Transfer of *Sejongia antarctica*, *Sejongia jeonii* and *Sejongia marina* to the genus *Chryseobacterium* as *Chryseobacterium antarcticum* comb. nov., *Chryseobacterium jeonii* comb. nov. and *Chryseobacterium marinus* comb. nov.

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The genus *Sejongia* was described in 2005, with the two species *Sejongia antarctica* and *Sejongia jeonii*, mainly on the basis of 16S rRNA gene sequence analysis. At that time, these organisms formed a quite separate branch in a 16S rRNA gene sequence-based tree, but, in subsequent studies, it became obvious that the species *S. antarctica* and *S. jeonii* and a third species, *Sejongia marina*, were most closely related (>95.0 % similarity) to some *Chryseobacterium* species (e.g. *Chryseobacterium hominis*, *C. formosense* and *C. haifense*). In addition, there is no evidence for clear phenotypic (i.e. chemotaxonomic) differences between these organisms that justifies their assignment to different genera. For these reasons, a proposal is made to transfer these species to the genus *Chryseobacterium* as *Chryseobacterium antarcticum* comb. nov. (type strain AT1013<sup>T</sup> = JCM 12381<sup>T</sup> = IMNSU 14040<sup>T</sup> = KCTC 12225<sup>T</sup>), *Chryseobacterium jeonii* comb. nov. (type strain AT1047<sup>T</sup> = JCM 12382<sup>T</sup> = IMNSU 14049<sup>T</sup> = KCTC 12226<sup>T</sup>) and *Chryseobacterium marinus* comb. nov. (type strain IMCC3228<sup>T</sup> = KCCM 42689<sup>T</sup> = NBRC 103143<sup>T</sup>) on the basis of 16S rRNA gene sequence data and published phenotypic data.

The genus *Chryseobacterium* was proposed by Vandamme *et al.* (1994) in the course of the subdivision of the genus *Flavobacterium*, which at that time contained a rather heterogeneous group of yellow-pigmented, Gram-negative organisms. At that time, the new genus *Chryseobacterium* contained the six species *Chryseobacterium balustinum*, *C. gleum*, *C. indologenes*, *C. indoltheticum*, *C. meningocepticum* and *C. scophthalmum*. These species were similar in many respects. They share many classical phenotypic features: they all contain menaquinone 6 (MK-6) as their major respiratory quinone and they have similar fatty acid profiles, which are characterized by large amounts of iso-15 : 0, iso-17 : 1<sup>0</sup>, iso-17 : 0 3-OH and summed feature 4 (iso-15 : 0 2-OH and/or 16 : 1<sup>0</sup>)<sup>7</sup>. Within this group, *C. meningocepticum* revealed the most aberrant fatty acid profile and was subsequently transferred to the new genus *Elizabethkingia* (Kim *et al.*, 2005b). Between 1994 and 2008, the number of *Chryseobacterium* species increased significantly, to 37 species with validly published names (de Beer *et al.*, 2005; Gallego *et al.*, 2006; Herzog *et al.*, 2008; Kämpfer *et al.*, 2003, 2009; Kim *et al.*, 2005a, 2008; Li *et al.*, 2003; Park *et al.*, 2006; Quan *et al.*, 2007; Shen *et al.*, 2005; Shimomura *et al.*, 2005, 2008; Li *et al.*, 2005; Tai *et al.*, 2006; Vaneechoutte *et al.*, 2007; Weon *et al.*, 2006; Young *et al.*, 2005). This increase in the number of species was accompanied by the proposal of two novel genera, *Kaistella* (Kim *et al.*, 2004) and *Sejongia* (Yi *et al.*, 2005), that share many features of *Chryseobacterium* species. The reclassification of the sole species of the genus *Kaistella* in the genus *Chryseobacterium* is proposed elsewhere (Kämpfer *et al.*, 2009).

Recently, several *Chryseobacterium* species, i.e. *Chryseobacterium haifense* (Hantsis-Zacharov & Halpern, 2007), *C. hominis* (Vaneechoutte *et al.*, 2007) and ‘C. anthropi’ (Kämpfer *et al.*, 2009), amongst others, have been described with high 16S rRNA gene sequence similarities to the species of the genus *Sejongia*. In comparisons of the 16S rRNA gene sequences of type strains, *C. haifense* showed similarities of 95.3 % to *Sejongia antarctica*, 95.8 % to *Sejongia jeonii* and 95.0 % to *Sejongia marina*, *C. hominis* showed similarities of 95.1 % to *S. antarctica*, 96.5 % to *S.
jeonii and 95.6% to S. marina and ‘C. anthropi’ showed similarities of 95.3% to S. antarctica, 95.9% to S. jeonii and 94.8% to S. marina. 16S rRNA gene sequence similarities of the type strain of C. formosense (Young et al., 2005) were 95.7% to S. antarctica, 96.3% to S. jeonii and 95.9% to S. marina. Similarities were calculated using the ARB software package (version December 2007; Ludwig et al., 2004) and the corresponding SILVA SSURef 95 database (release July 2008; Pruesse et al., 2007).

