

Erratum to: *Aurantibacter crassamenti* gen. nov., sp. nov., a bacterium isolated from marine sediment

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Published online: 24 October 2016
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Erratum to: Archives of Microbiology DOI:10.1007/s00203-016-1280-y

Subsequent to the publication of the above paper, it has been noticed that the characteristics of strain *Kriegella aquimaris* KMM 3665^T in Table 1, cellular fatty acids for strain *Kriegella aquimaris* KMM 3665^T in Table 2 and GenBank/EMBL/DDBJ accession number of strain *Aurantibacter crassamenti* HG732^T in Fig. 2 were incorrectly published. The corrected Tables 1 and 2 and Fig. 2 are provided here.

The online version of the original article can be found under doi:[10.1007/s00203-016-1280-y](https://doi.org/10.1007/s00203-016-1280-y).

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Table 1 Differential characteristics of strain HG732^T and other closely related taxa

Characteristic	1	2	3	4	5
Pigmentation	Orange	Orange to dark orange	Yellow to dark red (yellow ^b)	Yellow to dark orange (yellow ^d)	Orange to dark orange (dark orange ^e)
Gliding motility	–	+ ^a	+	± (+ ^d)	± (– ^e)
Temperature range for growth (°C)	20–37	4–37 ^a	13–45	4–50 (4–33 ^d)	4–40 (10–37 ^e)
pH range for growth	6–9	6–8	6–8.5	5.5–10.5 (5.5–10 ^d)	6–10
Highest NaCl tolerance (% w/v)	5	6 ^a	10	10	8 (7 ^e)
Nitrate reduction	–	–	+	± (+ ^d)	± (+ ^e)
Hydrolysis of					
Gelatin	–	+	+	± (– ^d)	± (– ^e)
ONPG	+	–	+	± (– ^d)	+
Starch	–	–	± (+ ^b)	± (+ ^d)	–
Urea	–	+	–	–	± (+ ^e)
Acid production from					
Cellobiose	–	–	± (+ ^c)	± (– ^d)	+
Galactose	–	–	–	± (– ^d)	± (+ ^e)
Glucose	–	–	± (– ^c)	± (– ^d)	+
Maltose	–	–	± (+ ^c)	± (– ^d)	± (+ ^e)
Melibiose	–	–	–	± (– ^d)	± (– ^e)
Lactose	–	–	–	± (– ^d)	+
Raffinose	+	–	± (– ^c)	± (– ^d)	± (+ ^e)
Polar lipids	PG, 3UAL, 2UL	ND	ND	PE, 2UAL, 4UL	PE, 2UL
DNA G + C content (mol %)	35.2	39.2 ^a	36.1–43.4 (43 ^c)	34.2–41.1 (37.5 ^d)	37–40 (37.5–38.2 ^e)

Strains: 1 HG732^T (*Aurantibacter crassamenti* gen. nov., sp. nov.; present study), 2 *Kriegella aquimaris* KMM 3665^T (data from this study), 3 *Zobellia* spp. (Barbeyron et al. 2001; Nedashkovskaya et al. 2004b), 4 *Maribacter* spp. (Nedashkovskaya et al. 2004a; Zhang et al. 2009; Hu et al. 2015; Jackson et al. 2015; Park et al. 2015), 5 *Arenibacter* spp. (Ivanova et al. 2001; Nedashkovskaya et al. 2006; Sun et al. 2010; Jeong et al. 2013)

Symbols: PE phosphatidylethanolamine, PG phosphatidylglycerol, UAL unidentified aminolipid, UL unidentified lipid, + positive, – negative, ND no data

Data for the type strain of the type species (*K. aquimaris* KMM 3665^T; *Z. galactanovorans* Dsij^T; *M. sedimenticola* KMM 3903^T; *A. latericius* KMM 426^T) from a, Nedashkovskaya et al. 2008; b, Barbeyron et al. 2001; c, Nedashkovskaya et al. 2004b; d, Nedashkovskaya et al. 2004a; e, Ivanova et al. 2001

Table 2 Comparison of cellular fatty acids for strain HG732^T and other closely related taxa

