Description of *Chryseobacterium anthropi* sp. nov. to accommodate clinical isolates biochemically similar to *Kaistella koreensis* and *Chryseobacterium haifense*, proposal to reclassify *Kaistella koreensis* as *Chryseobacterium koreense* comb. nov. and emended description of the genus *Chryseobacterium*

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A collection of eight strains, NF 1366^T, NF 450, NF 1101, NF 1107, NF 1123, NF 1413, CCUG 15260 and CCUG 15624, from various clinical origins, were characterized biochemically as similar to *Kaistella koreensis* and *Chryseobacterium haifense*. They differed from *K. koreensis*, which is unable to alkalinize acetate, and from *C. haifense*, which is ONPG-positive (β -galactosidase) and acidifies sucrose, fructose and lactose. Based on 16S rRNA gene sequence comparisons, this collection of strains was most closely related to the type strains of *K. koreensis* (97.3–97.5 %) and *C. haifense* (99.1 %). Representative strain NF 1366^T showed only 41.8 % DNA–DNA relatedness with *K. koreensis* DSM 12107^T and only 51.9 % with *C. haifense* DSM 19056^T. DNA–DNA hybridization of strains NF 450 and CCUG 15624 to strain NF 1366^T was 41.7 and 74.6 %, respectively, and relatedness of these strains with *C. haifense* DSM 19056^T was 72.6 and 70.2 %. With the present information, these two strains must be classified as intermediate between *C. haifense* and strain NF 1366^T. The fatty acid composition and polar lipid profile of strain NF 1366^T were similar to those reported for other *Chryseobacterium* species. Like other chryseobacteria, strain NF 1366^T exhibited a polyamine pattern with the predominant compound sym-homospermidine and a quinone system consisting of menaquinone MK-6 only. For this collection of clinical strains, the name *Chryseobacterium anthropi* sp. nov. is proposed, with NF 1366^T (=CCUG 52764^T =CIP 109762^T) as the type strain. *K. koreensis* was shown to be very similar genotypically and phenotypically to *Chryseobacterium*. Its polar lipid profile exhibited the major characteristics shown for recently described *Chryseobacterium* species and the fatty acid profile of *K. koreensis* was also very similar to those of the *Chryseobacterium* species. Hence, no striking genotypic or phenotypic differences could be found that could justify the classification of this species into a separate genus, and we therefore propose to reclassify *Kaistella koreensis* in the genus *Chryseobacterium* as *Chryseobacterium koreense* comb. nov. (type strain Chj707^T =IAM 15050^T =JCM 21512^T =KCTC 12107^T =NBRC 103027^T). An emended description of the genus *Chryseobacterium* is also proposed.

Abbreviation: tDNA-PCR, tRNA intergenic length polymorphism analysis.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strain NF 1366^T and the other seven strains reported in this study are AM982786 and AM982787–AM982793, as detailed in Table 1.

Within the family *Flavobacteriaceae* as emended by Bernardet *et al.* (2002), the genera *Bergeyella*, *Chryseobacterium*, *Elizabethkingia*, *Empedobacter*, *Kaistella*, *Riemerella*, *Sejongia* and *Weeksella*, and the recently described genus *Wautersiella* (Kämpfer *et al.*, 2006) form a distinct branch. The genus *Chryseobacterium* currently contains more than 20 species, including some of clinical importance (Quan *et al.*, 2007; Vaneechoutte *et al.*, 2007). The genus *Kaistella* was proposed by Kim *et al.* (2004) as a novel member of the *Chryseobacterium*–*Bergeyella*–*Riemerella* branch, mainly on the basis of 16S rRNA gene sequence comparisons, without reporting striking phenotypic features (i.e. chemotaxonomic traits) as differentiating characteristics. Interestingly, the species *Chryseobacterium haifense* (Hantsis-Zacharov & Halpern, 2007) clearly shows higher 16S rRNA gene sequence similarity to the sole species of *Kaistella* (97%) than to the *Chryseobacterium* species described at that time. However, these authors did not compare *C. haifense* to *Kaistella koreensis* in their paper.

Here, we report the characterization of eight strains of clinical origin (Table 1) that were biochemically most similar to *K. koreensis* and *C. haifense* and which displayed biochemical profiles that resembled those of CDC group II-e strains (Dees *et al.*, 1986).

