Contrasting adaptations in shallow and deep-sea bivalves from East Atlantic: transcriptome-wide analysis

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Bivalve molluscs play a significant role in nearshore reef ecosystems and constitute one of the dominant groups of macrofauna in the deep sea. In European waters, several intertidal bivalves including *Limecola (Macoma) balthica*, *Mya arenaria* and *Mytilus edulis* are widely presented in upper sublittoral communities. Typical subtidal species, particularly *Arctica islandica, Hiatella arctica* and *Mya truncata* occur from low tide level mark down to bathyal zone. Next-generation sequencing has recently catalyzed studies of local adaptations by obtaining a large number of co-dominant genetic markers, even when no reference genome is available. We used whole body transcriptomes of common bivalves inhabiting contrasting enviromental conditions, available from GenBank SRA database. Comparison of transcriptomes of phylogenetically close taxa showing contrastingadaptations, or phylogenetically distant taxa with similar adaptive traits allows to reveal convergence and parallelisms at the molecular level. This approach allows to test the hypothesis of the origin of mutations that lead to similar phenotype effects, and reveal the velocity at which mutation in the DNA may cause a phenotypic effect. Transcriptome-wide scans for common genes under selection were implemented by using the standart pipeline with estimation of dN/dS ratio in ortholog genes of studied species and computation of GO terms (Gene Ontology terms) enrichment. Ortholog genes were identified with protheinortho program and dN/dS values were determined in PAML codeml program for each orthogroup. GO enrichment analysis was performed with Webgestalt software. The results of comparative transcriptome analysis led to the identification of candidate genes responsible for intertidal, upper sublittoral and shelf habitat adaptations in common European marine bivalves. The research was supported by the RFBR 18-34-00572, RAS research projects AAAA-A17-117042410167-2 and AAAA-A17-117030310207-3, Programs of Presidium RAS "Dynamics of gene pools in natural populations" and "Development of vital and biosphere processes".

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