

**Apoptosis in the tissues of *Bathymodiolus* mussels under bathymetric pressurized/ versus unpressurized conditions: the possible role of apoptosis in regulating the branchial microbiota.**

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The deep-sea mussels *Bathymodiolus azoricus* (Bivalvia: Mytilidae) and *B. puteoserpentis* often dominate the endemic macrofauna of mid-Atlantic ridge vent sites. Their gills house methane- (MOX) and sulfur-oxidizing (SOX) bacteria that sustain most of the mussel's nutritional requirements. The association is flexible, symbiont abundances can vary depending on substrate availability. However, mechanisms regulating symbiont abundances are poorly understood. Transcriptomic analyses suggest that when the load of symbionts is high in the gills of *B. thermophilus*, the genes involved in the inhibition of apoptosis are depressed, suggesting that when the symbiotic load is high, apoptosis might be activated, and vice versa. Using the TUNEL method and immunohistology we followed apoptosis in the gills and other non-symbiotic tissues in *B. azoricus* and *B. puteoserpentis*. To avoid bias due to recovery stress, mussels had to be sampled in the pressure-maintaining device PERISCOP, which allow recovering animals at their native pressure. For the first time during the cruises BioBaz 2013 and BICOSE 2014, such collections were possible from sites between 800 and 3500m depth. We thus compared the apoptotic levels between mussels sampled in pressurized versus unpressurized conditions. Pressure did not significantly change the apoptotic levels in the gills of *Bathymodiolus*. Comparison with non-symbiotic *Mytilus edulis* indicate that levels of apoptosis are higher in *Bathymodiolus*. Altogether, results support that apoptosis is a possible mechanism to control the gill microbiota.