Biochemical and morphological tests were performed as described previously (Laffineur *et al.*, 2002; Schreckenberger *et al.*, 2003; Vaneechoutte *et al.*, 2007) on the eight clinical isolates and on the other strains listed in Table 2. Assimilation and alkalization of organic compounds was detected on Simmons' citrate agar base, replacing citrate with various organic substrates at 0.2% (w/v), according to Martin *et al.* (1981). Enzyme activities were detected using diagnostic tablets (Rosco). The KOH test was used to detect flexirubin pigments (Bernardet *et al.*, 2002). Table 2 summarizes the biochemical data obtained. All eight strains grew aerobically at 37 °C (with optimal growth at 30 °C) and were positive for oxidase and catalase activities and for acid production from glucose and

maltose. Acid production from mannose and hydrolysis of Tween 80 were strain-dependent. All strains were positive for indole production, hydrolysis of gelatin, starch and tyrosine, presence of alkaline phosphatase, trypsin and pyrrolidonyl aminopeptidase activities and alkalization of acetate. All strains were negative for production of flexirubin pigments, growth at 42 °C, nitrate reduction, H₂S production on Kligler agar, alkalization of citrate and urease, β -galactosidase, ornithine and lysine decarboxylase, arginine dihydrolase and L-phenylalanine deaminase activities. The phenotypic characteristics most useful to differentiate the eight clinical isolates from related taxa are highlighted in Table 2.

In summary, the strains can be differentiated from *K. koreensis* (Kim *et al.*, 2004) by alkalization of acetate, from *C. haifense* (Hantsis-Zacharov & Halpern, 2007) by the lack of acid production from fructose, lactose and sucrose and by a negative ONPG test (β -galactosidase), from *Chryseobacterium molle* and *Chryseobacterium pallidum* (Herzog *et al.*, 2008) by the lack of acid production from arabinose, cellobiose, xylose and ethylene glycol and by the lack of hydrolysis of aesculin, from *Chryseobacterium hispanicum* (Gallego *et al.*, 2006) and *Chryseobacterium caeni* (Quan *et al.*, 2007) by the absence of flexirubin pigments and by the lack of aesculin hydrolysis and from *Chryseobacterium hominis* (Vaneechoutte *et al.*, 2007) by the lack of aesculin hydrolysis and the lack of acid production from ethylene glycol.

Antibiotic susceptibility was determined by the disc diffusion method using the criteria for non-*Enterobacteriaceae* Gram-negative rods (CLSI, 2005). All strains were susceptible to erythromycin, ciprofloxacin, temocillin and trimethoprim-sulfamethoxazole. All but one were susceptible to tetracycline. Susceptibility to desferrioxamine, ampicillin, cephalothin, cefotaxime and gentamicin was strain-dependent.

In contrast to the original description of *K. koreensis* (Kim *et al.*, 2004), where oxidation–fermentation of glucose,

Table 1. Origin of the *Chryseobacterium* strains studied

Culture collections: CCUG, Culture Collection of the University of Göteborg, Sweden; CIP, Collection de l'Institut Pasteur, Paris, France; LMG, Laboratory of Microbiology Gent Culture Collection, Gent, Belgium. Strains prefixed with NF are non-fermenters (designation of the collection at UCL, Brussels, Belgium).

Strain	Location of isolation	Year	Clinical origin	16S rRNA gene sequence accession no.
NF 450, CCUG 52760	Ottignies, Belgium	1992	Blood	AM982787
NF 1101, CCUG 52762	Brussels, Belgium	2002	Bite wound	AM982788
NF 1107	Gosselies, Belgium	2002	Finger abscess	AM982889
NF 1123, CCUG 52763	Antwerp, Belgium	2003	Blood	AM982790
NF 1366 ^T , CCUG 52764 ^T , CIP 109762 ^T	Brussels, Belgium	2006	Blood	AM982786
NF 1413	Brussels, Belgium	2006	Blood	AM982791
CCUG 15260, CDC F4391, LMG 8325	Indiana, USA	1984	Lung biopsy	AM982793
CCUG 15624, Berger 7814	Heidelberg, Germany	1984	Urethra	AM982792

