

The nucleotide sequence of a tRNA gene cluster from *Spiroplasma meliferum*

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Submitted 28 February 1986

FEATURES: The recombinant plasmid containing a tRNA gene cluster from *Spiroplasma* species BC3 has been described (1). The ten tRNA genes presumably constitute a single transcriptional unit. Probable promoter and terminators are indicated. A sequence GGGG (155-158) may serve as a 'Discriminator' region (2). An o.r.f. starts at nucleotide 1251 if UGA codes for tryptophan (3).

COMMENTS: The order of the tRNA genes in this cluster, and the isoacceptors encoded (except for the first tRNA^{Cys} gene), is identical to that of two other tRNA gene clusters from Gram-positive eubacteria; from *Mycoplasma mycoides* (4), and a portion of the rrnB (trrnE) sequence from *Bacillus subtilis* (5,6). Similar clusters of tRNA genes implies an important transcriptional and regulatory mechanism for these gene clusters.

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TCGATGAAAGTTTTGATGTTGAATATGAATTTATTGATGGTGTCAAACTTATACCCATTTTAAATGCTGTTGAGTAAATAAAAATAAAATGAATTTAAGTTTTTTATTTATTTA 120
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TCTTGAAATGAATATGAATATGATAATATAGTAGGGGTTTAGATTTTATGGCACTATAGCCAAAGGTGGCTAAGGCATGGGACTGCACCTCCCGATCGTGGTTCGAATCCGACTAGTG 240
tRNACys
CCTCCATTTAAATCTGCTCAACATTTAAATATTGCTTTATTTCTTATGCGCCCATAGATCAATGGATAGATCGTTTGACTACGGATCAAAAGGTTGAGGGTTCGATTCCTCTGGGCGC 360
tRNAArg
GCCATTTTAAATGTTAATTTTTTTTCGGAAAGTAGCTTAGCTTGGTAGACACTCGGTTTGGACCCGAGGGGTCGAGGTTCGAATCCGTCTTCCSACCAATTTTTTATACTAITTT 480
tRNAPro
GGCCCGTAGCTCAGCTGGGAGACACCTGCTTGCACACGAGGGGTCGACGGTTCGATCCCGTTCCGGTCCACCAATTAACAATTAATAAAGCAATTAACCTTGATATGGCGGATAGCT 600
tRNAMet
CAGCTGGTAGAGCGCTCGGCTACACCCGGGAGGTCAGAGTTCAGGTCCTTTCTCGCTACCATGGACCGCTTAGCTCAGTTGGTTAGAGCATCCGGCTCATACCCGGATGGTCACTGG 720
tRNASer
TTCAAGTCCAGTAGGTTCCACCAATTTATTAATTTAGTTGCTTTACGAGCATTTTTGGAGATTACCCAAAGTCTGGTTGAAGGATCGGTCCTGAAAAATGACAGCGGGTGAAGGCCG 840
tRNAMet
CGCGGGGTTCGAATCCCTCATCTCCGCCAGTTTTTCAGAAAAAACTTGCAGTAATAAAGTAAAGTTGATGATAGATTAAAAATCGTGGGGTGGAGCAGTTGGTAGCTCGTTGGGCTCA 960
tRNAMet
TAACCCAAAGGTCGAGGTTCAAGTCTCGCCCCGCAACCAATGGCTTTGTAGTGAAGTTGGTTATCATGCTCTCTGTCACAGAGGAGATCGCGGGTCAAGTCCCGTCAAGACCCCA 1080
tRNAPhe
ATCGTGGTTCAGTAGCTCAGTTGGTAGACCATTTGATTTGAAGCTCAAAGTGTCCGGCAGTTCAATTCGTCTCTGACCCACCAATGAAATTTAGTTAAAAATAACCCTAGACTCTAAATTAAT 1200
<T2=====> <T1=====>
CATAGATTAATTTACAGTTTTTAAATTTTGTATATAAATAAAGGATGGATGTAATGTTTTCAAGATTAACAAAAGATATAACCTTTTATTTAAACGTTGAAGAGTGAAGTTACGTT 1320
TAAATGAAGATAATTTAAATATAAACCGCGCTTTGTTTTAGACGGTTATCAAAAAAAGATGGGAACGGAGAATTTCCGTAATTTTAAATATTGAATTTTTAAACGTTGAATTTAAAAA 1440
ATTTTGTCTACTACAGATTTTATTCACCGATTTTACAANAATCAACGGAAACTAAATTTAGTGTAAAC 1510
    
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ACKNOWLEDGMENTS: M.J.R. was a recipient of an EMBO short-term Fellowship, with additional support from the SERC.

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