



Biogeography of vent and seep mussels of the genus *Bathymodiolus*

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Deep-sea hydrothermal vent mussels of the genus *Bathymodiolus* with endosymbiotic bacteria are endemic in marine chemosynthetic environments such as hydrothermal vents and hydrocarbon seeps. They depend on the symbiotic primary production that is fueled by the oxidation of reduced inorganic compounds such as hydrogen sulfide or methane. Reduced deep-sea habitats are usually widely separated, and the question how *Bathymodiolus* species disperse over large distances and which biogeographic barriers affect species distribution remains unanswered. The equatorial Atlantic may represent a key area for investigating this question because large fracture zones may either act as biogeographic barriers for N-S directed gene flow along the ridge and/or as conduits for W-E directed genetic exchange between Gulf of Mexico and W-Africa seep populations.

The patterns of biogeographic distribution and evolutionary dispersal in *Bathymodiolus* have been investigated by analysis of the phylogenetic relationships among species collected from the Pacific, North Atlantic and the Central Indic Ocean based on mitochondrial and nucleic phylogenetic marker genes. However, the role of the southern and equatorial Atlantic for genetic exchange between these biogeographic provinces remains unclear to this date. We have for the first time included collections from this region in our investigations on the worldwide phylogenetic relationships in *Bathymodiolus*, based on newly analyzed and published gene sequences of mitochondrial Cytochrome Oxidase subunit I (COI), NADH-Dehydrogenase subunit 4 and the nuclear 28S rRNA gene.