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Biodiversity and genomics of diatoms

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Motivation and Aim: Diatoms are single-cell photosynthetic algae that fix up to 20 % of total marine primary productivity [1]. Biodiversity of diatoms is huge: *a.* 12000 diatom species have already been described, and *a.* 100000 are assumed to exist [2]. In this regard, joint analysis on the species richness assessment and genomes survey of Bacillariophyta are the crucial both for development of the measures to maintain the sustainable functioning of marine ecosystem chains and conservation of the gene pool. Based on the published sources and own surveys, the current taxonomic richness of Black Sea benthic diatoms was evaluated. Updated diatom inventory holds 1094 species and intraspecific taxa, pooled in 953 species, 149 genera, 61 families, 32 order and 3 classes Bacillariophyta [3]. At present, genomes of 8 diatom species have been obtained only [4–6]. The mainstream of diatom research is elicitation of genes responsible for the silicon transport during the valves morphogenesis, the uptake of high-affinity iron, biosynthetic enzymes, a complete urea cycle. An explanation of these mechanisms will help to understand the wide prevalence of diatoms, which able to survive even in soils, ice and hot springs. Another important aim is the study of diatom genetic regulatory elements that determine gene expression and the light response regulation [7]. According to some data, there is a mechanism for switching from phototrophic to heterotrophic feeding under limited light regime.

Conclusion: Combined taxonomical evaluation of diatom diversity and its genomes should be employed for necessity of environmental security measures and conservation of marine flora biodiversity at the modern transformation and anthropogenic development of the Black Sea and World Ocean shores. The obtained in future research results will allow to consider the diatom evolution, ecology and metabolism processes within the framework of the biodiversity concept.

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