

Ribosome profiling (Ribo-seq) – optimization of the method for the cyanobacterium *Synechocystis* sp. PCC 6803

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Ribosome profiling, also named ribosome footprinting, was first described in 2009 as a new method to study translation which employs deep sequencing of ribosome-protected mRNA fragments ^[1]. Mapping of these fragments provides a “snapshot” of all the ribosomes active in a cell at a specific point. Data obtained with this method show relative rates of protein synthesis, dynamics of ribosome movement along mRNAs and so provide insights into the mechanism of translational control.

This work that was supported by the International mobility project ^[2] is focused on optimization and mastering the ribosomal RNA profiling in the cyanobacterium *Synechocystis* PCC 6803. Since there is an apparent connection between regulation of protein translation and their subsequent assembly into complexes, the optimized method originally developed for plants ^[3] will be used to identify mechanisms regulating translation and assembly of Photosystem II (PSII) proteins. For this purpose, we will compare ribosome profiles in a number of *Synechocystis* strains lacking various PSII subunits and PSII assembly factors under different growth conditions (irradiance, temperature). The seminar will present theoretical basics of the methodology and the first results of its optimization, which is still in progress.

References:

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2. International mobility of the researchers of the Institute of Microbiology of the CAS, v.v.i. No. 2 (registr. Number CZ.02.2.69/0.0/18_053/0017705) within the framework of the Operational Programme Research, Development and Education funded from European Union Funds.
3. Chotewutmontri P., Stiffler N., Watkins K.P., Barkan A. (2018) Ribosome Profiling in Maize. In: Lagrimini L. (eds) *Maize. Methods in Molecular Biology*, vol 1676. Humana Press, New York, NY. <https://doi.org/10.1007/978-1-4939-7315-610>.