Summary for general public

Protein biosynthesis (translation) is a multi-stage process necessary for the life of every cell. Instructions for making proteins are encoded in DNA. Transcription is the process of copying of the DNA nucleotide sequence into an mRNA sequence, which is then translated into the language of amino acids. Another transcription product necessary for protein synthesis are tRNA molecules, which are responsible for providing amino acids - the building blocks of protein. The multidimensional relationship between translation and transcription is a fundamental scientific issue undertaken by scientists around the world, but due to the multitude of factors that regulate translation, many aspects remain unexplained. The current project is an attempt to elucidate the relationship between translation and tRNA biosynthesis. tRNA is produced by a specific enzyme RNA polymerase III (Pol III). The activity of Pol III is controlled by the Maf1 protein, a general negative regulator that is conserved through evolution, from yeast to humans. In cells with an inactive Maf1 protein (*maf1Δ*), improper Pol III regulation leads to increased transcription of tRNA precursors (pre-tRNA), leading to impaired pre-tRNA maturation and saturation of the tRNA export machinery. Thus, tRNA that accumulates in *maf1Δ* cells likely does not reach translation machinery or is not fully functional in reading mRNA codons. Our preliminary data indicate that the level of protein synthesis is decreased in *maf1Δ* cells and can be restored by overproduction of the translation elongation factor eEF-1α. eEF-1α is responsible for delivering tRNA to the ribosome. We hypothesize that an imbalance in levels of individual tRNAs adversely affects translation in *maf1Δ* cells, and eEF-1α overproduction compensates for this effect by facilitating codon adaptation to different tRNA pools. The aim of the proposed project is to understand the mutual influence of the tRNA pool and levels of the elongation factor on the rate and specificity of translation for specific mRNAs. To achieve this goal we will use high-throughput methods and a simple model organism, yeast *Saccharomyces cerevisiae*. We will identify and analyze the translation of individual mRNAs that are most affected in *maf1Δ* cells. We will also identify changes in the tRNA pool resulting from inappropriate Pol III regulation. The proposed research will elucidate the mutual influence of the tRNA pool and elongation factor levels on the rate and specificity of translation for specific mRNAs. Our data could contribute to a better understanding of the relationship between the two fundamental cellular processes - transcription and translation.