Table 2. Phenotypic characteristics of the novel strains and related taxa

Strains: 1–6, *C. anthropi* sp. nov. strains NF 1366^T (1), NF 1101 (2), NF 1107 (3), NF 1123 (4), NF 1413 (5) and CCUG 15260 (6); 7, *Chryseobacterium* sp. NF 450; 8, *Chryseobacterium* sp. CCUG 15624; 9, *K. koreensis* KCTC 12107^T; 10, *C. haifense* DSM 19056^T; 11, *C. hominis* (data for 11 strains); 12, *C. arothri* DSM 19326^T; 13, *C. hispanicum* JCM 13554^T; 14, *C. caeni* DSM 17710^T; 15, *C. molle* CCUG 52547^T; 16, *C. pallidum* CCUG 52548^T. All data were taken from this study. +, Positive; –, negative; –/+, most strains negative; (+), weak or delayed positive; v, strain-dependent. Characteristics highlighted in bold are considered the most useful for differentiation between the species listed. All strains are positive for acid production from glucose and maltose, production of indole and hydrolysis of gelatin. All strains are negative for acid production from mannitol, urease activity, growth at 42 °C and growth on MacConkey agar.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Acid production from:																
Arabinose	–	–	–	–	–	–	–	–	–	–	–	–	+	(+)	+	+
Cellobiose	–	–	–	–	–	–	–	–	–	–	–/+	(+)	(+)	(+)	+	+
Ethylene glycol	–	–	–	–	–	–	–	–	–	–	+	+	+	+	+	+
Fructose	–	–	–	–	–	–	–	–	–	+	v	+	+	+	–	+
Lactose	–	–	–	–	–	–	–	–	–	+	–	–	–	–	–	–
Mannose	–	–	+	–	+	+	(+)	+	+	+	+	+	+	+	+	+
Sucrose	–	–	–	–	–	–	–	–	–	+	v	+	+	+	–	+
Trehalose	–	–	–	–	–	–	–	–	–	–	–	–	–	+	–	+
Xylose	–	–	–	–	–	–	–	–	–	–	–	–	+	(+)	+	+
Hydrolysis of:																
Aesculin	–	–	–	–	–	–	–	–	–	–	+	+	+	+	+	+
Starch	+	(+)	(+)	(+)	(+)	(+)	+	(+)	(+)	+	+	+	+	+	+	+
Tween 80 (7 days)	–	(+)	(+)	–	–	–	–	–	+	–	–	–	–	–	–	+
Tyrosine	+	+	+	+	+	+	+	+	(+)	+	v	–	+	+	+	+
Growth at 37 °C	+	(+)	+	(+)	(+)	+	+	+	+	(+)	+	+	–	+	–	+
Nitrate reduction	–	–	–	–	–	–	–	–	–	–	v	–	+	–	–	+
Acetate alkalization	+	+	+	+	+	+	+	+	–	+	+	+	–	+	+	(+)
Production of flexirubin pigments	–	–	–	–	–	–	–	–	–	–	–	–	+	+	–	–
ONPG (β-galactosidase)	–	–	–	–	–	–	–	–	–	+	–	–	(+)	+	+	–
Desferrioxamine susceptibility	+	–	+	–	+	+	+	+	+	+	–	–	–	–	–	–

using the medium of Hugh & Leifson (1953), tested negative, we found *K. koreensis* KCTC 12107^T to be saccharolytic, producing acid from glucose, maltose and mannose, by three different methods, using (i) ammonium salt agar base, which is the method recommended by Bernardet *et al.* (2002), (ii) the conventional oxidation–fermentation medium of Hugh & Leifson (1953) and (iii) low-peptone phenol red agar base (Wauters *et al.*, 1998). Furthermore, we could not confirm the hydrolysis of aesculin.

