

Study of the COI Gene Fitness for a Population-Genetic Analysis of Endemic Baikal Sponges *L. Baikalensis*

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Introduction

Genetic structure of endemic Baikal sponges must differ from cosmopolitan sponges one due to life cycle peculiarities and it still remains unknown

Cosmopolitan sponges:

- Have resting stage – gemmules
- Have annual life cycle
- Distributed around the world
- Healthy

Baikal endemic sponges:

- Do not have resting stage – gemmules
- Some individuals live more than 50 years
- Found only in Lake Baikal
- Events of mass disease and mortality are recorded for the past decade

Studying of genetic structure might help to assess populations' recovery potential from disease, witch have been reported for the past decade

Here we check if universal molecular genetic marker COI could be used for population structure analyses of Baikal endemic sponges as it is successfully used for marine sponges population studies

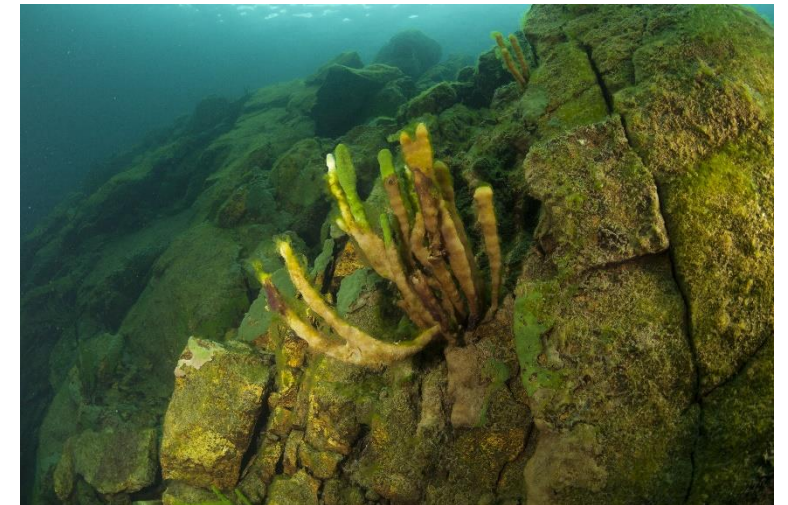


Figure 1. Picture of sick Baikal sponge *Lubomirskia baikalensis*
Photographer: Eugenie Saphonov

Methods & Results

Two parts of COI were taken into analyses. Standard 5 end fragment and fragment E3M11. For standard fragment were taken primers previously described by Folmer and for E3M11 part primers were developed by us using full sequence of COI of *Baikalospongia intermedia* from GenBank NCBI

Primers for fragment E3M11 of COI:

Forward primer 5'-GCTGGAGGAGGAGACCCAAT-3'

Reverse primer 5'-TGGAATCCGAATACCGTCTCG-3'

For 8 samples of *Lubomirskia baikalensis* species from tree different basins of Lake Baikal no differences were found in standard Folmer fragment, and just two haplotypes were found for E3M11 fragment

Thus we consider COI gene to be inappropriate for population genetic studies of endemic Baikal sponges and recommend using microsatellite markers instead

Work on microsatellites markers development is already underway

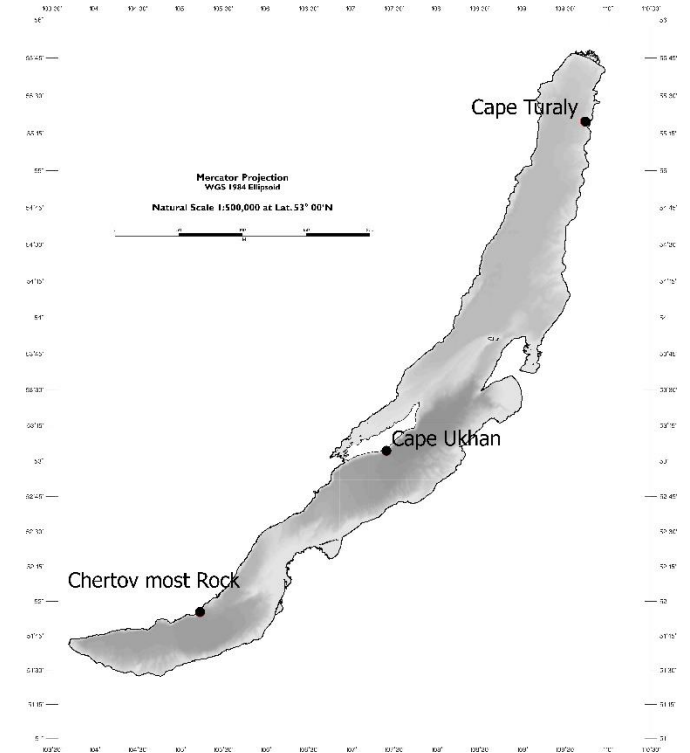


Figure 2. Sampling points on the map of Lake Baikal