

Nucleotide sequence of the genes encoding the L11, L1, L10 and L12 equivalent ribosomal proteins from the archaeobacterium *Halobacterium marismortui*

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A λEMBL3 clone (PP*10) containing a gene cluster coding for the ribosomal proteins L11, L1, L10 and L12 was identified in a genomic library of the halophilic archaeobacterium *Halobacterium marismortui* (Hma) using a heterologous hybridization probe (pBH327) from the related organism *Halobacterium halobium* (Hha) (1). A 3000 bp region of the PP*10 is shown in the figure. HmaL1 and HhaL1 share 79%, HmaL10 and HhaL10 66% and HmaL12 and HhaL12 68% identical amino acid residues, respectively. 78% identity was found for HmaL11 and HcuL11 (*Halobacterium cutirubrum*) (2).

The gene order strongly corresponds to that of the *E. coli* equivalent genes whereas the operon structure is different, namely the HmaL1 gene is fused to the HmaL10/HmaL12 operon leaving

HmaL11 in a monocistronic gene arrangement. Our results agree with those obtained for the other halobacteria (1, 2). Putative promoter and terminator structures are underlined.

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REFERENCES

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2. Shimmin, L.C. and Dennis, P.P. (1989) *EMBO J.* **8**, 1225–1235.

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1   ctccagcagttatccgtgaaacgcaatccctttaaactgcccggaggattccactatgtaTGGCTGGAACATAOGAAGTCCTCGTTCCCGGTGGGGAGGCC 100
101 AACCCCTGGCCCGCCACTCGGTCGGAACTCCGCCGACACCGGTGGAAGTCAGGCAGTGTACAGGAGATCAACGACCAGAGCGGAGCGTTGCAOCCGA 200
201 CCGAAGTCCCGTCAACGTCAGTATGACGACGACCGTTCCTTTOGAGATOGAAGTGGTGTCCCGCGAOCGGCGAACTCATCAAGGAOGACCGCTGGCTT 300
301 OGAAACCGGCAGCGGGAGCCAGGAGGACTTCGTCGTCAGCTCTCTGTGACACAGTCAAAACAGATGCCGAGCAGAAACCCCGACCTGCTCTCC 400
401 TAOGACCTCAOGAAACCGCAAAAGAAGTGTGGGAGGTGCACTCTCTCGGTGTCACTATTGAAGGOGAGAACCACCGGAGTTCAAGGAGCGCATOG 500
501 ACCGAGCGAGTAOGAOCAGTGTTCGCGCCGAAAGCCAAAGCGtaagtcggactggcgtgtgctgtgcactggcgtgtgttttcttctgtttcgaacc 600
601 tgcagagcaactgcacagtcgatggtaaccccgcttaacgactggcccttgcgaaccggaacacgcccgtcagcggctccttctgtctggttcgaacggttt 700
701 aagtgctgcattggcgtctactgcacagacagggcatccgctgttttactgaccctgagaacccgatiggcgtactacggaggtgaacaATGCCAGAT 800
801 CAGGAAATAGAGAAAGCAGTCTCGCGCCACTCGAGGAOCACCTGACCGGAATTTCCGCGAAAACCGTGGACCTCGCTGTGAACCTCGCGACTTAGATC 900