Our results for *C. caeni* N4^T are also significantly different from the original description (Quan *et al.*, 2007). The authors described an asaccharolytic species, whereas we found the type and only strain of this species to be one of the most saccharolytic strains among the *Chryseobacterium* species, rapidly acidifying glucose, maltose, sucrose, trehalose and L-arabinose and acidifying xylose and cellobiose more slowly. This contradiction may be explained by the fact that the authors used three API strips for carbohydrate metabolism, API 20 E, API 20 NE and API ID 32 GN (bioMérieux), although these are not suitable for the detection of oxidative acidification of carbohydrates by non-fermenters: API 20 E is intended primarily for fermentative bacteria and is not reliable for

non-fermenters, and API 20 NE and API ID 32 GN only score assimilation, which is often different from acidification. Moreover, indole production was reported as negative, whereas the strain was clearly positive in our hands.

16S rRNA gene sequences were determined for all eight isolates, as described previously (Wauters *et al.*, 2003), and a phylogenetic tree was constructed on the basis of the 16S rRNA gene sequences using the software package Genebase (Applied Maths). At first, a pairwise alignment was carried out using UPGMA (gap cost 100 %, unit gap cost 20 %), which was subsequently used for a global alignment with *Bacteroides fragilis* ATCC 25285^T as an outgroup on a common region corresponding to *Escherichia coli* 16S rRNA positions 211–1378, resulting in a similarity matrix. A dendrogram was constructed on the basis of this similarity matrix, using the neighbour-joining clustering method (Fig. 1). Bootstrap values, obtained from 1000 replicated calculations, are presented as percentages at each node, omitting values below 50 %. The similarity between strain NF 1366^T and the seven other strains ranged between 99.7 and 100 %. Based on 16S rRNA gene sequence similarity, this collection of strains was most closely related to *C. haifense* DSM 19056^T (99.1 %) and *K. koreensis* KCTC

The G+C content of the DNA of strain NF 1366^T was determined at the DSMZ (Braunschweig, Germany), according to the method of Mesbah *et al.* (1989), as being

trRNA-intergenic length polymorphism analysis (tDNA-PCR) was carried out as described previously (Baele *et al.*, 2000). The tDNA-PCR patterns of the eight strains studied were compared with patterns obtained from all strains of the family *Flavobacteriaceae* available in the collection of the LBR UGent. A similarity tree (Fig. 2) was constructed

Fig. 2. Clustering of tDNA-PCR profiles of the novel strains, related *Chryseobacterium* species and other representatives of the family *Flavobacteriaceae*. Bar, 10% distance as calculated by the differential base pairs algorithm (Baele *et al.*, 2001).

as follows: the distance matrix was calculated with the differential base pairs algorithm, using a 1 bp tolerance threshold (Baele *et al.*, 2001), clustering was done with the UPGMA algorithm using the NEIGHBOR software and the tree was constructed with the PHYLIP software (TreeView; <http://taxonomy.zoology.gla.ac.uk/rod/treeview.html>).

Two of the strains studied, NF 450 and CCUG 15624, showed a pattern that was intermediate between that of the six other strains and that of *C. haifense* DSM 19056^T. All eight strains studied and *C. haifense* DSM 19056^T had a tRNA intergenic spacer with a length of 135.2 ± 0.1 bp (mean $\pm$ SD) in common, all eight strains studied had fragments of 106.9 ± 0.1 and 205.9 ± 0.1 bp in common and the two intermediate strains had spacers of 210.4, 229.1 and 243.1 bp in common with *C. haifense* DSM 19056^T, but could be differentiated from it by the presence of fragments of 108.3, 109.1 and 205.1 bp in *C. haifense* DSM 19056^T. The two intermediate strains could be differentiated from the other six strains studied by the presence of fragments of 212.0, 230.3 and 244.6 bp in the

latter. *K. koreensis* KCTC 12107^T had tRNA spacer fragments of 101.0, 144.5, 197.6, 211.8, 245.3 and 284.2 bp.

For DNA–DNA hybridization, a microtitre plate method was used, modified after Lind & Ursing (1986), as described previously (Ziemke *et al.*, 1998). Strain NF 1366^T showed only 41.8% DNA–DNA relatedness with *K. koreensis* DSM 12107^T and only 51.9% with *C. haifense* DSM 19056^T, and therefore was considered to represent a separate species. Strains NF 450 and CCUG 15624 were phenotypically identical to the six other strains, but their tDNA-PCR pattern was intermediate between that of *C. haifense* DSM 19056^T and those of the six other strains. The DNA–DNA relatedness of these two strains was 41.7 and 74.6% with strain NF 1366^T and 72.6 and 70.2% with *C. haifense* DSM 19056^T, respectively. Hence, both strains must be classified as intermediate between *C. haifense* and the novel species described below, in agreement with their intermediate tDNA-PCR pattern.

