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Genomics and Symbiosis Readings Summary

Symbiosis, the functional interaction among organisms, facilitates the persistence of many species in environments that are less than ideal (Fisher, Henry, Cornwallis, Kiers, & West, 2017). This interdependence can drive evolutionary change and even promote speciation (Brucker & Bordenstein, 2012). Thus, symbiosis is often reflected in the genomes of symbiotic organisms, making genomics a tractable method for studying symbiotic relationships (Brucker & Bordenstein, 2012). Belcaid et al. (2019) and Hansen & Moran (2011) explore relationships between model organisms and their symbiotic microbial communities by examining their genomes. They reveal that many questions regarding the nature of the relationship between two symbiotic organisms, as well as the evolutionary origin of the symbiosis can be revealed through genomic analysis.

Belcaid et al. used genomics to determine the evolutionary origin of two symbiotic organs in cephalopod *Euprymna scolopes*, whereas Hansen & Moran looked at the genomes of aphid ﻿*Acyrthosiphon pisum*, and its bacterial endosymbiont, *Buchnera aphidicola* to better understand how they coordinate the production of amino acids to meet their differing dietetic needs. In short, Belcaid et al. studied the process, while Hansen & Moran studied the result of symbiosis-driven evolution. Both Belcaid et al. and Hansen & Moran were able to answer these questions because their model organisms, *Euprymna* and *Acyrthosiphon*,host symbiotic microbial communities within specific organs. These organs are specific to a single unique endosymbiotic community. *Euprymna* has two of these types of organs: The Light Organ (LO), and the Accessory Nidamental Gland (ANG). The LO hosts bioluminescent bacteria, *Vibrio fiscerhi*,allowing the squid to camouflage with its environment. In contrast, the ANG, which hosts many different types of microbes, “is hypothesized to play a role in egg defense” (Belcaid et al., 2019). *Acyrthosiphon* has only one symbiotic organ, the bacteriocyte. The bacteriocyte plays a role in coordinating the production of amino acids between the aphid and bacteria to meet their differing metabolic needs. The isolation of the endosymbionts in the hosts bodies enabled the researchers to compare gene expression between symbiotic-specific organs against non-symbiotic organs. This comparison enabled them to isolate the effects of symbiosis on gene expression in bacteriocytes.

The work in these two papers illustrate the coevolution of the two organisms in question with their internal microbial communities. The aphid-*Buchnera* study shows physiological complementarity between the two species. The study revealed that enzymatic pathways necessary for the production of six essential amino acids in *Buchnera* are puzzle-pieced together with enzymes encoded by the *Acyrthosiphon* genome. The complementarity of these metabolic pathways provides evidence for the idea that gene expression in the symbiotic hosts are coordinated with expression in their endosymbionts. Genes with enzymatic processes present in the aphid were lost in *Buchnera* shortly after its association with *Acyrthosiphon*. Each of the two species encodes enzymes that are necessary to biosynthesize a “balanced profile” of amino acids, that are then imported into either the bacteriocyte or *Buchnera* cells, depending on the metabolic needs of each species. Neither participant could survive without the other in the relationship, and this interdependence sustains their ecological association. Hansen & Moran also found that genes in the squid have also rapidly been exchanged after its associations with microbes began. While complementarity in the squid-microbe relationship is not heavily discussed in the Hansen & Moran paper, they do mention that portion of the *Euprymna* genome encoding the LO includes genes that encode an antimicrobial compound that “is thought to contribute to the specificity of the squid-vibrio association.” The Hansen & Moran study takes a different approach to studying the coevolution of organisms and rather than looking at complementarity, examined the evolution of symbiotic organs. They found that the squid’s two symbiotic organs have different origins. The LO was found to share many paralog genes with the eyes, and the authors conclude that the LO and ANG are mostly composed of tandemly-duplicated genes that are “involved in development and function of cephalopod eyes and the nervous system.” However, while LO genes many genes in the ANG organ were found to be novel, suggesting “high evolutionary turnover” in that specific organ. The authors found that the ANG has a higher proportion of repetitive elements than other bodily organs and suggest that this may result in rapid “genomic innovation” (Hansen & Moran, 2011). While the study uncovered the mechanisms of evolution of symbiotic organs in the squid, the authors posit that because the symbioses present in *Euprymna* are not nutritionally-based, that “the mechanisms for the evolution of [the squid’s] symbiotic organs may be different from what has been proposed for insect bacteriocytes.” However, this is not discussed in the Belcaid et al. paper.

In conclusion, symbiotic organs isolating endosymbionts from other bodily tissues allowed Belcaid et al. and Hansen & Moran to study the genomic aspects of host-microbe associations. While Belcaid et al. examined the extensive complementarity in enzymatic pathways between hosts and the symbionts, Hansen & Moran looked at different mechanisms of the evolution of symbiotic organs in hosts with endosymbionts. These papers contribute extensively to the emerging field of ecological and evolutionary genomics by providing unique insights into the genomics of symbiotic organisms.

References:

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