Nucleotide sequence of the *unc* operon of *Vibrio alginolyticus*

Lee R.Krumholz, Ursula Esser and Robert D.Simoni*

Department of Biological Sciences, Stanford University, Stanford, CA 94305, USA
Submitted August 21, 1989 EMBL accession no. X16050

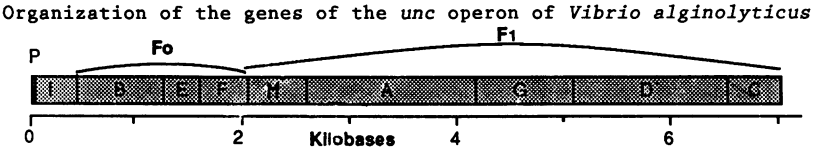
Vibrio alginolyticus is an aerobic marine bacterium. It produces energy through oxidative phosphorylation as is typical of a variety of aerobic bacteria. It contains a unique sodium pumping NADH/ubiquinone oxidoreductase (1). The sodium gradient generated by this process can be used to produce ATP via a sodium dependent ATP synthase activity which has been observed to be present in this organism (2). The ATP synthase is a membrane protein which converts an electrochemical cation gradient into energy in the form of ATP. When no electron acceptor is present, ATP hydrolysis can be used for the formation of a cation gradient. Because of interest in the structure function relationships of ATPases which pump different cations, we sequenced the F1Fo ATPase of *V. alginolyticus*.

A chromosomal DNA library was constructed in bacteriophage lambda Dash (Stratagene Inc.) which for screening was plated on *E. coli unc* deletion strain DK-8. Plaques were screened by hybridization with pRPG44, a plasmid containing most of the *unc* operon (ATPase genes) of *Escherichia coli*.

Restriction fragments which hybridized with the unc genes were subcloned into pBluescript (Stratagene Inc.) and the fragments were sequenced.

The sequence of the entire *unc* operon of *V. alginolyticus* is presented here. It includes the transcriptional promotor region (TATA box is underlined) and the 9 open reading frames (ORF's) designated uncIBEFHAGDC based on homology with the same genes in the *E. coli unc* operon (unpublished data). The structural organization of this operon is similar to that of the *unc* operon in *E. coli*. All the ORF's have Shine-Dalgarno sequences which are properly placed. The uncH gene has an unusual Shine-Dalgarno sequence (GGGGG). All the genes have ATG as a start codon except uncF which uses GTG.