Biomass used for the extraction of quinones, polar lipids and polyamines was obtained after culture at 28 °C in $3.3 \times$ PYE medium (10 g peptone from casein and 10 g yeast extract l⁻¹, pH 7.2). Polar lipids were extracted and analysed as described previously (Tindall, 1990; Altenburger *et al.*, 1996). Polyamines were extracted and analysed as reported by Busse & Auling (1988) and Stolz *et al.* (2007). The polyamine pattern consisted of the major compound *sym*-homospermidine [$36.5 \mu\text{mol (g dry weight)}^{-1}$], minor amounts of spermidine [$2.9 \mu\text{mol (g dry weight)}^{-1}$] and spermine [$3.1 \mu\text{mol (g dry weight)}^{-1}$] and traces of putrescine [$<0.1 \mu\text{mol (g dry weight)}^{-1}$], which is consistent with the characteristics of other chryseobacteria (Hamana & Matsuzaki, 1990, 1991; Kämpfer *et al.*, 2003). It is worth mentioning that, in the original genus description, major amounts of 2-hydroxyputrescine were also reported in *Chryseobacterium indologenes* (Vandamme *et al.*, 1994; Hamana & Matsuzaki, 1991). However, the diamine 2-hydroxyputrescine has so far been reported only from betaproteobacteria whereas, for all chryseobacteria for which polyamine patterns have been determined, including the type species of the genus, *Chryseobacterium gleum*, and the species *Chryseobacterium balustinum*, *C. daecheongense*, *C. defluvii*, *C. hispanicum*, *C. indoltheticum* and *C. scopthalmum*, only *sym*-homospermidine has been reported as the major compound (Hamana & Matsuzaki, 1990, 1991; Kämpfer *et al.*, 2003; Kim *et al.*, 2005; Hamana *et al.*, 2008). Possibly, 2-hydroxyputrescine was identified erroneously in *C. indologenes*. Hence, the genus description of *Chryseobacterium* should be emended to indicate that members of the genus contain *sym*-homospermidine as the major polyamine.

The quinone system of strain NF 1366^T consisted exclusively of menaquinone MK-6, which also is in agreement with the assignment of NF 1366^T to the genus *Chryseobacterium* (Vandamme *et al.*, 1994). The polar lipid profile of NF 1366^T exhibited the major compounds

phosphatidylethanolamine, an unknown aminophospholipid, an unknown aminolipid and two unknown polar lipids and minor to trace amounts of four unknown aminolipids and seven unknown polar lipids (Fig. 3a). This polar lipid profile is almost indistinguishable from that of *C. gleum* (data not shown) and is also similar to that of *C. defluvii*, except that no rather hydrophilic aminophospholipid was detected in NF 1366^T.

The polar lipid profile of *K. koreensis* KCTC 12107^T consisted of the predominant compounds phosphatidylethanolamine, an unknown aminolipid (AL1) and three unknown polar lipids L2, L3 and L4, with the first two exhibiting a very weak reaction with ninhydrin, indicating that they may contain amino groups (Fig. 3b). Further-

more, moderate amounts of an unknown polar lipid L6 and an aminophospholipid APL1 and minor amounts of three unknown polar lipids and three aminolipids could be detected. So far, polar lipid analysis has been carried out for the species *C. defluvii* (Kämpfer *et al.*, 2003), *C. daecheongense* (Kim *et al.*, 2005), *C. aquaticum* (Kim *et al.*, 2008) and *C. gambrini*, *C. molle*, *C. pallidum* and *C. ureilyticum* (Herzog *et al.*, 2008). Unfortunately, only the papers describing *C. defluvii*, *C. gambrini*, *C. molle*, *C. pallidum* and *C. ureilyticum* (Kämpfer *et al.*, 2003; Herzog *et al.*, 2008) provided figures showing the complete polar lipid profiles. This information is of the highest importance when lipid profiles are composed mainly of unknown components, as is the case in *Chryseobacterium*. When detailed comparative chromatographic results are missing from the description, the presence of the same unknown lipid in two strains can only be estimated by visual comparison of its chromatographic behaviour, together with the staining behaviour of the unknown lipid and in correlation with known lipids in the same chromatogram. Still, from the available data, it is possible to conclude that the polar lipid profile of *K. koreensis* KCTC 12107^T is quite similar to those of *C. defluvii*, *C. gambrini*, *C. molle*, *C. pallidum* and *C. ureilyticum*, indicating a close relatedness, which supports the inclusion of *K. koreensis* in the genus *Chryseobacterium*.

