Nucleotide sequence of the 10Sa RNA gene of the β-purpl eue bacterium Alcaligenes eutrophus

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In the course of cloning the gene for the RNA component of ribonuclease P (RNase P) from the β-purpl eue bacterium Alcaligenes eutrophus, we have also isolated a clone which contains significant sequence similarity to Escherichia coli 10Sa RNA, a 363 nucleotide, stable RNA of unknown function (1, 2, 3). The cloned DNA hybridizes to a ∼340 nucleotide RNA in Northern blots of total RNA from A. eutrophus and another β-purpl eue bacterium, Pseudomonas testosteroni, but not other organisms tested, including E. coli (data not shown). The 10Sa RNA of A. eutrophus comigrates in 8M urea polyacrylamide gels with the 341 nucleotide RNase P RNA (also known as 10Sb RNA (1)) (data not shown), as is the case in E. coli (1). The A. eutrophus 10Sa RNA structural gene (underlined below) is clearly homologous to that of E. coli, with overall sequence identity of 51%. Much of the similarity between these sequences is found in the 5' and 3' terminal regions of the genes, whereas the central region shows significantly less similarity. Interestingly, the conservation of primary sequences does not end at the 3' terminus of the mature E. coli 10Sa RNA, but continues for an additional 12 nucleotides into the 3' flanking sequence, which in E. coli is removed endonucleolytically from the precursor 10Sa RNA (2, 3).

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REFERENCES

1 GTGCACCCGC GCCAGTGCGT CTATGTGGGC GATGACCTGC GCGACATCCA GGGCGCAAC GGGCGCATG
71 ATCACCGAC AGCCGCTAT GCTATTCGGG CGACGAGCCG CCGAGACCTG GGGCGCCGAC CACCTGATT
141 GCGACCACGC CGGCTGCTGT CGGCTGCTGT TGCCCGCCGT GTGCCTGCTA TTTGCTGCTA GGGGTATCTG
211 GCCGGTCCGA ACTCCCGCGA CAGCTGCGTC AAAGGCTGAC CAGCTGCGTT CCGACCTGTT
281 TTGGCGAGGG GTCACGGGCAC GCCAGGGGAG CCCGACGCCG GCCAGCCGCC AATCAATGTT ATTGCAATAA
351 CTGCTAGCGA CGGAGGCCTG ACGAGCCTG ATTTGCGGC GCTTCCGGGC TGGCTGCTAT ACGGCTTAGG
421 GTGCCAAGAG CAGCCGAGGT AATCCAGCTA GATAGGACTA CAAGGACCGG CAGGAAACC
491 TACGTACGAG CGTCTGGTAG GCGTGTTGCT GCGAGCCGC GCTGTAAATG AATGAGAAGA CTCTACCTAGT
561 AGAATCTCCT GTGCAGGGGC TACGGACCGG GCTTCCGGAT CACCAGCTT CAGTCCGGATG
631 CAGCACCTGC AG

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