Arch Microbiol (2001) 176 : 391–392
DOI 10.1007/s002030100334

ERRATUM

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A *Desulfitobacterium* strain isolated from human feces that does not dechlorinate chloroethenes or chlorophenols

Arch Microbiol (2001) 175:389–394

In the Results section, formation was erroneously omitted from the first paragraph of the subsection “Phylogeny” on p. 392, which should read:

The main part of the 16S rRNA gene of strain DP7 was amplified by PCR, cloned, and sequenced, resulting in a nearly complete sequence of 1,644 nucleotides. Phylogenetic analysis was carried out with related species (Fig. 3). Comparison of strain DP7 with *D. dehalogenans* JW/IU-DC1, *Desulfitobacterium* sp. strain PCE1, *D. chlororespirans* Co23, *D. hafniense* DCB-2, *D. frappieri* strain PCP-1, and *D. frappieri* strain TCE1 revealed that strain DP7 is more related to *D. frappieri* strain TCE1 (using sequence 1 for analyses, accession number X95742; see below) (99.4% similarity and only nine mismatches, both based on the total sequences) than to the other *Desulfitobacterium* species. However, two 16S rRNA gene sequences from *D. frappieri* TCE1 are known. Both sequences come from the same pure culture (J. Gerritse, personal communication). Previously, only sequence 2 (accession number X95972) from strain TCE1 was used for phylogenetic analyses (Gerritse et al. 1999). This sequence is less related to that of strain DP7 (95.8%) and resembles more the sequence of strain PCP1. After *E. coli* position 117, however, sequences 1 and 2 from strain TCE1 are identical and differ only in two bases from the sequence of strain DP7. Recently, it was shown that *Desulfitobacterium* species contain more than one 16S rRNA gene (Ebersbach et al. 2000). This is the case for strain TCE1, and it can be assumed that also strain DP7 contains more that one 16S rRNA gene. The sequence similarity of the 16S rRNA of strain DP7 with the other *Desulfitobacterium* strains and *Desulfosporosinus orientis* was determined (Table 1) and it was shown that phylogenetic analysis of this group could be biased by the inclusion of a hypervariable region between *E. coli* positions 75–94. When this region was included in the analysis, strain DP7 had only 95% similarity with *D. frappieri* PCP1, while it had 99% similarity with *D. frappieri* PCP1 when this region was excluded. However, strain DP7 and the two *D. frappieri* strains all had a long insert, unlike the other *Desulfitobacterium* strains, which indicated the relationship between the *D. frappieri* strains.

The following reference has been added:

Ebersbach H, Breitenstein A, Lechner U (2000) All species of *Desulfitobacterium* contain two types of 16S rRNA genes of different length. Biospektrum (special issue) p. 157 (Abstract 15.P.13.01)

A strain was erroneously omitted from Table 1, and some numbers in the last column were incorrect. The table should be replaced by the following:

The online version of the original article can be found at:
http://dx.doi.org/10.1007/s002030100276

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Table 1 Similarities (%) and comparison of insert size (nucleotides) of 16S rRNA sequences of *Desulfitobacterium frappieri* DP7 with other *Desulfitobacterium* species and *Desulfosporosinus orientis.* *NS* No sequence information available

Strain	Sequence accession number	Similarities including *E. coli* positions 117–1,489	Similarities including all positions	Insert size between *E. coli* positions 75 and 94
Desulfitobacterium frappieri DP7	AJ276701	100	100	139
Desulfitobacterium frappieri TCE1 (1)	X95742	99.93	99.38	139
Desulfitobacterium frappieri TCE1 (2)	X95972	99.93	95.83	120
Desulfitobacterium frappieri PCP1	U40078	99.78	95.82	120
Desulfitobacterium hafniense	X94975	99.78	98.00	22
Desulfitobacterium chlororespirans	U68528	98.34	96.88	22
Desulfitobacterium dehalogenans	L28946	97.23	96.26	22
Desulfitobacterium sp. PCE1	X81032	96.47	96.45	NS
Desulfosporosinus orientis	Y11570	93.87	92.72	22