Fatty acid analysis was carried out as described previously (Kämpfer & Kroppenstedt, 1996; Kämpfer *et al.*, 2003) on the eight isolates and on the type strains of *C. haifense* and *K. koreensis*. The fatty acid profiles of the eight strains studied were very similar to those of the type strains of *C. haifense* and *K. koreensis* (Table 3) and in accordance with the fatty acid patterns reported for other *Chryseobacterium* species.

Hence, all data resulting from this polyphasic study demonstrate that the six clinical isolates NF 1366^T, NF 1101, NF 1107, NF 1123, NF 1413 and CCUG 15260 represent a novel species in the genus *Chryseobacterium*, for which the name *Chryseobacterium anthropi* sp. nov. is proposed.

K. koreensis was shown to be genotypically and phenotypically very similar to *Chryseobacterium* species. Its polar lipid profile exhibited the major characteristics shown for recently described *Chryseobacterium* species and the fatty acid profile of the type strain of *K. koreensis* was also very similar to those of *Chryseobacterium* species. The species *C. anthropi* sp. nov., *C. haifense* and *K. koreensis* cluster most closely according to 16S rRNA gene sequences and tDNA-PCR patterns and are negative for aesculin hydrolysis and ethylene glycol production, whereas these biochemical characteristics are positive for most other *Chryseobacterium* species. Because no genotypic or phenotypic differences could be found to justify the classification of *K. koreensis* in a separate genus, it is proposed to reclassify *Kaistella koreensis* in the genus *Chryseobacterium* as *Chryseobacterium koreense* comb. nov.

Fig. 3. Two-dimensional TLC separation of the total polar lipids of strain NF 1366^T (a) and *K. koreensis* KCTC 12107^T (b). PE, Phosphatidylethanolamine; APL1, unknown aminophospholipid; AL1–5, unknown aminolipids; L1–7, unknown polar lipids.

Table 3. Fatty acid compositions of the novel strains and the most closely related species

Strains: 1, *C. anthropi* sp. nov. (ranges of values for six strains); 2, *Chryseobacterium* sp. NF 450; 3, *Chryseobacterium* sp. CCUG 15624; 4, *C. haifense* DSM 19056^T; 5, *K. koreensis* DSM 12107^T. All data are from this study. Values are percentages of total fatty acids. tr, Traces (<0.5%); ND, not detected. Unknown fatty acids could not be identified with the MIDI system; numbers indicate their equivalent chain-lengths. For unsaturated fatty acids, the position of the double bond is located by counting from the methyl (ω) end of the carbon chain; *cis* isomers are indicated by the suffix *c*.

