
Nucleotide sequence of the 5S rRNA from *Listonella (Vibrio) ordalii* ATCC 33509 and *Listonella (Vibrio) tubiashii* ATCC 19105

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The 5S ribosomal RNA nucleotide sequences of *Vibrio tubiashii* ATCC 19105 and *Vibrio ordalii* ATCC 33509 have been determined. The 5S rRNA was extracted, purified, and sequenced enzymatically (1), as previously described (2). The sequences are shown below:

V. ordalii ATCC 33509

5'UGCUUGGGAUCAUAGCGUUGUGGACCCACCUGACUCCAUGCCGAACUCAGAAGUGAAAC
ACAACAGCGCCGAUGGUAGUGUGGGGUUCCCAUGUGAGAGUAGGACAUCGCUAGGCAU 3'

V. tubiashii ATCC 19105

5'UGCUUGCGCACCAUAGCGUUGUGGACCCACCUGAUCCAUGCCGAACUCAGAAGUGAAAC
GCAAUAGCGCCGAUGGUAGUGUGGGGUUCCCAUGUGAGAGUAGGACAUCGCCAGGCAU 3'

The most accurate secondary structure model for these sequences is that of Erdmann *et al.* (3). This model has been depicted for a closely related organism, *Listonella (Vibrio) aestuariana* ATCC 35048, in (4). Cluster analysis of the sequences shows that both organisms belong to the gamma-3 subdivision of the Rhodobacteria, and are members of the newly proposed genus *Listonella* (5). Based on comparative sequence analysis, *V. ordalii* is closely related to *L. pelagia*, *L. anguillara*, and *V. tubiashii* (95.5%, 94.8%, and 94.8% sequence similarity, respectively). *V. tubiashii* is also closely related to *L. pelagia*, as well as to *L. aestuariana* and *Photobacterium logei* (5) (99.3%, 97.0%, and 97.0% sequence similarity, respectively).

These results suggest that *Vibrio ordalii* ATCC 33509 and *Vibrio tubiashii* ATCC 19105 are misnamed. Further work is required to define the genus *Listonella* and determine its position within the family Vibrionaceae.

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