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Nucleotide sequence of the 5S ribosomal RNA gene of Bartonella bacilliformis

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Eubacterial rRNA genes are usually organized in operons containing the 16S, 23S and 5S rRNA genes, in that order (1). A cluster of structural rRNA genes was discovered during nucleotide sequencing of a cloned 3.6-kb BamHI fragment of DNA from B. bacilliformis, the agent of Oroya fever in humans. The 5S rRNA gene is 119 bp in length and is located 107 bases 3' to the 23S rRNA gene of the bacterium (Figure 1A). The gene contains the highly conserved eubacterial 5S rRNA sequence GAAC (Figure 1B), which is believed to interact with tRNA's during translation (2). The 5S gene is immediately preceded and followed by a 12-base inverted repeat flanked by adenine-rich sequences (Figure 1B). Previous homology searches using the 16S rRNA sequence of B. bacilliformis indicated that the bacterium was closely related to Rochalimaea quintana, Brucella abortus, and Agrobacterium tumefaciens, with 91.7%, 91.3%, and 88.8% identity, respectively (3). In keeping with the high degree of 16S rRNA homology (3), searches with the 5S rRNA gene from this study show 84% sequence identity to the 5S gene of A. tumefaciens. The 5S sequence homology also suggests that B. bacilliformis may be closely related to Vibrio cyclotis, with 91.6% 5S rRNA sequence identity (4). As the 16S rRNA sequence from V. cyclotis and the 5S rRNA sequences of R. quintana and B. abortus become available, a further homology comparison will be useful for the proper classification of B. bacilliformis. The bacterium is presently placed in the order Rickettsiales. However, it is the only motile species in the order and is one of just two genera, including Rochalimaea, which can be cultured axenically (5).

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