Chryseobacterium chaponense sp. nov., isolated from farmed Atlantic salmon (*Salmo salar*)

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Two bacterial strains, designated Sa 1147-06^T and Sa 1143-06, were isolated from Atlantic salmon (*Salmo salar*) farmed in Lake Chapo, Chile, and were studied using a polyphasic approach. Both isolates were very similar; cells were rod-shaped, formed yellow-pigmented colonies and were Gram-reaction-negative. Based on 16S rRNA gene sequence analysis, strains Sa 1147-06^T and Sa 1143-06 shared 100 % sequence similarity and showed 98.9 and 97.5 % sequence similarity to *Chryseobacterium jeonii* AT1047^T and *Chryseobacterium antarcticum* AT1013^T, respectively. Sequence similarities to all other members of the genus *Chryseobacterium* were below 97.3 %. The major fatty acids of strain Sa 1147-06^T were iso-C_{13:0}, iso-C_{15:0}, anteiso-C_{15:0} and iso-C_{17:1}ω9c, with iso-C_{15:0} 3-OH, iso-C_{16:0} 3-OH and iso-C_{17:0} 3-OH constituting the major hydroxylated fatty acids. DNA–DNA hybridizations with *C. jeonii* JMSNU 14049^T and *C. antarcticum* JMNSU 14040^T gave relatedness values of 20.7 % (reciprocal 15.1 %) and 15.7 % (reciprocal 25.7 %), respectively. Together, the DNA–DNA hybridization results and differentiating biochemical properties showed that strains Sa 1147-06^T and Sa 1143-06 represent a novel species, for which the name *Chryseobacterium chaponense* sp. nov. is proposed. The type strain is Sa 1147-06^T (=DSM 23145^T =CCM 7737^T).

A large number of novel species of the genus *Chryseobacterium* have been described within the last 15 years (Hugo *et al.*, 2003; Li *et al.*, 2003; de Beer *et al.*, 2005; Shen *et al.*, 2005; Shimomura *et al.*, 2005; Young *et al.*, 2005; Park *et al.*, 2006; Tai *et al.*, 2006; Herzog *et al.*, 2008; Behrendt *et al.*, 2008; Weon *et al.*, 2008; Szoboszlay *et al.*, 2008; Hantsis-Zacharov *et al.*, 2008; Kim *et al.*, 2005, 2008; Kämpfer *et al.*, 2009a, b, c, 2010; Benmalek *et al.*, 2010; Pires *et al.*, 2010; Yassin *et al.*, 2010) and, recently, species of the genera *Sejongia* and *Kaistella* have been added to the still growing number of species of the genus *Chryseobacterium* (Kämpfer *et al.*, 2009a, b). Members of the genus *Chryseobacterium* can be found in a wide variety of samples from clinical sources (Bernardet *et al.*, 2006) but also in samples of aquatic origin (de Beer *et al.*, 2006; Ilardi *et al.*, 2009).

Two bacterial strains, designated Sa 1147-06^T and Sa 1143-06, that formed yellow-pigmented colonies were recovered from diseased Atlantic salmon farmed in Lake Chapo, located 43 km north-west of Puerto Montt (X Región), Chile. These strains were isolated from the external lesions, gills and fins of diseased fish as mixed cultures with *Flavobacterium psychrophilum*, a notorious salmonid pathogen, and were initially diagnosed as such.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains Sa 1147-06^T and Sa 1143-06 are GU345045 and GU345046, respectively.

Both strains were maintained and subcultured on nutrient agar (NA, Oxoid) at 30 °C for 48 h and were subsequently analysed to determine the 16S rRNA gene sequences, fatty acid methyl ester composition of whole cell hydrolysates, further phenotypic characteristics and DNA–DNA relatedness to those species most closely related on the basis of 16S rRNA gene sequence similarities.

