



Reevaluating the classification of *Halobacteroides* and  
*Halococcus* species based on sequence comparisons of the

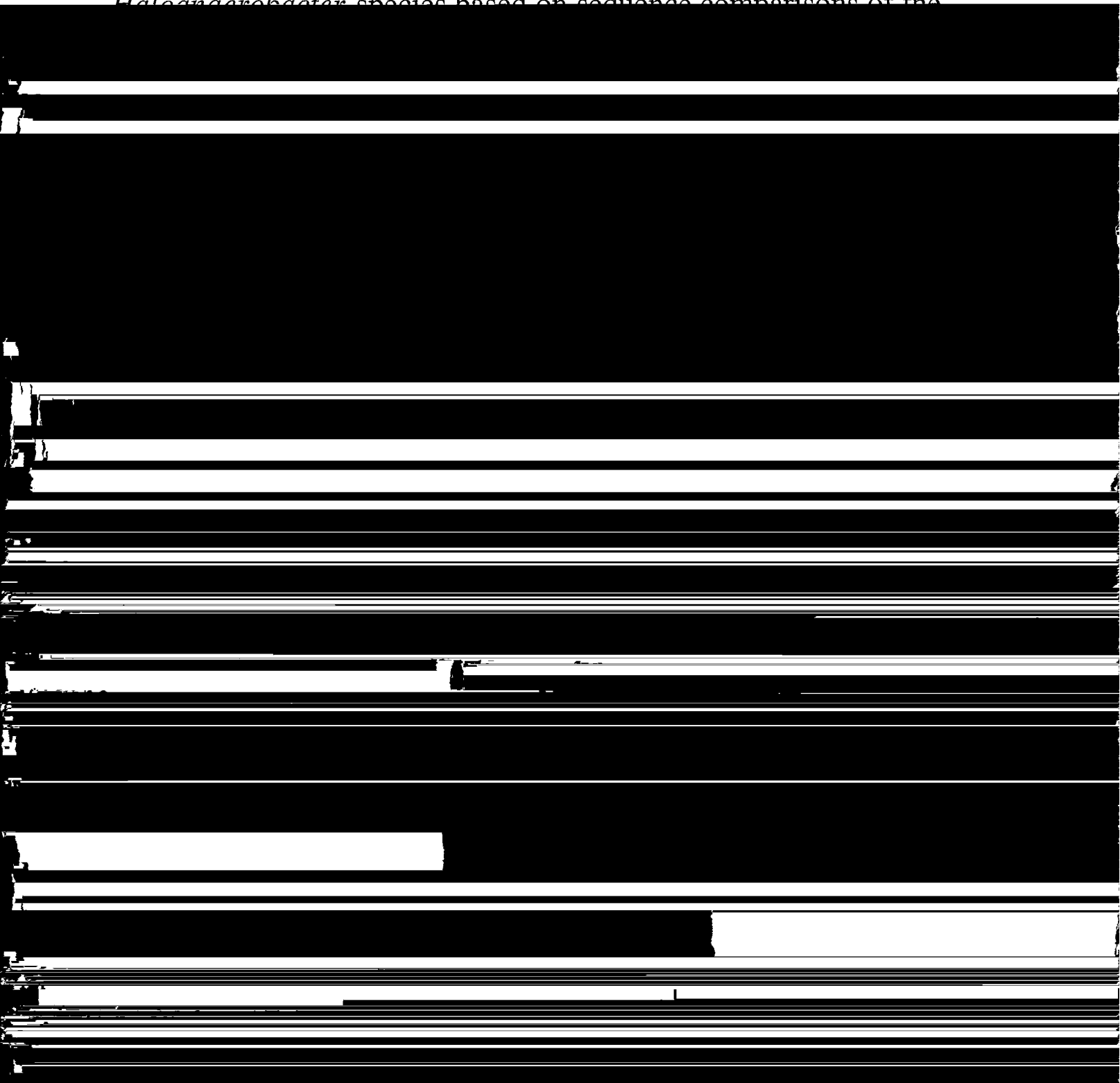




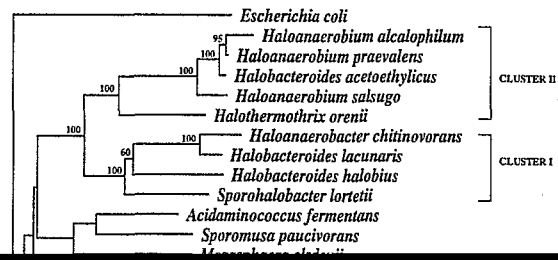
Table 1

Evolutionary distances of members of the family Haloanaerobiaceae and various representatives of the Gram-positive phylum based on the method of Jukes and Cantor [6]

