Molecular Phylogenetic Analysis of Tryptophanyl-tRNA Synthetase of *Actinobacillus actinomycetemcomitans*

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Aminoacyl-tRNA synthetase family enzymes are of particular interest for creating universal phylogenetic trees and understanding the gene flow as these enzymes perform the basic and analogous biochemical function of protein synthesis in all extant organisms. Among them, tryptophanyl-tRNA synthetase (Trp-RS) plays a foremost role in phylogeny owing to the close relationship with tyrosine-tRNA synthetase. In this study, the sequence of the gene *Trp-RS* was amplified using degenerated adenylation domain primers in the periodontal bacterium *Actinobacillus actinomycetemcomitans*. The sequence of the cloned PCR amplicon confirmed the adenylation domain sequence with glutamic acid residue, which is absent in five other oral bacteria used in this study as well as in a number of other bacteria described in the database. The Trp-RS sequence analysis prevailed the identify elements such as Rossmann-fold sequence and tRNA^{Trp} binding domains including acceptor stem and anticodon. A theoretical model of Trp-RS of *A. actinomycetemcomitans* was generated. Guided docking of the ligand tryptophanyl-5′-AMP revealed a highly identical active site in comparison with the bacterial template. The phylogenetic positioning of Trp-RS among a group of oral bacterial species revealed that *A. actinomycetemcomitans* is closely related to *Haemophilus influenzae*, *H. ducreyi* and *Pasteurella multocida*.

Key words: Aminoacyl-tRNA Synthetase (AARS), Tryptophanyl-tRNA Synthetase (Trp-RS), *Actinobacillus actinomycetemcomitans*, Phylogenetic Tree