Colony characteristics were observed on nutrient agar. The Gram reaction was performed using the modified Hucker method as described by Gerhardt *et al.* (1994) and motility was assessed under a light microscope using cells grown in nutrient broth (Oxoid) for 3 days at 30 °C. Growth was determined at 4, 11, 15, 20, 25, 30, 37, 45 and 50 °C in nutrient broth and in 0.5–8.0 % (w/v) NaCl in tryptic soy broth. Both strains stained Gram-negative and formed visible yellowish colonies ~2 mm in diameter within 48 h of growth at 30 °C. No growth was observed below 4 °C or above 37 °C. Both strains were able to grow in the presence of up to 1 % (w/v) NaCl. Colonies were translucent and shiny with entire edges but on prolonged incubation the colonies were not visible as single entities, probably due to the profuse production of extracellular substances. A bright yellow pigment was produced on nutrient agar. The flexirubin test using the KOH method according to Reichenbach (1992) was negative. Oxidase activity was tested using oxidase reagent (bioMérieux) according to the manufacturer's instructions. Both strains showed a positive

oxidase reaction. Cells were non-motile, non-spore-forming rods ($1 \times 2 \mu\text{m}$). Good growth was observed on nutrient agar, R2A agar and tryptic soy agar but no growth was visible on MacConkey's agar (Oxoid).

Physiological characterization and additional biochemical tests were performed as described previously (Kämpfer *et al.*, 1991) on both isolates to assess carbon source utilization and hydrolysis of chromogenic substrates. Additional biochemical tests for the production of hydrogen sulphide (using the lead acetate paper and triple-sugar-iron methods), indole reaction (using Ehrlich's and Kovacs' reagents), activities of arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, DNase (Oxoid CM321; supplemented with 0.01 % toluidine blue), β -galactosidase (ONPG) and urease on Christensen's urea agar and the hydrolysis of casein, gelatin (plate method), starch and tyrosine (Smibert & Krieg, 1994) were performed. Both strains utilized a few carbon sources, similarly to other members of the genus *Chryseobacterium*, but were also able to hydrolyse some chromogenic substrates.

Indole production, hydrolysis of casein, gelatin, starch and tyrosine, hydrogen sulphide production and urease, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase

Table 1. Characteristics of strains Sa 1147-06^T and Sa 1143-06 and type strains of closely related species of the genus *Chryseobacterium*

Taxa: 1, Sa 1147-06^T; 2, Sa 1143-06; 3. *C. jeonii* JMNSU 14049^T; 4, *C. antarcticum* JMNSU 14040^T. +, Positive; (+), weakly positive; –, negative; ND, not determined. All strains were able to utilize D-glucose, maltose and acetate. All strains were unable to utilize the following compounds: N-acetyl-D-galactosamine, N-acetyl-D-glucosamine, L-arabinose, L-arbutin, cellobiose, D-fructose, D-galactose, gluconate, glycerol, D-mannose, D-mannitol, maltitol, α -melibiose, L-rhamnose, D-ribose, sucrose, salicin, trehalose, D-xylose, adonitol, myo-inositol, D-sorbitol, putrescine, *cis*- and *trans*-aconitate, 4-aminobutyrate, adipate, azelate, fumarate, glutarate, DL-3-hydroxybutyrate, itaconate, DL-lactate, 2-oxoglutarate, pyruvate, suberate, citrate, mesaconate, L-alanine, β -alanine, L-ornithine, L-phenylalanine, L-serine, L-aspartate, L-histidine, L-leucine, L-tryptophan, 3- and 4-hydroxybenzoate and phenylacetate. All data from this study.

Characteristic	1	2	3	4
Aesculin hydrolysis	–	–	–	+
Indole production	–	–	+	+
Growth at:				
5 °C	+	+	–	+
37 °C	+	+	+	–
α -Glucosidase production	+	+	–	+
Utilization of:				
D-Mannose	(+)	(+)	–	–
D-Xylose	–	–	–	+
Propionate	–	–	–	+
Urease activity	+	+	–	+

and β -galactosidase (ONPG) activities were negative in the novel strains. Biochemical and physiological data are given in Table 1 and in the species description.

For both isolates, cellular fatty acid analyses after extraction of whole cell hydrolysates were performed according to Kämpfer & Kroppenstedt (1996). The two isolates contained iso-C_{15:0}, anteiso-C_{15:0}, iso-C_{13:0} and iso-C_{17:1} ω 9*c* as the predominant fatty acids and contained smaller proportions of iso-C_{15:0} 3-OH, iso-C_{16:0} 3-OH and iso-C_{17:0} 3-OH, which was consistent with fatty acid profiles of other members of the genus *Chryseobacterium*. Comprehensive fatty acid profiles of strains Sa 1147-06^T and Sa 1143-06 and type strains of closely related species of the genus *Chryseobacterium* are shown in Table 2.

