

Analysis of the evolutionary relationships of Melainabacteria, Cyanobacteria, Sericytochromatia and Margulisbacteria based on the study of the cation binding site in the c-subunit of rotor membrane ATPases

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Phylogenetic trees provide per se no information on the order of appearance of different groups of organisms; evolutionary scenarios should rely on additional data sets. For prokaryotic organisms, it appears useful to analyze the ion-specificity of their membrane bioenergetic machinery, which can be determined from the amino acid sequences of ion-translocating subunits of rotary ATP synthases [4]. Earlier, the evolutionary primacy of sodium-dependent bioenergetics was shown; it was argued that proton-dependent bioenergetics got widespread mostly after the oxygenation of the atmosphere some 2.5 Gy ago [5].

We have checked for the ion-specificity of bioenergetics within Cyanobacteria phylum, which contains Oxyphotobacteria and two apparently non-photosynthetic phyla, namely Melainabacteria and Sericytochromatia [6]. We also included in the analysis Margulisbacteria and Saganbacteria – two newly described phyla closely related to Cyanobacteria [1]. Cyanobacterial genomes were selected from the representative set of 711 prokaryotic genomes, Melainabacterial genomes were selected in NCBI Taxonomy Browser; the genomes of Sericytochromatia and Margulisbacteria were selected in accordance with the GTDB taxonomy. Gene predictions were made with Prodigal, and gene annotation was performed with BLAST and HMMER, using the set of HMM-profiles of Clusters of Orthologous Groups [2]. The set of protein sequences was aligned using MUSCLE, and the phylogenetic tree was reconstructed using MEGA X.

Sequences of the c-subunits of Na⁺-dependent ATP-synthases are characterized by a specific amino acid pattern [3, 4]. The Na⁺-binding c-subunits were found in several genomes of Margulisbacteria, which made a separate clade on the phylogenetic tree, and in one Sericytochromatia genome. These organisms could closely resemble the ancestors of Margulisbacteria and Cyanobacteria, respectively. Photosynthetic Cyanobacteria (Oxyphotobacteria) and Saganbacteria contain no organisms with sodium-dependent bioenergetics and could be derived groups that appeared after the oxygenation of the atmosphere.

Источники и литература

- 1) Carnevali P. B. M. et al. Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria //Nature communications. – 2019. – Т. 10. – №. 1. – С. 463.
- 2) Dibrova D. V. et al. COGcollator: a web server for analysis of distant relationships between homologous protein families //Biology direct. – 2017. – Т. 12. – №. 1. – С. 29.
- 3) Meier T. et al. Complete ion-coordination structure in the rotor ring of Na⁺-dependent F-ATP synthases //Journal of molecular biology. – 2009. – Т. 391. – №. 2. – С. 498-507.
- 4) Mulkidjanian A. Y. et al. Evolutionary primacy of sodium bioenergetics //Biology direct. – 2008. – Т. 3. – №. 1. – С. 13.
- 5) Mulkidjanian A. Y., Dibrov P. The past and present of sodium energetics //BBA. – 2008. – Т. 1777. – №. 7-8. – С. 985-992.

- 6) Soo R. M. et al. On the origins of oxygenic photosynthesis and aerobic respiration in Cyanobacteria //Science. 2017. – Т. 355. – №. 6332. – С. 1436-1440.