Organization of the genes of the *unc* operon of *Vibrio alginolyticus*




```
1    AATTGCCAAGCTTGAGGCCTAGATGAGATAATTGATTTAGGTCAATTAATCTAATTAATCGAATTTTGTGCGAAAGTTGTCGTTTTGTAA
91   ACAAAACTGTAAGTTTTTGATGCAATCGAATTGCTTTACGTTGAACTGAACGTATAATTTTCGCCAATTTCCCAGCACAGAGAGTTTAGT
                                  /===>uncI
181  GCGAAGTGGATATTACTAGAGGTACGAATACATGGTAGCTGCGTTAGCTAGACCAGGACGAGAGCTCGCAAGGCAATTGTTAATGATCCA
271  GTCTGGCGCGGTTATTTTTGTGGCAGCAGGAATGGCGGTAGCCATAAATCCTGACTGGGGATTTTCAGCGCTGATTGGCGGAGGCATTTT
361  TGTTGTTGCCAATGCAGTATTCGCGCTGTGTGCTTTCATGTTTAGTGGGGCTCGCGCTGCCAAGCGCATCGCGGCTTCCTTCTATACGGG
451  TGAAGTACTGAAAATTCTCATCACGGTTGCACTGTTCTATGTTGCCTACATGTATATGCAGGTGGAACTTGTTCCCCTCAAACTAACCTA
                                                    uncI==>\\        /===>uncB
541  TTTGCTGGTACTAGGTATTAATATCTGTGCACCAGTGCTATTCATTAACAACAAAAAATAGGATGAGTTATGGCTGCGCCAGGTGAAGCG
631  CTAACATCGTCCGGTTACATTGCCCACCACCTTTCTAACCTATCGCTGTATAAGTTGGGTTTAGTAGGGTCGGAGACAAGTTTCTGGAAC
721  GTACATATCGATAGCCTGTTTTTTTCTTGGTTTACTGGTTTAATCTTCCTCGGAATTTTTTACAAAGTAGCGAAGAGAACAACAGCGGGT
811  GTACCGGGTAAGCTTCAGTGTGCTGTAGAAATGATCGTTGAATTTGTCGCCGATAACGTCAAAGACACGTTCCATGGACGCAACCCACTG
901  ATCGCGCCTTTAGCACTGACTATCTTTTGTTGGGTATTTTTGATGAACGTGATGGACTTAGTTCCTATCGACTTCTTACCGTACCCAGCA
991  GAACATTGGCTAGGTATCCCTTACCTTAAGGTTGTACCGTCTGCTGATGTGAATATCACCATGGCTATGGCTCTAGGCGTTTTTGCATTG
1081 ATGATTTACTACAGCATCAAAGTGAAAGGTCTAGGTGGATTCGCAAAAGAACTTGCACTACATCCATTCAATCACCCACTTATGATTCCG
1171 TTTAACCTACTGATTGAAGTGGTATCGCTACTGGCGAAACCTCTATCACTTGGTATGCGTTTATTCGGTAACATGTTCGCGGGTGAGGTT
1261 GTATTCATTCTTTGTGCGGCAATGCTACCATGGTACTTACAATGGATGGGTTCACTACCGTGGGCAATCTTCCATATCTTGGTTATTACG
                                                                  uncB==>\\
1351 ATTCAAGCCTTCGTATTCATGATGTTGACAATTGTTTACCTGTCAATGGCACACGAAGATCCTGATCATTAATTTTTTTAAAGCTTTTTA
                                          /===>uncE
1441 TTTGGGCACTAAGCCAACAACTATAAATTGGAGATAGTAATGGAAACTTTACTGAGCTTTTCTGCAATCGCCGTAGGTATTATCGTCGGT
1531 CTTGCTTCTCTTGGTACAGCGATTGGTTTCGCACTGCTAGGTGGTAAATTCCTAGAAGGTGCTGCACGTCAACCAGAAATGGCTCCTATG
1621 CTACAAGTTAAGATGTTCATCATCGCGGGTCTACTTGATGCGGTTCCAATGATCGGTATCGTAATCGCGCTACTATTCACTTTCGCAAAC
                    uncE==>\\
1711 CCATTCGTTGGTCAACTAGGTTAATCACCTTTAACTCGGGACGAGCGATTAGCGCTTGTCACTGATTAACACTAAGTCCAAATAGAGGGT