Fatty acid	1	2	3	4	5
iso-C _{13:0}	1.2–3.7	ND	3.3	1.8	8.3
anteiso-C _{13:0}	ND–0.5	ND	ND	ND	0.7
Unknown 13.565	2.3–3.5	3.4	2.2	0.8	4.4
iso-C _{14:0}	tr–1.0	ND	ND	2.8	2.0
C _{14:0}	ND–0.5	ND	ND	ND	tr
iso-C _{15:0}	33.9–44.8	34.8	35.4	28.6	43.6
anteiso-C _{15:0}	12.4–20.3	13.9	19.0	12.9	13.0
C _{15:0}	tr	ND	ND	ND	0.5
iso-C _{16:0}	tr	ND	ND	1.2	0.5
Summed feature 3*	1.4–5.9	5.8	5.8	5.0	2.4
C _{16:1} ω 5 <i>c</i>	ND–0.5	ND	ND	1.2	ND
C _{16:0}	ND–3.7	ND	ND	0.5	1.7
iso-C _{15:0} 3-OH	2.4–5.5	3.9	5.5	3.5	2.4
C _{15:0} 2-OH	tr–2.4	2.1	ND	0.9	0.6
iso-C _{17:1} ω 9 <i>c</i>	6.4–12.6	7.4	12.4	22.3	8.0
Summed feature 4*	0.5–2.1	ND	ND	1.2	0.8
Unknown 16.582	ND–1.5	ND	ND	0.6	0.9
iso-C _{16:0} 3-OH	0.8–2.5	4.6	ND	1.6	2.3
C _{18:1} ω 5 <i>c</i>	0.9–1.5	ND	ND	1.0	0.5
iso-C _{17:0} 3-OH	5.3–11.6	22.3	14.3	11.9	6.0
C _{17:0} 2-OH	tr–1.6	ND	ND	2.3	0.5

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

Description of *Chryseobacterium anthropi* sp. nov.

Chryseobacterium anthropi (an'thro.pi. Gr. n. *anthropos* a human being; N.L. gen. n. *anthropi* of a human being, since all strains so far recovered are from human clinical specimens).

Non-motile, Gram-staining-negative rods, 2–4 μ m long and 0.5–1 μ m wide, growing aerobically at 20, 30 and 37 °C on standard media such as tryptic soy agar and blood agar, with optimal growth at 30 °C. No growth on MacConkey agar, cetrimide agar or 3% NaCl agar. Colonies are circular and may be mucoid or dry; most are also sticky. No flexirubin pigments are produced. Acid is produced oxidatively from glucose and maltose, whereas acid production from mannose is strain-dependent. No

acid is produced from ethylene glycol. Indole is produced. Urease, lysine decarboxylase, ornithine decarboxylase and arginine dihydrolase activities are absent. Acetate is alkalinized but citrate is not. Nitrate is not reduced. Gelatin is hydrolysed but aesculin is not. Alkaline phosphatase, pyrrolidonyl aminopeptidase and trypsin activities are present. Hydrolysis of Tween 80 is strain-dependent. The major cellular fatty acids are iso-C_{15:0} and anteiso-C_{15:0}, followed by C_{17:1} ω 9*c*, iso-C_{13:0} and iso-C_{17:0} 3-OH. The polyamine pattern consists of the major compound *sym*-homospermidine and minor amounts of spermidine and spermine. The quinone system is menaquinone MK-6. The major polar lipids are phosphatidylethanolamine, an unknown aminophospholipid, an unknown aminolipid and two unknown polar lipids with minor to trace amounts of four unknown aminolipids and seven unknown polar lipids.

The type strain is NF 1366^T (=CCUG 52764^T =CIP 109762^T), isolated from the blood of a hospitalized patient. Strains NF 1101 (=CCUG 52762), NF 1107, NF 1123 (=CCUG 52763), NF 1413 and CCUG 15260 (=CDC F4391 =LMG 8325) are also members of the species.

Description of *Chryseobacterium koreense* comb. nov.

Chryseobacterium koreense (ko.re.en'se. N.L. neut. adj. *koreense* of Korea, from where the organism was first isolated).

Basonym: *Kaistella koreensis* Kim *et al.* 2004.

The phenotypic characteristics are those described by Kim *et al.* (2004) with the following amendments, based on the study of the type strain. No flexirubin pigments are produced, acid is produced from glucose, maltose and mannose, aesculin is not hydrolysed, acetate and citrate are not alkalinized and alkaline phosphatase, pyrrolidonyl aminopeptidase and trypsin activities are present. The major polar lipids are phosphatidylethanolamine, an unknown aminolipid (AL1) and the unknown polar lipids L2, L3 and L4. Moderate amounts of an unknown polar lipid L6 and aminophospholipid APL1 are present.

The type strain is strain Chj707^T =IAM 15050^T =JCM 21512^T =KCTC 12107^T =NBRC 103027^T.

Emended description of the genus *Chryseobacterium* Vandamme *et al.* 1994

The description of the genus is as given by Vandamme *et al.* (1994), with the exception that the major polyamine is *sym*-homospermidine.

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