Physiological basis of the Riftia pachyptila symbiosis

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In the giant deep-sea tubeworm Riftia pachyptila, the association between chemosynthetic bacteria and their invertebrate host is driven to the extreme: The adult animal lacks a digestive system, but instead totally relies on one species of sulfur-oxidizing, chemosynthetic Gammaproteobacteria for nutrition. The bacteria dwell in the trophosome, a specialized organ in the worm's body cavity. This intricate symbiosis probably requires complex communication and coordination between both partners, to ensure a stable symbiosis under the seemingly hostile deep-sea conditions. However, even today, after decades of research, the molecular interactions between the worm and its symbiont remain poorly understood. Especially interconnections of metabolic pathways and coordination of immune responses are of great interest not only for profound insights into this symbiosis, but also for a better understanding of how beneficial host-microbe interactions in general differ from harmful ones. Here, we present a comprehensive study of the physiological basis of the Riftia symbiosis, employing state of the art mass spectrometric methods. These allow for a detailed proteomic comparison of symbiont-containing and symbiont-free tissue. We thus characterize the metabolic networks and communication pathways between the host and its bacterial symbiont in high resolution. Additionally, we address the influence of environmental conditions, such as the availability of sulfur and thus energy, on the adaptation mechanisms of this fascinating symbiosis.