

Marine thiotrophic symbioses - examined by physiological proteomics

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Chemosynthetic symbioses of marine invertebrates with sulfur-oxidizing bacteria are a widespread phenomenon across a variety of sulfidic habitats, from hydrothermal vents to shallow water seagrass bed ecosystems. Hosts and symbionts cooperate in an intricate and delicately tuned network of molecular interactions. Many of these processes have not been deciphered to date, which is – to a considerable extent – due to the uncultivability of the bacterial symbionts. Physiological proteomics circumvents this problem: A culture-independent global proteome analysis allows for comprehensive and very detailed metabolic profiling of the individual symbiotic partners or even of the symbiosis as a whole. We therefore pursued a proteogenomic approach to investigate symbiont physiology and microbe-host interactions in a) the giant tubeworm *Riftia pachyptila*, b) deep-sea mussels of the genus *Bathymodiolus*, and c) the shallow water clam *Codakia orbicularis*. Our results revealed a remarkable degree of metabolic flexibility in these systems: In *Riftia*, individual symbiont subpopulations display distinct metabolic pathway strategies, likely allowing them to play different roles in the consortium. In *Bathymodiolus* symbioses, some metabolic functions are missing in the thiotrophic symbiont, but seem to be complemented by the host – and vice versa. The symbiont of *C. orbicularis*, on the other hand, does not only produce organic carbon and detoxify harmful sulfide to its host's benefit, but is also able to fix molecular nitrogen. This enormous metabolic versatility on the symbionts' side, combined with the hosts' ability to effectively buffer unsteady ambient conditions, might be the key to success for these remarkable symbioses.