

Epitranscriptome of bacterial tRNA: function of sulfur and selenium-modified uridines present in the wobble position of tRNA anticodons

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In the translational machinery the transfer RNAs (tRNAs) are adapter molecules that supply amino acid residues to a growing peptide chain following genetic information encoded by messenger RNA (mRNA). The reading of mRNA codons by tRNA anticodons is a dynamic process orchestrated by cellular conditions and the structure of both interacting molecules. The post-transcriptional modifications of tRNA are main functional players of its epitranscriptome. So far more than 40 modifications (out of ca. 100 total present in transfer RNAs) have been found in the wobble position (a position 34 of tRNA molecule, the first letter of the anticodon), and most of them are R5-substituted uridines (R5U), 2-thiouridines (R5S2U) and 2-selenouridines (R5Se2U). These modified nucleosides were identified in all domains of life, although it was shown only in bacterial systems that (c)mmm5Se2U-tRNA are formed from their sulfur precursors. The S2U modifications are important for fine-tuning of protein biosynthesis through modulation of the codon-anticodon interactions, however less is known about function of selenium-modified tRNAs.[1,2]

Recently we have proposed a cellular two-step mechanism of the S2U-RNA→Se2U-RNA transformation, in which (i) 2-thiouridine is S-geranylated, and (ii) the resultant geS2U intermediate is selenated to form 2-selenouridine-RNA. Interestingly, both processes are catalyzed by the same enzyme - 2-selenouridine tRNA synthase (SeIU in bacteria).[3]

In the lecture we will try to answer two questions: 1) why the Nature introduced selenium into nucleosides located in the wobble position; 2) to what extent the palette of functions of S2U was changed/enriched by the presence of Se2U units. Thus, we will discuss the difference between codon reading properties of selenium and sulfur-modified tRNAs, as well as between the susceptibility to oxidation of S2U and Se2U in transfer RNA in the context of survival of bacteria under oxidative stress conditions.[4]

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References

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