

The tRNA^{sup} (anticodon TTU) gene and its upstream sequence coding for a homolog of the *E. coli* large ribosome-subunit protein L14 in the *Tetrahymena* mitochondrial genome

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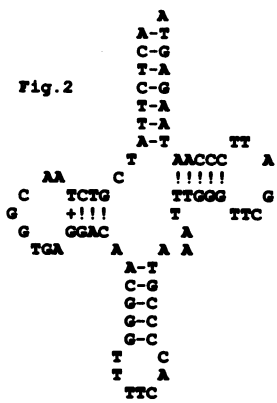
The linear mitochondrial (mt) DNA (55 kbp) of the ciliate protozoan *Tetrahymena* encodes only 8 tRNA genes, seven of which have already been sequenced (4,5,7,8). We present the sequence of the eighth tRNA gene and its flanking sequence. The internal 0.57 Sau3A fragment of E3B1 (1.9kbp) (7) which showed hybridization with mt-tRNA, was cloned and sequenced. The derived tRNA sequence [in lower case letters in Fig.1] is 72 bases long with 44% G+C and can be folded into the standard cloverleaf structure (Fig.2) by Staden's program (6). This tRNA has 8 bases at the DHU loop just like an eukaryotic cytoplasmic tRNA^{sup} and shows the highest nucleotide identity (67%) with *Drosophila* cytoplasmic tRNA^{sup}.

Immediately upstream of this tRNA gene is found a coding sequence for mt-L14 [underlined in Fig.1], a homolog of the large ribosomal subunit protein (LRSP) L14 of *E. coli* (1). Alignment by FASTP program (2) shows identity of 42/119 amino acids and both proteins are highly basic; the number of K and R residues in *E. coli* and mt protein is 23 and 28, respectively. This is the first report of a LRSP encoded in mitochondrial DNA. The present finding is consistent with our previous report (3) that mitochondrial ribosomal proteins <25,000 MW are synthesized in *Tetrahymena* mitochondria.

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1  GATCTATAAAAAAAAAAATTTAATTAATGATACAAAAGAACTAATTTTAAACCAATAGATBAATGCGG
71  AGTTTGATCAGTAAGGGCGCTTTCATTTATATGGTGGTTCGTTTAgAABATCAATCTCAATAAGTAACTTT
141 TTAAGGTTAGTGTAABAAAAAACBAGAGCAAAATAATTGAGTACCGAABAAAAACAAAATTTAAAGCAATAA
211 TTGTTACACTAAAAAAGAAATTAABAAAAATAGATGGTAGCTATATAAAAATTTAGAACAAAATAATGTTGT
281 CCTATTAABAAAAAGATTAAACCCCTAAAGGAAAAAATATTAATGGGGCCCGTTAGTTCAAATTTAAGGAGA
351 AAAGGTTTCTTAACTTCTTTTGTGGATCTATTTAAATCATAGAAATTTTTATTTAAAATTAactcttat
421 cgtctaacgggtgaggacaacgggttttcaccccgtaaatTTgggttcgataccacaagagtaATATGT
491 TTAGATGACTTTTTTATATTTGGTATAACGTAAGTACTGATACACCATCAGCTATTTCAAAAATTAATTTATG
561 ATCGATC
    
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Fig.1



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