Nucleotide sequence of the *tuf* gene from *Mycoplasma gallisepticum*Julia M. Inamine¹⁺, Steve Loechel¹ and Ping-chuan Hu^{1,2,3*}¹Departments of Pediatrics, ²Microbiology and Immunology and ³Center for Environmental Medicine, University of North Carolina, Chapel Hill, NC 27599-7220, USA

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Both strands of a 1.4-kilobase *Eco*47 III/*Eco*R V fragment from *Mycoplasma gallisepticum* (ATCC 19160) were sequenced, and analysis revealed that it contained an open reading frame coding for a protein of 393 amino acids. It has 83% identity (with conservative replacements) with elongation factor Tu (Ef-Tu) of *Escherichia coli* (1). Southern blot hybridization showed that *M. gallisepticum* (MGAL) contains a single *tuf* gene. Alignment of nucleotide and amino acid sequences demonstrated that the single UGA (TGA) codon in the MGAL *tuf* sequence (indicated by *) corresponds to Trp in the EF-Tu of *E. coli*. We previously identified both tRNA-UCA and tRNA-CCA genes in MGAL (2), and the above alignment provides supporting evidence that, as in *Mycoplasma capricolum* (3), UGA is translated as Trp in MGAL. Flanking the *tuf* gene are putative ribosome binding site, promoter, and transcription terminator sequences.

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              30              60              90              120
TAGCAATTAGTTATATGTTACATATAGCGCTATAAGTACACCGGTGCAAAACCGTTTCACTTTAGAAATTTTCAAGGAGAAATATTTAAAGAAAGGTTTCGATCGTAGTAA
              (N) A K E R F D R S K

              150              180              210              240
ACCTCAGGTTAATATTGGCAAAATCGGTATATTGACACGGGAAACATACATTAACCGCAAGCAATTTGTACCGTGTATCAAAAGCCGGTACATCTGAAGCTAAAAAATATGATGAAAT
P R V N I G T I G H I D N G K T T L T A A I C T V L S K A G T S E A K K Y D E I

              270              300              330              360
TGATGCTGCACAGAGAAAGAGCTCGTGGATTACATTAAACACTGCACACGTAGATACCGCAACTCAAAATCGTCACTATGCACAGCTTGACTGTCCGGTCCACGCCGACTACGTTAA
D A A P E E K A R G I T T I N T A B V E Y A T O N N R R Y A H V D C P G H A D Y V K

              390              420              450              480
AAACATGATTACAGGTGCTGCTGACAGCGGTATCTTAGTGTCTGCAACTGATGGTCCAAATGCTCAAACTCGTGAACACATCTTAGCTGCGCAAGTTGGTGTCTCTAA
N X I T G A A O N D G G I L V V S A T D G P M P O T R E I I L L A R O V G V P K

              510              540              570              600
GATGGTGTATTTCTTAAACAAATGATGATGCTGATGCTCAGAAATGCAAGAAATAGTGAATGGAAGTTAGAGATCTTCTTAAATCTTACGGATTGATGGTGATACTACCTCAAGT
M V V F L N K C D V A D D P E M O E L V E M E V R D L L K S Y G F D G D N T P V

              630              660              690              720
AATCAGAGGTTCTGCTTTAGGTGCTCTTATGGTGAACCTGTCATCAGAGAGAAAAATTCATGAACATTAATGAAGCAGTTGATGAATACATCCCACTCTGACCGTGAAGTTGATAAAC
I R G S A L G A L N G E P A M E E K I R E L N K A V D E Y I P T P D R E V D K P

              750              780              810              840
ATTTTTATTACCAACCGAAGTACTATGACAAATTACTGGTCTGGTCTAGTAACTGATAGCTTGAACCTGGTCAACTTAAAGTTGGTGAAGAAATGAAATCGTTGGTATTACTGA
F L L P I E D T M T I T G R G T V V T G R V E R G O L K V G E E V E I V G I T D

              870              900              930              960
CACTAGAAAAGTAGTAACTGGTATTGAAATGTTGAGAAAAGAACTAGATGCTGCTATGGCTGGTGACACCGCTGGGATCTTACTCTGGTGGTAGACCGTAAAGATGTACACCGTGC
T R K V V V T G I E M F R K E L D A M A G D N A G I L L R G V D R K D V O R G

              990              1020              1050              1080
TCAAGTTTGTAGTAAACCTGGTTCATTAATCTCCACACAGAAATTCAGAGCTGAAATTTATGCGCTTAAGAAGGATGAAGGTGGTCTCACACAGCTTCTTAAATGGTTACAGACCTCA
O V L A K P G S I T P H K K F R A E I Y A L K K D E G G R H T A F L N G Y R P O

              1110              1140              1170              1200
ATTCTACTTCAGAACAACTGACGTATGGTTCAATCAATTAAGAAAGGAAGTGAATGGTTATGCTGGTGATAACACAGAAATTCGTTGAATTAATTTCTCAATCGCTTGTGA
F Y F R T T D V T G S I O L K E G T E M V M P G D N T E I I V E L I S S I A C E

              1230              1260              1290              1320
AAAAGGTTCTAAGTTCTCTATCGGTGAAGGTGAGTAACTGTAGTGTGCTGGTACAGTTGTGAAGTACTTGAATAGGCCCTATTTAAATTTAAAAAATATAATGGCTAAGGAACCTTGT
K G S K F S I R E G G R T V G A G T V V E V L E *

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