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Sequencing the transcriptome of Bathymodiolus azoricus: new possibilities for the understanding of biological processes at deep-sea hydrothermal vents

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Sequencing the transcriptome of Bathymodiolus azoricus: new possibilities for the understanding of biological processes at deep-sea hydrothermal vents

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Abstract

Deep-sea hydrothermal vents are regarded as extreme environments, yet the animals dwelling around the vent sites exhibit high productivity and therefore must cope with environmental microbes and mechanical stress whether ensuing from animal predation or venting activity. Investigating the exceptional physiological reactions that vents mussels have adopted in their habitat remains an overwhelming challenge for deep-sea biologists.

In an attempt to better understand the responses of deep-sea mussels to different hydrothermal vent conditions we carried out a high-throughput sequence analysis of B. azoricus transcriptome using gills tissues from animals freshly collected from the bottom of the sea. The Roche 454 GS FLX sequencing technology was used to generate a substantial EST data set from which a comprehensive collection of genes coding for putative proteins was organized in the dedicated database, DeepSeaVent accessible through the website http://transcriptomics.biocant.pt:8080/deepSeaVent/. This is the first deep-sea vent animal transcriptome database based on the pyrosequencing technology. In addition, a metatranscriptome analysis from the bacterial community associated to the vent mussel gills was also performed. Results from the metatranscriptome analyses point at the presence of an unprecedented number of bacterial phylotypes. The present study reports on the detection of a large numbers of novel sequences in both the transcriptome in the metatranscriptome of vent mussel and its associated microbial communities and discusses new possibilities to find protein-coding genes with potential use in biotechnology. The presence of bacterial marine enzymes such as chitinase, alpha-amylase, xylose isomerase, 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, 1-deoxy-D-xylulose 5-phosphate synthase and polyketide synthase, ribulose-1,5-bisphosphate carboxylase oxygenase, methane monooxygenase, methanol dehydrogenase, sulfur oxidation sox y and methanol dehydrogenase, is discussed within the context of their gene expression in gill tissues of B. azoricus mussels retrieved from the Lucky Strike and Menez Gwen hydrothermal vent sites.