Fatty acid	1	2	3	4	5
iso-C13:0	tr	tr	–	tr	tr–1.1
C13:0	–	–	–	–	–
iso-C14:0	–	–	–	1.4	–
C14:0	1.4	tr	tr–1.0	tr–1.7	tr–1.0
C15:0	–	11.1	7.5–14.4	2.9–15.5	4.1–22
C15:0 2-OH	tr	–	–	tr	tr–1.0
C15:0 3-OH	–	–	tr	1.4–3.9	tr–2.2
iso-C15:0	33.1	12.3	16.8–22.5	9.4–42.6	6.8–15
iso-C15:0 3-OH	4.3	3.2	4.6–8.3	2.0–12.6	3.5–7.2
iso-C15:1 G	10.5	19.7	–	5.2–16.7	9.3–12.7
anteiso-C15:0	1.2	tr	1.0–1.8	tr–9.0	1.8–13.5
C15:1 ω 6c	2.6	2.5	1.1–3.2	tr–4.8	tr–4.2
C16:0	1.3	tr	tr–2.6	tr–1.9	tr–2.7
C16:0 3-OH	1.4	tr	2.4–4.9	1.1–5.5	tr–3.7
iso-C16:0	–	tr	–	tr–1.8	tr–1.7
iso-C16:0 3-OH	tr	tr	–	tr–6.8	tr–7.2
C17:0 2-OH	1	tr	–	1–3.8	tr–5.1
C17:1 ω 6c	tr	tr	1.0–1.2	tr–1.7	tr–3.0
iso-C17:1 ω 9c	–	6.4	2.4–5.1	2.0–9.4	2.2–5.3
iso-C17:0 3-OH	22.2	12.8	15.1–25.9	4.8–29.2	6.9–21.9
C18:0	–	tr	–	tr	–
Summed feature 3 ^a	8.2	9.4	9.9–15.5	1.7–14.8	9.6–20.4
Summed feature 9 ^b	6.2	–	–	7.9	–

Strains: 1 HG732^T (*Aurantibacter crassamenti* gen. nov., sp. nov.; present study), 2 *Kriegella aquimaris* KMM 3665^T (Nedashkovskaya et al. 2008), 3 *Zobellia* spp. (Barbeyron et al. 2001; Nedashkovskaya et al. 2004b), 4 *Maribacter* spp. (Nedashkovskaya et al. 2004a; Zhang et al. 2009; Hu et al. 2015; Jackson et al. 2015; Park et al. 2015), 5 *Arenibacter* spp. (Ivanova et al. 2001; Nedashkovskaya et al. 2006; Sun et al. 2010; Jeong et al. 2013)

Symbols: *tr* trace (less than 1.0 %), – not detected. The data were typically obtained by GLC using the MIDI system

^a Summed feature 3 consists of C16:1 ω 7c and/or C16:1 ω 6c

^b Summed feature 9 consists of C16:0 10-methyl/iso-C17:1 ω 9c

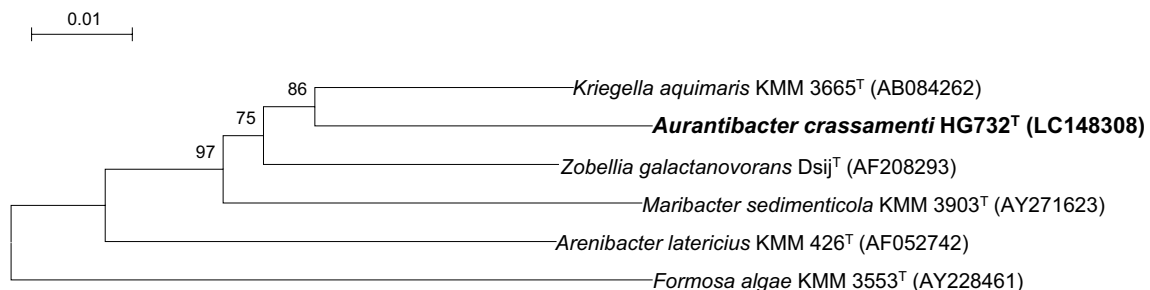


Fig. 2 Neighbor-joining tree of 16S rRNA gene sequence similarity, showing the phylogenetic position of strain HG732^T and representatives of the family *Flavobacteriaceae*. The sequence of *Formosa*

algae KMM 3553^T was used as an outgroup. The sequence determined in this study is shown in *bold*. Bootstrap values from neighbor-joining analysis are shown. *Bar*, 1 % sequence divergence