

Computational study of translation elongation features in *Mycoplasma*

V.S. Sokolov

Institute of Cytology and Genetics SB RAS, Novosibirsk, e-mail: sokovlad1@bionet.nsc.ru

V.A. Likhoshvai, Y.G. Matushkin

Institute of Cytology and Genetics SB RAS, Novosibirsk

In a modern biology, study of genes expression efficiency and its optimization is timely and significant problem both for theory and for practice. From the fundamental point of view, a solution of this problem is important for theoretical estimation of expression level of genes, which experimental data is not available yet. The results of this research can also be helpful in practical biology, for instance in planning genetic engineering experiments or increasing producers (genetically modified organisms) productivity.

It is known, that for unicellular and many multicellular organisms level of genes expression depends on such factors as gene codon composition, presence and distribution of secondary structures in mRNA and their stability [1]. According to various combinations of these factors five groups of organisms, that optimized the primary structure of their genes in different ways during the evolution, are identified [2].

We have implemented the algorithm for research of completely sequenced genomes. For each gene in a genome, the algorithm calculates parameters associated with mRNA codon composition and stability of its secondary structures. Consequently, so-called elongation efficiency index (EEI) is assigned to each gene.

We have analyzed genomes of 42 various *Mycoplasma* strains. It was found, that genes expression level in almost all organisms depends on number of mRNA secondary structure and doesn't depend on codon composition. Also three strains which significantly differed from others were revealed (*Mycoplasma haemocanis Illinois*, *Mycoplasma haemofelis Ohio2* and *Mycoplasma haemofelis Langford1*). Genomes of these particular organisms are distinguished by much lower average number of local inverted repeats, which can form secondary structures in mRNA. For additional investigation we have constructed

and analyzed the average profiles of local inverted repeats localization in mRNA for all *Mycoplasma* genomes.

Based on our data and information available in literature about *Mycoplasma* phylogeny we suppose, that particular *Mycoplasma* strains evolved in the line of reducing number of mRNA secondary structures for increasing genes expression level. Parasitic life style of these organisms can be the main cause of such changes.

1. N.V.Vladimirov, V.A.Likhoshvai, Y.G.Matushkin. (2007) Correlation of codon biases and potential secondary structures with mRNA translation efficiency in unicellular organisms, *Molecular Biology*, V. 41. № 5. P. 843-850.
2. V.A.Likhoshvai, Y.G.Matushkin. (2002) Differentiation of single-cell organisms according to elongation stages crucial for gene expression efficacy, *FEBS*.