```

```
          /===>uncF
1801 AGCTGTTGTGAACATAAACGCAACTCTGCTAGGTCAAGCAATCTCGTTTGCACTATTTGTGTGGTTCTGCATGAAGTATGTATGGCCACC
1891 ATTGATGAAAGCGATCGAAGAGCGTCAGAAGAAAATTGCTGATGGCCTTCAAGCAGCAGAACGTGCTGCGAAAGACTTGGATCTAGCACA
1981 AGCCAACGCTTCTGATCAATTGAAAGAAGCGAAGCGCACAGCAACTGAGATCATCGAACAAGCGAACAAGCGCAAGTCTCAAATTCTTGA
2071 TGAAGCTCGCGAGGAAGCTCAGGCAGAACGCCAGAAAATCCTAGCGCAAGCAGAAGCAGAACTTGAAGCTGAACGCAATCGTGCGCGCGA
2161 TGACCTGCGCAAACAAGTTGCTACTCTGGCTGTAGCTGGTGCTGAGAAAATCCTTGAGCGTTCTATCGATAAAGATGCGCAAAAAGATAT
                        uncF==>\\              /===>uncH
2251 TCTCGACAACATTACTGCAAAACTTTAAGTCTGGGGGCGCATATGTCTGATTTGACTACTATCGCACGCCCCTATGCTAAAGCAGCCTTC
2341 GACTTTGCTTTAGAGAAAGACCAGTTGGACCAATGGGGCCAAATGTTATCTTTTGCTGCTGAAGTGGCCAAAAACGAACAAATGAACGAA
2431 CTTCTAACCGGTTCGGTTTCTGCTGATAAAATGGCAGAGATTTTTGTTGCAGTTTGCGGCGAACAAGTTGATACGCACGGTCAAAACCTT
2521 TTGAAGGTGATGGCTGAGAATGGTCGTTTAGCGGCCCTTCCTGATGTTTGCACAGAGTTTTACACTCTGAAGAAAGAGCATGAGAAAGAA
2611 ATCGATGTTGAAGTCATTTCAGCTACAGAACTTTCTGATGAGCAACTTGCAAACATTGGCAGCAAACTTGAAAAGCGTCTTGAACGCAAA
2701 GTGAAGCTGAATTGCAGTGTAGATGAGACCCTACTTGGTGGGGTTATTATTCGAGCCGGAGACCTAGTCATCGATGACTCAGCGCGTGGT
                              uncH==>\\              /===>uncA
2791 CGTTTGAACCGCCTGAGCGATGCATTGCAGTCTTAATGGGGATTGGAGCATGCAACTTAATTCCACGGAAATTAGCGATCTAATCAAACA
2881 ACGTATCGAATCTTTCGAAGTTGTTAGTGAAGCTCGCAACGAGGGTACTATCGTATCGGTAAGCGATGGTATCATCCGCATCCACGGCCT
2971 AGCGGACGTGATGCAAGGTGAAATGATTGAATTACCGGGTGGCCGTTATGCACTGGCACTTAACCTTGAGCGTGACTCGGTTGGTGCGGT
3061 TGTAATGGGCCCATATGCTGACCTTAAGGAAGGCATGAAAGTTACAGGTACTGGCCGCATTCTTGAAGTGCCAGTTGGTCCAGAACTACT
3151 AGGCCGCGTAGTAAACACGCTCGGTGAGCCTATCGATGGTAAAGGTCCAATCGAAGCCAAAATGACTTCGCCTGTAGAAGTGATCGCACC
3241 AGGTGTAATCGACCGTAAATCGGTAGACCAACCTGTGCAAACTGGTTATAAGTCAGTTGACTCAATGATCCCTATCGGTCGTGGTCAGCG
3331 TGAGCTTATCATCGGTGACCGTCAGATTGGTAAAACAGCACTGGCGATCGACGCGATCATCAACCAGAAAGACTCTGGTATTTTCTCTAT
3421 CTACGTAGCAATTGGTCAGAAAGCATCGACTATCGCTAACGTAGTTCGCAAACTAGAAGAGCACGGCGCACTACAAAACACTATCGTTGT
3511 AGTTGCATCAGCTTCTGAATCTGCAGCGCTGCAATACCTAGCGCCATACGCAGGTTGTGCGATGGGTGAATACTTCCGCGATCGCGGTGA
3601 AGACGCACTGATTGTTTACGATGACCTATCTAAGCAAGCGGTAGCTTACCGTCAGATCTCTCTACTACTTAAACGTCCACCAGGCCGTGA
3691 GGCATTCCCAGGTGACGTATTCTACTTACACTCGCGTCTACTAGAGCGTGCAGCTCGTGTAAACGAAGAGTACGTAGAACGTTTCACAAA
