.0	14.8	10.6
C _{15:0} 2-OH	1.0	–	TR
C _{15:0} 3-OH	4.0	5.2	3.2
iso-C _{16:0} 3-OH	2.5	2.1	8.4
C _{16:0} 3-OH	3.7	6.2	2.2
iso-C _{17:0} 3-OH	1.1	1.4	2.9
Summed feature 3*	3.8	4.8	11.0

*Summed features are groups of two or three fatty acids that cannot be separated by GLC using the MIDI system. Summed feature 3 comprises C_{16:1} ω 7c and/or iso-C_{15:0} 2-OH.

modified by Huß *et al.* (1983). The experiment was performed at 45 °C in 2 × SSC (1 × SSC is 0.15 M sodium chloride plus 0.015 M sodium citrate at pH 7.0) using a Cary 100 Bio UV/visible spectrophotometer equipped with a Peltier-thermostatted 6 × 6 multicell changer and temperature controller with an *in situ* temperature probe (Varian). The DNA–DNA relatedness value between strain 35/09^T and *T. ovolyticum* DSM 18103^T was 12.9%. On the basis of the data presented, strain 35/09^T should be classified as a representative of a novel species of the genus *Tenacibaculum*, for which the name *Tenacibaculum dicentrarchi* sp. nov. is proposed.

Description of *Tenacibaculum dicentrarchi* sp. nov.

Tenacibaculum dicentrarchi [di.cen.trar'chi. N.L. n. *Dicentrarchus* a zoological genus name; N.L. gen. n. *dicentrarchi* of *Dicentrarchus*, isolated from the sea bass (*Dicentrarchus labrax* L.)].

Cells are strictly aerobic, Gram-stain-negative, straight rods, 0.3–0.5 µm in diameter and 2–40 µm in length (filamentous cells up to 150 µm long may occur; Fig. 2a), and motile by gliding. Degenerative spherical cells are observed in ageing cultures (Fig. 2b). Colonies on FMM or MA are flat, circular with uneven edges, pale-yellow-pigmented and do not adhere to agar. The pale yellow pigment is not a flexirubin-type pigment. Growth occurs in media containing 30–100% strength seawater (optimum,

70%), but not in media supplemented with NaCl only. Growth occurs at 4–30 °C (optimum, 22–25 °C), and at pH 6.0–9.0 (optimum, pH 7.0). Catalase and cytochrome oxidase activities are present. Gelatin and casein are hydrolysed, but Tween 80 and starch are not. The Voges–Proskauer test is negative. No acid is produced from carbohydrates. H₂S and indole are not produced. L-Proline, L-glutamate, D(+)–sucrose, D(–)-ribose, D(+)–galactose, D(+)–glucose and L-tyrosine are not utilized. In the API ZYM system, alkaline phosphatase, esterase (C4), esterase lipase (C8), lipase (C14), leucine arylamidase, valine arylamidase and cystine arylamidase are present, but trypsin, α-chymotrypsin and all enzymes related to the metabolism of carbohydrates are absent. Susceptible to ampicillin, novobiocin and pteridine. The major fatty acids (>5% of the total fatty acids) are iso-C_{15:0}, iso-C_{15:0} 3-OH, anteiso-C_{15:0}, C_{15:1}ω6c and iso-C_{15:1}.

The type strain is 35/09^T (=CECT 7612^T=NCIMB 14598^T), isolated from diseased sea bass (*Dicentrarchus labrax* L.) reared in Spain. The DNA G + C content of the type strain is 31.3 mol%.

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Fig. 2. Light micrographs of cells of strain 35/09^T grown on MA at 22 °C for 48 h (a) and 168 h (b). The arrow indicates the presence of degenerative spherical cells. Bars, 20 µm.

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