Understanding mechanisms of host-microbe interactions in lucinid clams

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Mutualistic associations between invertebrate animals and chemosynthetic bacteria form the foundation of deep-sea hydrothermal vents and cold seeps and are highly abundant in shallow-water ecosystems, like the Lucinidae bivalves. The lucinidae symbioses are natural low-diversity associations and offer unique opportunities for understanding the mechanisms that underlie host-microbe associations. Most research on lucinids has focused on the phylogeny, physiology and metabolism of the symbionts, but much less is known about the host's physiology and response to the symbionts. We sequenced and assembled metatranscriptomes of the symbiont-hosting lucinid Loripes orbiculatus. This dataset enabled us to simultaneously assess both host and symbiont gene expression, and also allowed us to identify symbiont- and host-encoded proteins in the holobiont. We show that host digestive enzymes are highly expressed in the symbiont-hosting gill tissue, indicating active symbiont digestion that would provide nutrition for the host and control the symbiont population size. A small subset of symbiont proteins including the key glycolytic enzyme glyceraldehyde-3-phosphate dehydrogenase, was highly abundant in the symbiont-free foot tissue and it is termed a 'moonlighting' protein in pathogens due to its dual roles in bacterial metabolism and host immune modulation. These proteins may be secreted by an unconventional mechanism, as they lack recognizable signal peptides. Due to the natural simplicity of this symbiosis, we could identify potentially secreted symbiont proteins that could have 'long-distance' effects on the host physiology. This study helps to bridge the gap between animal and symbiont responses, both of which are essential for the long-term persistence of beneficial associations.