3781 CGGTGAAGTGAAAGGTAAGACTGGTTCATTGACTGCTCTTCCTATCATCGAAACTCAAGCAGGTGACGTCTCAGCATTCGTACCGACTAA
3871 CGTAATCTCGATTACCGATGGTCAGATCTTCCTACAAACTGAGCTATTCAACGCCGGTGTTCGTCCAGCGGTTGACCCAGGTATCTCAGT
3961 ATCTCGTGTAGGTGGTTCAGCTCAGACGAAAATCATCAAGAAACTATCAGGTGGTATCCGTACAGCACTAGCTGCATACCGCGAACTAGC
4051 AGCATTTGCTCAGTTCTCTTCTGACCTTGATGAAGCAACGAAGAAACAGCTAGACCATGGTCAAAAAGTAACAGAACTAATGAAGCAGAA
4141 GCAGTACGCTCCAATGTCTGTATTTGACCAAGCTCTAACTATCTTCGCGGCAGAGCGCGGTTACCTTGATGATGTAGAACTTAACAAAGT
4231 TCTAGATTTCGAGGCGGCTCTACTATCGTACGCTCGCGGTCAATACGCTGAACTAGCAGCTGAGATCGACAAGTCTGGCGCTTACAACGA
                                                        uncA==>\\
4321 TGAAATCGAAGCTCAGTTGAAGAAACTGACTGACGACTTCAAAGCAACCCAAACTTGGTAATTAGGTCGGTGGCAGTTTCTGCCACCAAC
                    /===>uncG
4411 TAACGGAGAGTAACGATGGCCGGCGCAAAAGAGATACGTAATAAAATCGGTAGTGTTAAAAGCACGCAGAAAATTACGAAAGCGATGGAA
4501 ATGGTAGCAGCTTCAAAAATGCGTCGTTCTCAAGATGCAATGGAAGCTTCTCGTCCATACGCTGAAACAATGCGTAAAGTGATCGGTCAT
4591 GTGGCTAACGCAAACCTAGAGTACCGTCATCCGTACCTAGAAGAGCGTGAAGCTAAACGTGTTGGTTACATCATCGTTTCGACAGACCGT
4681 GGTCTGTGTGGTGGTTTGAACATTAACGTGTTCAAAAAAGCCGTTACAGACATGCAAACATGGAGAGAGAAAGGTGCTGAGATTGAGCTT
4771 GCCGTAGTTGGCTCAAAAGCAACAGCTTTCTTTAAACATGGTGGCGCAAAAGTTGCGGCACAGGTTTCTGGCCTGGGTGATAACCCAAGC
4861 TTAGAAGACCTAATCGGTTCTGTTGGCGTAATGCTGAAGAAATACGATGAAGGTGAGCTGGACCGTCTATACGTAGTATTCAACAAGTTT
4951 GTTAATACTATGGTTCAGCAACCAACGATCGATCAATTGCTACCTTTGCCTAAATCGGACAGCGAAGAGATGCAGCGTGAGCACTCATGG
5041 GACTACATCTATGAGCCTGAGCCAAAACCTCTACTGGATACGCTACTAGTGCGTTACGTAGAGTCTCAGGTATACCAAGGTGTGGTTGAG
5131 AACCTTGCTTGTGAACAAGCGGCTCGAATGATTGCGATGAAGGCTGCAACGGATAACGCAACCAACTTGATTGACGATTTGGAACTTGTG
                                                              uncG==>\\
5221 TACAACAAAGCCGTCGGCTGCGATCACACAAGAACTATCGGAAATCGTTGGTGGTGCAGCTGCGGTTTAAGCTTAGGTAAAACGAAAT
                    /===>uncD
5311 AGTTTAGAGGATTAACGATGGCTACAGGTAAGATCGTACAGATCATCGGTGCGGTAGTCGACGTAGAGTTCCCACAGAGCAATGTACCTA
5401 GTGTATATGACGCTCTAAACGTAACGGACTCAAAAGAGCGTCTAGTTCTTGAAGTTCAACAACAGCTAGGCGGTGGCGTAGTTCGTTGTA
5491 TCGTAATGGGTAGCTCTGATGGTTTACGTCGTGGAGTTGAAGTGGTTAACACTGGCGCTCCAATTTCAGTACCAGTCGGTACTAAAACTC
5581 TAGGTCGTATCATGAACGTCCTAGGTCACGCGATTGATGAGCGTGGTGAAGTGGGCGCGGAAGAGGTTTACTCTATCCACCGCAGCGCAC