The 16S rRNA gene sequences for all strains under comparison were analysed as described above. Trees were reconstructed using the maximum-likelihood method with fastDNAml (Olsen et al., 1994) and a 50% conservation filter (only alignment columns in which the frequency of the most abundant nucleotide is equal to or more than 50% are included in the calculation). Tree topology was further tested with no conservation filter and with 30 and 40% conservation filters. No significant differences could be detected between these trees. For tree reconstruction, 90 sequences were included. For better clarity, only a subset of the sequences used for treeing are shown in Fig. 1.

On the basis of these comparisons, the type strains of the three Sejongia species fell clearly in the Chryseobacterium cluster at a depth similar to other Chryseobacterium species groups.

Although respiratory quinones have low resolution within this group, the presence of MK-6 supports affiliation of the Sejongia species to the genus Chryseobacterium, where all species investigated to date have MK-6 as the major quinone.

The fatty acid profiles of all Sejongia species were very similar to those of species of Chryseobacterium, as reported already by Yi et al. (2005). All Sejongia species reveal iso-15:0, anteiso-15:1 and iso-17:1o9c as the major fatty acids (Yi et al., 2005; Lee et al., 2007), which is essentially in agreement with the fatty acid patterns of Chryseobacterium species (de Beer et al., 2005; Gallego et al., 2006; Herzog et al., 2008; Kämpfer et al., 2003, 2009; Kim et al., 2005a, 2008; Li et al., 2003; Park et al., 2006; Quan et al., 2007; Shen et al., 2005; Shimomura et al., 2005; Tai et al., 2006; Vaneechoutte et al., 2007; Weon et al., 2006; Young et al., 2005).

In conclusion, the species of Sejongia and Chryseobacterium show a strong congruence in phenotypic characters, in that they all produce MK-6 as the major menaquinone and the fatty acid profiles are very similar. Only a few differences have been reported with regard to cell morphology and certain physiological tests.

For these reasons, it is proposed to reclassify Sejongia antarctica, Sejongia jeonii and Sejongia marina in the genus Chryseobacterium as the new combinations Chryseobacterium antarcticum comb. nov., Chryseobacterium jeonii comb. nov. and Chryseobacterium marinum comb. nov.

**Description of Chryseobacterium antarcticum comb. nov.**

Chryseobacterium antarcticum (ant. arc.’tium. L. neut. adj. antarcticum southern, named after Antarctica, the geographical origin of the type strain).


The description is that of Yi et al. (2005). The type strain is AT1013 (ATCC 12225 = KCTC 12225 = JCM 12381).

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**Fig. 1.** Phylogenetic analysis based on 16S rRNA gene sequences available from the EMBL database (accession numbers in parentheses). The phylogenetic tree was constructed using the ARB software package (version December 2007; Ludwig et al., 2004) and the corresponding SILVA SSURef 95 database (version July 2008; Pruesse et al., 2007). Tree building was performed with 90 sequences using the maximum-likelihood method with fastDNAml (Olsen et al., 1994) and 50% conservation filter. For better clarity, only a subset of the sequences used for treeing is shown. Bar, 0.05 substitutions per nucleotide position.

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Description of Chryseobacterium jeonii comb. nov.

Chryseobacterium jeonii (jeo’ni.i. N.L. gen. n. jeonii named in honour of the late Jae Gyu Jeon, who devoted his life to polar research).


The description is that of Yi et al. (2005). The type strain is AT1047^T (=KCCM 14049^T =KCTC 12226^T =JCM 12382^T).

Description of Chryseobacterium marinum comb. nov.

Chryseobacterium marinum (ma.r'i.num. L. neut. adj. marinum of the sea).

Basonym: Sejongia marina Lee et al. 2007.

The description is that of Lee et al. (2007). The type strain is IMCC3228^T (=KCCM 42689^T =NBRC 103143^T).

References


