Chryseobacterium arothri Campbell *et al.* 2008 is a later heterotypic synonym of *Chryseobacterium hominis* Vaneechoutte *et al.* 2007

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The type strains of the species *Chryseobacterium arothri* (DSM 19326^T) and *Chryseobacterium hominis* (NF802^T) were compared in order to clarify the taxonomic relationship of the two species. The 16S rRNA gene sequences of the two strains shared 99.9 % identity. DNA–DNA pairing studies between the two strains showed 100 % (reciprocal, 76.0 %) relatedness. Phenotypic data, including fatty acid patterns and substrate utilization profiles, showed no pronounced differences between the type strains of the two species. On the basis of these results, we propose the reclassification of *Chryseobacterium arothri* Campbell *et al.* 2008 as a later heterotypic synonym of *Chryseobacterium hominis* Vaneechoutte *et al.* 2007.

Chryseobacterium arothri was described by Campbell *et al.* (2008) for a novel strain isolated from the kidney of a pufferfish. A few months earlier, *Chryseobacterium hominis* was described by Vaneechoutte *et al.* (2007) for clinical isolates biochemically similar to CDC groups II-c and II-h. The two species were described at nearly the same time. Soon after the publication of the two studies, it became obvious that the type strains of these species were closely related on the basis of 16S rRNA gene sequence similarities. The 16S rRNA gene sequences of *C. arothri* P2K6^T (GenBank accession no. EF554408) and *C. hominis* NF802^T (AM261868) shared 99.9 % similarity. A further comparative phenotypic analysis supported this finding.

The original descriptions were based on the properties of strains of the two species grown on tryptic soy agar at 28 °C. However, the duration of incubation differed (i.e. 24 h for the type strain of *C. arothri* and 48 h for four *C. hominis* strains). In order to compare the fatty acid profiles of the two species grown under exactly the same conditions, the type strain of *C. arothri* (DSM 19326^T) was grown in this study for 48 h on tryptic soy agar at 28 °C. Fatty acid methyl esters were prepared, separated and identified according to the instructions of the Microbial Identification System (MIDI, Microbial ID; Kämpfer & Kroppenstedt, 1996), in order to study the strains simultaneously. The fatty acid profiles of the two strains are shown in Table 1. No significant differences in the fatty acid profiles were found.

Biochemical and morphological tests were again performed as described previously (Laffineur *et al.*, 2002; Schreckenberger *et al.*, 2003). Assimilation–alkalinization

of organic compounds was detected on Simmons' citrate agar base, replacing citrate with 0.2 % (w/v) of various organic substrates, according to Martin *et al.* (1981). Enzyme reactions were determined using diagnostic tablets from Rosco. The KOH test was used to detect flexirubin pigments (Bernardet *et al.*, 2002). All 11 strains of *C. hominis* and the type strain of *C. arothri* were positive for oxidase and catalase activities, growth at 30 and 37 °C (with optimal growth at 30 °C), aerobic growth, acid production from glucose, maltose and ethylene glycol, indole production, hydrolysis of aesculin, starch and gelatin, alkaline phosphatase, trypsin (benzyl arginine arylamidase) and pyrrolidonyl aminopeptidase (except CCUG 36749) activities and resistance to desferrioxamine. Acid production from sucrose, reduction of nitrate and nitrite and hydrolysis of tyrosine were variable among the *C. hominis* strains. Schreckenberger *et al.* (2003) reported a positive nitrate reduction (90 %) in group II-c and a negative result in group II-h. However, in our series, four strains out of seven with a II-h profile reduced nitrate. All strains were negative for production of flexirubin pigments, growth at 42 °C, H₂S production on Kligler agar, Tween 80 hydrolysis, alkalinization of citrate on Simmons' agar and activities of ornithine and lysine decarboxylases, urease, arginine dihydrolase and L-phenylalanine deaminase. Other important characteristics used to differentiate *Chryseobacterium* species are shown in Table 2 for *C. hominis* and *C. arothri*.

DNA–DNA hybridization experiments were performed with strains *C. hominis* NF802^T and *C. arothri* DSM 19326^T. DNA isolation and DNA–DNA hybridization were done as described previously (Kämpfer *et al.*, 2003). Results

Table 1. Cellular fatty acid profiles of strains of *C. hominis* and *C. arothri*

Data for *C. hominis* strains were taken from Vanechoutte *et al.* (2007). 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*. Values are percentages of total fatty acids; fatty acids amounting to <1 % of the total fatty acids in all strains studied are not shown. tr, Traces (<1 %); ND, not detected.

Fatty acid	<i>C. hominis</i> (n=4)	<i>C. arothri</i> DSM 19326 ^T	
		This study	Campbell <i>et al.</i> (2008)
iso-C _{13:0}	tr–4.8	1.3	5.0
Unknown 13.565*	ND–6.9	7.1	ND
iso-C _{15:0}	22.4–35.8	27.5	35.3
anteiso-C _{15:0}	8.1–9.6	6.4	5.5
Summed feature 3†	7.5–17.8	12.2	13.9
C _{16:1} ω5 <i>c</i>	ND	1.3	2.1
C _{16:0}	ND–3.0	tr	1.5
iso-C _{15:0} 3-OH	4.3–6.0	5.2	4.5
C _{16:0} 3-OH	ND–4.8	3.8	5.1
iso-C _{17:1} ω9 <i>c</i>	15.6	7.2	ND
Summed feature 4†	2.4	1.0	6.3
iso-C _{17:0} 3-OH	16.3–19.9	19.0	14.9
C _{17:0} 2-OH	ND	tr	tr

*This fatty acid could not be identified with the MIDI system; its equivalent chain length is provided.

†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}ω7*c* and/or iso-C_{15:0} 2-OH; summed feature 4 contained anteiso-C_{17:1} B and/or anteiso-C_{17:1} I.

Table 2. Physiological and biochemical properties of strains of *C. hominis* and *C. arothri*

Data were obtained in this study. +, Positive; (+), delayed positive; –, negative; v, variable, strain-dependent.

Characteristic	<i>C. hominis</i> (n=11)	<i>C. arothri</i> DSM 19326 ^T
Acid production from:		
Glucose	+	+
Sucrose	v	+
Mannitol	–	–
Arabinose	–	–
Cellobiose	v	(+)
Lactose	–	–
Maltose	+	+
Trehalose	–	–
Xylose	–	–
Ethylene glycol	+	+
Hydrolysis of:		
Aesculin	+	+
Tween 80 (7 days)	–	–
Starch	+	+
Tyrosine	v	–
Gelatin	+	+
Growth at 36–37 °C	+	+
Growth on MacConkey agar	–	–
Nitrate reduction	v	–
Urease activity	–	–
Indole production	+	+
Acetate alkalization	+	+
Flexirubin pigments	–	–
β-Galactosidase activity (ONPG)	–	–

of the DNA–DNA cross-hybridization yielded a relatedness of 100 %, whereas in reciprocal hybridization a lower value of 76 % was obtained.

Based on the presented results, it is proposed to unite the species *Chryseobacterium arothri* Campbell *et al.* 2008 and *Chryseobacterium hominis* Vaneechoutte *et al.* 2007. According to Rules 38, 42 and 24b(2) of the Bacteriological Code (Lapage *et al.*, 1992), the name *Chryseobacterium hominis* has priority and hence should be used for the unified taxon, with *Chryseobacterium arothri* as a later heterotypic synonym.

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