Nucleotide sequences of 16S rRNA encoding genes from halophilic archaea *Halococcus morrhuae* NRC16008 and *Haloferax mediterranei* ATCC33500

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The authors have reported that several strains of halophilic archaea, including *Hc.morrhuae* NRC16008 (NCMB746) and *Hf.mediterranei* R4 ATCC33500, produced extracellular halophilic proteases on agar plates containing 3 to 4 M NaCl (1). Later investigation showed that ten more unidentified halophilic archaeal strains recently isolated from saline samples exhibited extracellular protease activities. Since several complete and partial sequences of 16S rRNA encoding genes have been reported from halophilic archaea, the authors sequenced the genes of the above mentioned two species to enrich the 16S rRNA data base for the future use for the identification of the halophilic archaeal isolates.

Four primers were synthesized, 20 nucleotides long each, designed from very conserved regions of 16S rRNA of halophilic archaea (sense, 1−20 and 688−707: antisense, 720−739 and 1453−1472, numbering according to ref.2 for *Halobacterium cutirubrum* 16S rRNA), and used in PCR for the amplification of rDNA, approximately 740 and 785 bp. The partially overlapping rDNAs were sequenced by the dideoxy method with dye-labelled M13(−21) universal-primers using ABI 373A DNA sequencer. The result is shown in Figure 1 in an aligned form with a total of 164 substitutions including 5Ns. On the other hand *Hc.morrhuae* NRC 16008 16S rRNA differed from that of *Hc.morrhuae* ATCC17082 (3) in only 12 bases except for 5Ns, while there were 24 substitutions between *Hf.mediterranei* and *Hf.volcanii* (4).

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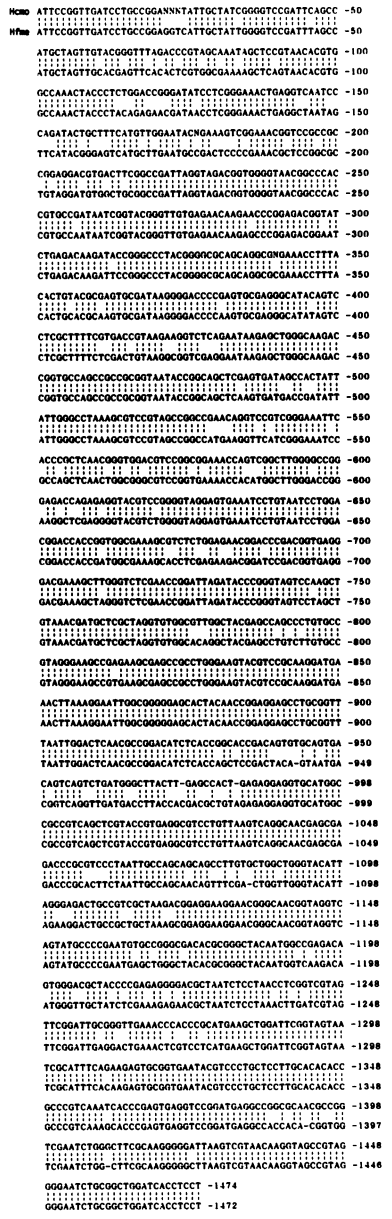

Figure 1. Sequences of 16S rRNA encoding genes from *Halococcus morrhuae* NRC 16008 (National Research Council Canada) (Hcmo) and *Haloferax mediterranei* ATCC33500 (Hfme). N, ambiguous bases; dashes, gaps required to maintain the alignment.