Table 2. Fatty acid compositions (%) of strains Sa 1147-06^T and Sa 1143-06 and type strains of closely related species of the genus *Chryseobacterium*

Data for strains *C. jeonii* JMNSU 14049^T and *C. antarcticum* JMNSU 14040^T were obtained in this study using the same method. Taxa: 1, Sa 1147-06^T; 2, Sa 1143-06; 3. *C. jeonii* JMNSU 14049^T; 4, *C. antarcticum* JMNSU 14040^T. tr: Trace (<0.4 %); –, not detected.

Fatty acid	1	2	3	4
iso-C _{12:0}	–	–	1.0	0.5
iso-C _{13:0}	7.0	8.7	2.9	2.5
anteiso-C _{13:0}	2.9	3.4	3.6	3.2
Unknown 13.565*	2.0	1.5	0.4	0.7
iso-C _{14:0}	2.3	1.1	5.0	1.5
C _{14:0}	tr	tr	–	–
iso-C _{15:0}	23.6	26.8	12.2	13.6
anteiso-C _{15:0}	19.4	17.8	24.2	15.2
anteiso-C _{15:1} A	–	–	–	6.6
C _{15:0}	–	–	1.5	2.6
iso-C _{16:0}	3.2	1.1	5.7	2.8
iso-C _{16:1} H	2.2	1.1	9.1	3.6
Summed feature 3†	5.6	5.5	2.6	2.7
iso-C _{15:0} 3-OH	3.5	2.9	1.3	1.0
C _{15:0} 2-OH	1.0	1.9	1.9	1.9
iso-C _{17:1} ω 9 <i>c</i> ‡	8.3	8.2	8.6	21.3
anteiso-C _{17:1} ω 9 <i>c</i>	–	–	1.9	2.5
Summed feature 4†	1.2	1.0	–	–
Unknown 16.582*	0.5	0.8	0.4	0.5
iso-C _{16:0} 3-OH	5.3	4.2	9.0	5.1
C _{18:1} ω 5 <i>c</i>	1.0	1.5	0.8	1.5
iso-C _{17:0} 3-OH	9.1	10.3	4.4	5.6
C _{17:0} 2-OH	1.6	2.1	–	–

*These fatty acids could not be identified with the MIDI system. The number indicates their equivalent chain-length.

†Summed features are groups of two or three fatty acids that cannot be separated by GLC with the MIDI system. Summed feature 3 comprises C_{16:1} ω 7*c* and/or C_{15:0} iso 2-OH; summed feature 4 comprises C_{17:1} iso I/anteiso B.

‡For unsaturated fatty acids, the position of the double bond is located by counting from the methyl (ω) end of the carbon chain. The *cis* and *trans* isomers are indicated by the suffixes *c* and *t*, respectively.

Fig. 1. Phylogenetic analysis of strains Sa 1147-06^T and Sa 1143-06 and closely related species based on 16S rRNA gene sequences available from the EMBL database (accession numbers are given in parentheses). Multiple alignments were performed and distances (distance options according to the Kimura-2 model) and clustering were determined using the neighbour-joining method in the MEGA version 4 software package (Tamura *et al.*, 2007). Bootstrap values >70 %, based on 1000 replications, are given as percentages at the branching points. Bar, 0.1 substitutions per nucleotide position.

The 16S rRNA gene of strains Sa 1147-06^T and Sa 1143-06 was sequenced as described by Kämpfer *et al.* (2003). Isolation of the DNA was performed using a GenElute Plant Genomic DNA extraction kit (Sigma). Multiple sequence alignment analysis was performed using the MEGA version 4 software package (Tamura *et al.*, 2007). Genetic distance calculations (distance options according to the Kimura-2 model) and clustering using the neighbour-joining (Fig. 1) and maximum-parsimony (results not shown) methods were performed using bootstrap values based on 1000 replications. The 16S rRNA gene sequence of strains Sa 1147-06^T and Sa 1143-06 was a continuous stretch of 1398 bp. The two strains shared 100 % 16S rRNA gene sequence similarity and showed 98.9 and 97.5 % sequence similarity to *Chryseobacterium jeonii* AT1047^T and *Chryseobacterium antarcticum* AT1013^T, respectively. Sequence similarities between the two novel strains and other members of the genus *Chryseobacterium* were found to be 97.3 % and below. The recently described species *Chryseobacterium solincola* (Benmalek *et al.*, 2010), *Chryseobacterium treverense* (Yassin *et al.*, 2010) and *Chryseobacterium palustris* (Pires *et al.*, 2010) showed sequence similarities of 97.2, 97.0 and 97.0 %, respectively, to the novel strains.