5671 CAAGCTACGAAGAACAATCAAACGAGATCGCACTTCTAGAAACGGGCGTTAAAGTAATCGACCTAATTTGTCCATTCGCTAAGGGTGGTA
5761 AAATCGGTCTATTCGGTGGTGCAGGTGTAGGTAAGACCGTTAACATGATGGAACTTATCAACAACATCGCACTACAGCACTCAGGTCTAT
5851 CCGTATTTGCGGGTGTTGGTGAGCGTACTCGTGAAGGTAACGATTTCTACTACGAGATGCAGGAAGCGGGCGTTGTAAACGTTGAGAAGC
5941 CTGAAGAATCGAAAGTAGCGATGGTTTACGGTCAGATGAACGAGCCACCAGGTAACCGTCTACGTGTTGCACTGACTGGTCTAACATATGG
6031 CAGAACGTTTCCGTGACGAAGGTCGTGACGTACTACTGTTCATTGATAACATCTACCGTTACACACTTGCAGGTACAGAGGTATCGGCAC
6121 TGCTAGGTCGTATGCCTTCTGCGGTAGGTTACCAGCCAACTCTTGCAGAAGAGATGGGTGTACTTCAGGAGCGTATCACGTCAACGAAAT
6211 CAGGTTCTATCACGTCTGTACAGGCGGTATACGTACCTGCGGATGACTTGACTGACCCGTCTCCAGCAACCACGTTCGCGCACTTGGATG
6301 CAACGGTTGTACTTAACCGTAACATCGCTGCTATGGGTCTATACCCTGCGATCGACCCACTAGATTCAACATCTCGTATGCTTGATCCAC
6391 TAGTAGTTGGTCAAGATCACTACGAAGTTGCTCGTGGCGTTCAGCAGACACTTCAGCGCTACAAAGAGCTGAAAGACATCATTGCTATCC
6481 TAGGTATGGACGAGCTATCTGAAGAAGATAAGCAAGTTGTATCTCGTGCACGTAAGATTGAGCGTTTCGCTAACTCAGCCTTACCACGTAG
6571 CAGAAGTATTTACAGGTGACCCTGGTATTTACGTACCTCTAAAAGAGACTCTACGTGGCTTCAAAGGTCTACTAGCTGGTGAATACGACG
                                                        uncD==>\\              uncC/>
6661 ACATTCCTGAGCAGGCATTCATGTACTGCGGTAGCATCGACGATGCTATTGAGAATGCGAAGAAGCTATAAGGCTAACTAGGAGGCGATA
6751 TGGCAGCAATAACCTTTCACCTAGACGTAGTAAGCGCTGAGAAGAAAATCTTCTCTGGTCGTGTTGAAACGTTTCAGGTGACCGGTAGCG
6841 AAGGTGAACTTGGTATTTTCCATGGTCACACCGCTGCTGACCGCTATCAAGCCTGGTATGGTGCGTATTGTGAAACAGCACGGCCACG
6931 AAGAAATCATTTATGTTTCTGGTGGTATGGTAGAGATTCAGCCTGGTACAGCGACTGTACTGGCTGATACCGCTATCCGTGGTGAAGAGC
7021 TAGACGCAGCGAAGGCAGAAGAAGCCAAGCGCCGCGCTGAGGAGCAAATCCAGAATCAGCATGGTGACATGGACTTCGCACAAGCGGCCA
                                                              uncC==>\\
7111 GTGAACTGGCTAAAGCCATTGCTCAGCTACGAGTTATCGAGCTGACAAAAAAGCGTCGCTAAGCTCAATTAGCAACGTTGCATGACAAAA
7201 GGCGGCCCAATGGTCGCCTTTTTGATTAATTTTAGTTGGAAATTTACCTTACTCCATTAACTATTTTAAAAGAGCTGTTTAAAATAACGG
7291 CCAATTAACATAAAACGTCAATAGGTTATCAATGAAATTCAGTGCTGTGATTCTTGCTGCGGGTAAAGGTACCCGTATGCATTCGAACAT
7381 GCCTAAAGTGCTACACACTTTG
```

*To whom correspondence should be addressed

References

1. Tokuda,H. and Unemoto,T. (1984). J. Biol. Chem. 259,7785-7790.
2. Dibrov,P.A., Lazarova,R.L., Skulachev,V.P. and Verkhovskaya,M.L. (1986). Biochim. Biophys. Acta. 850,458-465.