

Symbiosis under pressure: effects of isobaric recovery and in situ translocation on gene expression patterns in *Bathymodiolus azoricus*

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The deep-sea mussel *Bathymodiolus azoricus* harbor both thiotrophic and methanotrophic bacterial endosymbionts in its gills. Their density and relative proportion change in response to varying conditions in their environment. This flexibility remains difficult to explain on a molecular basis and few studies have been conducted on the effect of this variability on the physiological status of the mussel or the identification of the different genes and metabolic pathways potentially related to symbiosis control in mussels. In order to study the interplay between symbiosis partners we used high density micro-arrays to examine a wide range of gene expression patterns on mussels subjected to experimental in situ translocation. But a question remains: how does recovery from the deep affect gene expression? During the 2013 BioBaz expedition we were able to sample mussels from vent sites located south of the Azores at increasing depths (Menez Gwen at 800m, Lucky Strike at 1700m and Rainbow at 2400m) in two ways: normal recovery using regular sampling boxes, and isobaric recovery using the Periscop® device. We observed a significant difference in gene expression patterns only for mussels living below 2000m, validating our approach for mussels from MG and LS. Analyzing the results in relation to the symbiont content of each individual, we have evidenced that the physiological responses of mussels exhibit specific patterns highlighting a more complex picture than initially expected. The results of these studies will be presented as well as some interesting outcomes of the characterization of *B. azoricus* genome.