1 <i>Escherichia coli</i>																		
2 <i>Haloanaerobacter chitinovorans</i>	30.2																	
3 <i>Halobacteroides lacunaris</i>	29.7	4.4																
4 <i>Halobacteroides halobius</i>	28.9	11.9	13.8															
5 <i>Sporohalobacter lortetii</i>	29.5	11.6	13.4	13.1														
6 <i>Halobacteroides acetoethylicus</i>	29.0	18.8	20.1	19.0	17.9													
7 <i>Haloanaerobium praevalens</i>	29.2	18.7	20.1	17.9	18.1	1.3												
8 <i>Haloanaerobium salsugo</i>	28.5	20.3	21.3	21.2	18.4	3.5	4.6											
9 <i>Haloanaerobium alcaliphilum</i>	30.7	20.0	21.4	20.3	19.4	2.6	2.0	5.9										
10 <i>Halothermothrix orenii</i>	27.6	18.3	19.4	19.4	15.7	13.1	14.0	12.3	15.5									
11 <i>Sporomus paucivorans</i>	26.6	23.4	24.4	23.2	22.3	23.4	23.5	22.9	25.2	22.0								
12 <i>Megasphaera elsdenii</i>	25.1	24.1	26.1	23.2	22.5	23.4	23.5	24.0	25.5	22.2	16.2							
13 <i>Heliobacterium chlorum</i>	25.2	22.9	24.4	24.0	22.2	23.8	24.1	22.5	25.7	20.7	18.3	19.8						
14 <i>Acidaminococcus fermentans</i>	27.1	23.2	24.8	22.0	21.2	22.0	21.7	21.3	23.7	19.3	12.1	15.1	18.7					
15 <i>Moorella thermoacetica</i>	26.1	21.6	22.8	21.0	19.6	22.2	22.9	21.4	24.1	20.0	21.7	19.4	17.2	19.6				
16 <i>Thermoanaerobacterium saccharolyticum</i>	25.4	19.4	20.6	18.6	18.4	19.6	19.8	19.8	21.6	19.3	17.9	17.2	16.7	18.0	13.6			
17 <i>Syntrophospora bryantii</i>	23.1	19.6	20.7	20.3	19.6	22.2	22.6	21.7	24.4	19.4	19.0	18.8	16.1	18.3	16.9	13.8		
18 <i>Syntrophomonas wolfei</i>	23.5	20.3	21.9	21.4	22.0	22.3	22.5	21.7	24.3	21.3	20.6	19.0	16.6	19.1	17.6	14.2	4.6	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18

The sequences used in distance calculations were obtained from the Ribosomal Database Project, version 5.0 [10] with the exception of the sequence of *H. alcaliphilum*, which was extracted from EMBL (accession number X81850). A total of 906 unambiguous nucleotides were used in the analysis. *Clostridium thermoaceticum* and *Clostridium thermosaccharolyticum* have been recently renamed *Moorella thermoacetica* and *Thermoanaerobacterium saccharolyticum* [4].

their 16S rDNA sequence analysis indicates that they are very close phylogenetic relatives of each other (an evolutionary distance of 4.5). The 16S rDNA sequence analysis also established that *H. lacunaris* and *Hb. chitinovorans* are phylogenetic relatives of *H. halobius* (evolutionary distances of 13.8 and 11.9, respectively). Based on these results, we propose that *Hb. chitinovorans* be transferred to the genus



recently from its original description [20] and in-

[10] Maidak, B.L., Larsen, N., McCaughey, M.J., Overbeek, R.,

*et al.*, *Appl. Environ. Microbiol.* 61 (1995) 3623–3631.