DNA–DNA hybridization experiments were performed between strain Sa 1147-06^T and the type strains of the two most closely related species of the genus *Chryseobacterium* according to the method of Ziemke *et al.* (1998) (except that, for nick translation, 2 µg of DNA was labelled during 3 h of incubation at 15 °C). DNA–DNA hybridizations between strain Sa 1147-06^T and *C. jeonii* JMSNU 14049^T and *C. antarcticum* JMNSU 14040^T resulted in relatedness values of 20.7 % (reciprocal 15.1 %) and 15.7 % (reciprocal 25.7 %), respectively.

Taken together, these results suggest that strains Sa 1147-06^T and Sa 1143-06 represent a novel species in the genus

Chryseobacterium, for which the name *Chryseobacterium chaponense* sp. nov. is proposed.

Description of *Chryseobacterium chaponense* sp. nov.

Chryseobacterium chaponense (cha.po.nen'se. N.L. neut. adj. *chaponense* pertaining to Lake Chapo, Chile, from which the Atlantic salmon harbouring the two isolates was obtained).

Cells are Gram-reaction-negative, aerobic, non-motile, non-spore-forming rods ~1 × 2 µm. Oxidase- and catalase-positive. Growth occurs after 48 h of incubation at 11–36 °C on nutrient agar, R2A agar and tryptic soy agar (Oxoid). No growth occurs on MacConkey's agar (Oxoid) at 28 °C. No growth occurs at temperatures below 4 °C and above 37 °C. Cells grow in the presence of 0–1 % NaCl. Colonies are smooth, yellowish, circular, translucent and shiny with entire edges when grown on nutrient agar. A yellow pigment (KOH test-negative) is non-diffusible and non-fluorescent. Acid is not produced from D-glucose, trehalose, D-mannitol, adonitol, L-arabinose, D-arabitol, dulcitol, erythritol, *myo*-inositol, lactose, maltose, melibiose, methyl- α -D-glucoside, raffinose, L-rhamnose, salicin, D-sorbitol, sucrose or D-xylose. Negative for indole production, hydrolysis of casein, gelatin, starch, DNA and tyrosine, hydrogen sulphide production and urease, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase and β -galactosidase (ONPG) activities. The following compounds are utilized as sole carbon sources: D-glucose, maltose, acetate, propionate and L-proline. The following compounds are not utilized as sole carbon sources: acetate, propionate, N-acetyl-D-galactosamine, N-acetyl-D-glucosamine, L-arabinose, L-arbutin, cellobiose, D-fructose, D-galactose, gluconate, glycerol, D-mannose, D-mannitol, maltitol, α -melibiose, L-rhamnose, D-ribose,

sucrose, salicin, trehalose, D-xylose, adonitol, *myo*-inositol, D-sorbitol, putrescine, *cis*- and *trans*-aconitate, 4-amino-butyrate, adipate, azelate, fumarate, glutarate, DL-3-hydroxybutyrate, itaconate, DL-lactate, 2-oxoglutarate, pyruvate, suberate, citrate, mesaconate, L-alanine, β -alanine, L-ornithine, L-phenylalanine, L-serine, L-aspartate, L-histidine, L-leucine, L-proline, L-tryptophan, 3- and 4-hydroxybenzoate and phenylacetate. The chromogenic substrates *p*-nitrophenyl α -D-glucopyranoside, bis-*p*-nitrophenyl phosphate, bis-*p*-nitrophenyl phenyl phosphonate, bis-*p*-nitrophenyl phosphorylcholine, 2-deoxythymidine-2'-*p*-nitrophenyl phosphate, L-alanine-*p*-nitroanilide, γ -L-glutamate-*p*-nitroanilide and L-proline-*p*-nitroanilide are hydrolysed. *p*-Nitrophenyl- β -D-glucopyranoside, *p*-nitrophenyl- β -D-galactopyranoside, *p*-nitrophenyl- β -D-xylopyranoside and *p*-nitrophenyl- β -D-glucuronide are not hydrolysed. The major cellular fatty acids are iso-C_{15:0}, anteiso-C_{15:0}, iso-C_{13:0} and iso-C_{17:1}9c. The major hydroxylated fatty acids are iso-C_{15:0} 3-OH, iso-C_{16:0} 3-OH and iso-C_{17:0} 3-OH.

The type strain, Sa 1147-06^T (=DSM 23145^T =CCM 7737^T), was isolated from Atlantic salmon (*Salmo salar*) farmed in Lake Chapo, Chile.

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