

Investigation of proteome of Baikal endemic amphipod *Eulimnogammarus cyaneus* (Dybowsky, 1874) using LC-MS

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Motivation and Aim: Lake Baikal is unique ancient ecosystem, currently threatened by the anthropogenic impact and climate change [1]. Thus, developing of the monitoring bioassays for this lake is of the great importance. Aim of the current study was to investigate proteome of a potential model biotest species for Lake Baikal – amphipod *Eulimnogammarus cyaneus* (Dybowsky, 1874), using a proteogenomic approach.

Methods and Algorithms: We used 1D-PAGE of total protein lysate of *E. cyaneus*, followed by gel fragmentation, in-gel trypsinolysis and nano-HPLC/nano-ESI-MS/MS using LTQ Orbitrap XL™ (Thermo Fisher Scientific). Transcriptome assembly of the respective species was used to generate a specific database for protein identification, which was carried out with MaxQuant software [2].

Results: MS-spectra were assigned to 1028 protein groups. Among them the first five major groups were belonging to the following families (identified by InterProScan Ids): tubulins, ubiquitin, heat shock protein 70 kDa, actin and hemocyanin. Used approach allowed us to validate approximately 9 % of the transcriptome. Label free quantification using MaxQuant revealed 16 differently expressed ($p < 0.05$, Bonferroni correction) protein groups in males and females of the studied species.

Conclusion: Thus, for Baikal endemic amphipod *E. cyaneus* experimentally-validated proteomic database was established and a sexual dimorphism of proteomes was investigated. This database will allow to carry out a broad spectrum of eco-physiological and eco-toxicological researches with amphipods and to reveal new specific biomarkers of anthropogenic impact to the unique ecosystem of Lake Baikal.

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References

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