901 TTAACGACCCGTCGAACCGCGTGAAGAGTCCGTCGCTTCCTGCTGGCAGCGTCAAGGAGACCACTATTGTGCTCTCCCGAGGGCGAAACCGCCCT 1000
1001 TCGTCCGAGGAAAGTCCGAGAACGCTACTGACGAGGATGAACCTGAGGAACTGGTGGGACGAGACGCGCCCAAGGACCTTGCCTGACACTGAC 1100
1101 TTCTTCATTCGGGAGAAAGGACTGATGACGAGACATCGGTGCTACCTGGGACCGTCTCGGTCCGCGTGGGAAGATGCCGAAACCGCTGACCCCGAOG 1200
1201 ACGAGCTGTGAGGTCATGAAAGCATGAAAAACAACCGTGCAGCTCCGAGCGGGGAAOCGGGAACGTTCCACACGCGGGTGGCGGGGAGGACATGTC 1300
1301 GCGGAGAATATCCCGGACAACATGAGCTTATCTCCCGCTGCAACCGGACCTCGAGAAGGGCCCGCTCAACATCGACACTGTCTAGCTGAAGACG 1400
1401 ACGATCCGGCCCTGCGATGGAGGTTGCCtgaLATGAGCGCGAAATCCGAAOCGAAGACCGAAACCAATCCCGAGTGAAGCAGGAAGAGGTGCAOCCCATC 1500
1501 GTAGAGATGATCGAGTCTAOGAGAGCGTCCGCTGTCAACATGCGCGGATTCCTCCCGCAACTGCAGGACATGOGAAGTGAACCTGCAOCCGAGCG 1600
1601 CCGAAGTCCCGTTCGCGCAACCGCTGCTTGAGCGTGCACCTGAGGATGTGATGACGCACTGGAAGACCTCAACCGCTACATCACCGGCAAGTGG 1700
1701 ACTCATGCGGACGCAAGATAACCCGTTCTCGCTGTTTTCAGGAACCTGAGCCCTCCAAAGACGCGCCCAOCCATCCGTCGCGGTGAGGTGGCCCGAAGAT 1800
1801 ATCTGATTTCCGGAAGGCGCAOCCGCGTGCACCCCGTCCGTTGTTGGGAACTCCAGAGCGTGGGTCCGGAOGCAOCCATTCAGGAAGGCTCCATTTC 1900
1901 AGTTCCTTTCTGACTCGAOCGCTGCTGACACCGCGGAGGAAGTCTCTCAGGAACCTTTOGAAOCTGCTGAACGAACTCCGATOGAAACCGAAGGAGGTCC 2000
2001 TCTGACCTTCCGCGCTTTCGCGAGGTTGCTGTTTGAACCCGAGGAACTGGAACCTGACATGACGAGTACCGGAGCGACATCCAGGCGGCTGCC 2100
2101 GCGGAGCGTTCAATCTCTCGTCAAOCGCGACTACCCGACCGGAGGAGGCGCCGCAOAGTCTCCAGTCCGATCGTGGCAAOCGCAAGGACCTCGCGC 2200
2201 TCCAGGGCGCCATOGAGGACCCGAGGTGCTGCTGACCTGCTGAGCAAGGCTGAOCGACAGGTCCGTCGCTGCGCTCGCAAAATGAAGATGAAGAGCC 2300
2301 ACTCCCGAGGAGCTTCAGGCGGTGAGGCGAOGTCCGGACAGAGAAOCGACTGAAGACCAAGGAGGACACCGCATCCGAGGAGCGGCGGACGCC 2400
2401 GAOGACCGCGCCGAGGAGCGCAOAGATGAOAGATGAOCGAGGAGCGTGGCGAOCGCTCCGAGCGATGTTTcaacaacacagactacaacaATGGA 2500
2501 ATAOGTATAOCTGCACCTATCCTGAACGAAGCTGAOAGAGATCAAOGAAGACAACCTCAOCCGAGTGTGCAOCCGCGCGGCTGCAOCTGAGGAG 2600
2601 TCCCGTTCAGGCGCTTGTGCGCGCTCGAAGAGTGCACATGAGGAGGCGGTGACAGCGCGCTCCGCGCACCGTCCCGGCAACCGGTGGCGCG 2700
2701 CCGCACCGCAGAGGGTGAOCGCAOAGAGCCGAGGCGCAOAGGAAOCCGAAGAAGGAGGCTCCGACGACCGGGGCAOAGATGACGCAAGA 2800
2801 GAGCAGGCAAGCGGTGAGGCGCTCCGCGAAGCTTTCGCTtaactcggttcaacacagctcaglttttcttcttggcgtgcgctcagccggtgagaggagtc 2900
2901 aactgaccccgccgatagccgtgtttctatatacattatgctgagccacgtccagacatgtaactctgactgtaccctgcacacagagccgttctca 3000
    
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