

Transfer of *Sejongia antarctica*, *Sejongia jeonii* and *Sejongia marina* to the genus *Chryseobacterium* as *Chryseobacterium antarcticum* comb. nov., *Chryseobacterium jeonii* comb. nov. and *Chryseobacterium marinum* 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^T = JCM 12381^T = IMSNU 14040^T = KCTC 12225^T), *Chryseobacterium jeonii* comb. nov. (type strain AT1047^T = JCM 12382^T = IMSNU 14049^T = KCTC 12226^T) and *Chryseobacterium marinum* comb. nov. (type strain IMCC3228^T = KCCM 42689^T = NBRC 103143^T) 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. meningosepticum* 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 ω 9c, iso-17:0 3-OH and summed feature 4 (iso-15:0 2-OH and/or 16:1 ω 7c). Within this group, *C. meningosepticum* 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; 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 fastDNAmI (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-17:1 ω 9c 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; Vanechoutte *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'ti.cum. L. neut. adj. *antarcticum* southern, named after Antarctica, the geographical origin of the type strain).

Basonym: *Sejongia antarctica* Yi *et al.* 2005.

The description is that of Yi *et al.* (2005). The type strain is AT1013^T (=IMSNU 14040^T =KCTC 12225^T =JCM 12381^T).

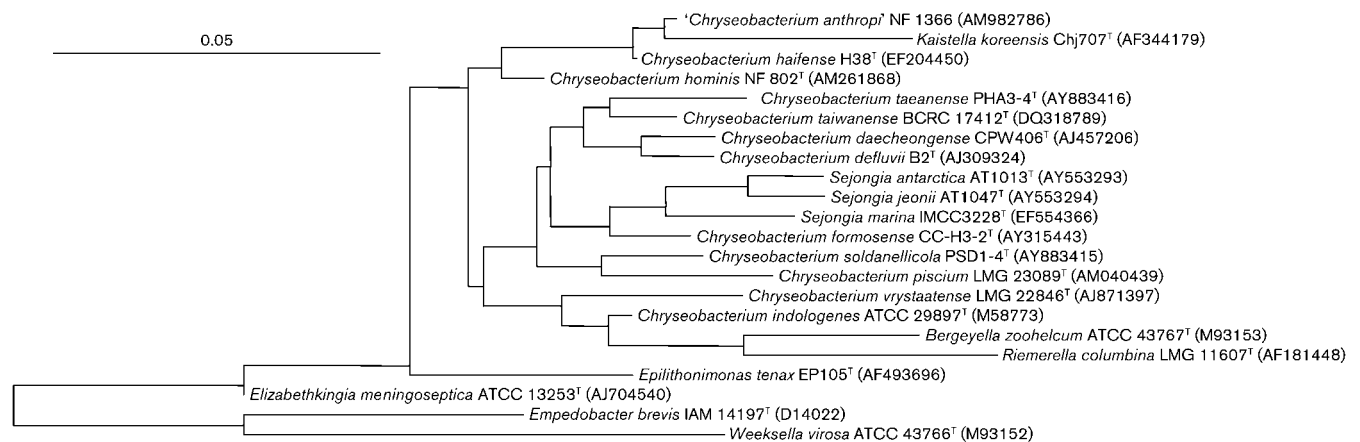


Fig. 1. Phylogenetic analysis based on 16S rRNA gene sequences available from the EMBL database (accession numbers in parentheses). The phylogenetic tree was constructed using the ARB software package (version December 2007; Ludwig *et al.*, 2004) and the corresponding SILVA SSURef 95 database (version July 2008; Pruesse *et al.*, 2007). Tree building was performed with 90 sequences using the maximum-likelihood method with fastDNAmI (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.

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).

Basonym: *Sejongia jeonii* Yi *et al.* 2005.

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

Description of *Chryseobacterium marinum* comb. nov.

Chryseobacterium marinum (ma.ri'num. L. neut. adj. *marinum* of the sea, marine).

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).

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