Calcification and gene expression patterns of *Mytilus edulis* under elevated pCO_2 (BIOACID subproject 3.1.3)

Jörn Thomsen[1], Anne Hüning[2], Magdalena Gutowska[3], Isabel Casties[1], Magnus Lucassen[2], Eva Philipp[4], and Frank Melzner[1]
[1]IFM-GEOMAR, Kiel, Germany
[2]Alfred-Wegener-Institute, Bremerhaven, Germany
[3]Kiel University, Institute of Physiology, Kiel, Germany
[4]Kiel University, Institute of Clinical Molecular Biology, Kiel, Germany

Juvenile mussels were acclimated to four pCO_2 levels between 39 and 400 Pa for two months. Following incubation, calcification, growth, oxygen consumption and NH_4^+ excretion were assessed. Additionally, outer (mantle folds) and inner mantle tissue samples were taken separately from control and 400 Pa mussels and analyzed for gene expression patterns using real-time PCR and pyrosequencing. In total about 26,000 transcripts have been identified so far, 50 % of which could be annotated. Elevated aerobic metabolism at moderate acidification and a linear increase of NH_4^+ excretion rates indicate higher protein turnover at higher pCO_2. Whereas somatic growth was not significantly affected, calcification rates decreased linearly with increasing pCO_2. Nevertheless, mussels were able to calcify at high rates in all treatments. Analysis of the mantle transcriptome showed remarkable differences between inner and outer mantle and a significant response to elevated pCO_2. Distinct matrix proteins could be identified exclusively in the outer mantle and a Ca^{2+} -binding protein was found 16-fold higher in the outer than in the inner mantle. Under hypercapnia, the expression of a chitin synthase decreased 5 fold. This is in line with reduced shell growth rates, as chitin is a major component of the organic matrix of the mussel shell. Our results suggest that mussel calcification under acidified conditions may be affected by elevated energy expenditure and loss of nitrogen components which may impair the production of shell matrix components. Future work is going to focus on how the expression of candidate genes is affected by elevated pCO_2 in space and time.