Symbiosis Summary

Maggie Schedl

Words: 775

Symbioses can involve a wide variety of organisms, but most studied are between a metazoan and a bacterial symbiont. Two studies, Hansen & Moran, (2011) and Belcaid et al. (2019), looked the symbiotic relationships between the host species: pea aphids and bobtail squids respectively, and various bacterial symbionts. Both papers utilized a symbiotic relationship that has been relatively well studied in the literature, and took a gene expression approach to unraveling their complex relationships.

Hansen & Moran's (2011) study system, the pea aphid and their bacterial symbiont *﻿Buchnera,* are an incredibly well studied pair. The full genome is sequenced for the both of them, and as they pointed out blatantly, “[they] exploited these recourses.” The amount of data they gathered was actually quite small; the transcriptomes of the aphid body tissue, bacteriocyte tissue, and of *Buchnera* at only one time point. This is because their focus questions were very directed. It is known that *Buchnera* is vertically transferred, and there are various studies on the development of bacteriocytes (ex: Braendle et al. 2003). However, the foundation of an obligate symbiosis most likely requires changes in the genome, and certainly changes in gene expression. Previous research recognized gaps in amino acid synthesis pathways in the genomes of both species. The authors had the very specific goal to look for expressed genes in either of the species that filled in pathway gaps in the other species. They concluded with direct evidence of metabolic complementation that takes place within bacteriocytes that allows pea aphids to thrive on the very nutrition-poor diet of phloem. It was also necessary to elucidate how nitrogen is created in the system, because previous research was unable to determine this, and nitrogen is an essential component of all amino acids.

While the paper was not necessarily heavily based in evolutionary theory, the strong evidence the authors put forward of metabolic complementation is a very good indicator of co-evolution. Nonetheless, the term co-evolution is incredibly broad, and the nuanced and intricate intertwining of these two organisms seems to beg for more complexity. Considering the incredible amount of research already gathered on this symbiotic pair, it would be very interesting to use this system to investigate the holobiont theory of evolution. How one would go about characterizing that, however, is another question completely.

While there is less known about the symbioses between the bobtail squid and its two bacterial symbiotic communities, ﻿*Vibrio fischeri* in the light organ, and many microbes in the accessory nidamental gland (ANG), than the aphids and *Buchnera,* this allowed Belcaid et al. (2019) to investigate broader patterns in the evolution of multiple symbioses in the squid. Interestingly, they did this with the same type of data that Hansen & Moran (2011) collected: transcriptomes from multiple host tissues. However, they did not look at the transcriptome of any of the symbionts. The obvious hurdle these authors had to overcome was the comparative lack of genomic resources: they assembled their own bobtail squid genome, and the genome of any of the symbionts is unknown. The highlight of this study system is the presence of two symbioses in the same organism. This allowed the authors to investigate how various symbioses could have evolved. The expression pattern from the light organ contained many genes from gene duplication events, while the expression from the ANG mapped to orphan genes. I found this particularly interesting considering that the ANG the more ancestral symbiosis. Further investigation of this dynamic is where I would like to see the research go. The differing genetic architecture that underlies the expression of the two symbioses-related organs indicated vastly divergent evolutionary histories.

This type of analysis was lacking in the Hansen & Moran (2011) paper, they did not investigate the potential genomic signatures eluding to the loss of various amino acid synthesis components. However, one must ask what is most biologically relevant, and understanding the meshing of fundamental biosynthetic pathways of obligate symbionts is a much more urgent question for the pea aphids. Depending on the symbiotic community under study, the two groups of authors leveraged what was unique about their system to shape their transcriptomic analysis. These are two examples of using similar data to either focus narrowly on specific molecules, or widely on larger processes. In a sense, this could be driven by the type of symbioses under questioning. If it is obligate, there is more of a chance for co-evolution of essential biological processes. Facultative symbioses may not have such distinct genomic signatures. The tissue specific annotation of functional genes transcriptomics provides, and their increasingly easier sample and bioinformatic processes, has opened them up widely to being used for studying symbioses.

**References**

Belcaid, M. et al., 2019. Symbiotic organs shaped by distinct modes of genome evolution in cephalopods. *Proceedings of the National Academy of Sciences*, p.201817322.

Braendle, C. et al., 2003. Developmental Origin and Evolution of Bacteriocytes in the Aphid–Buchnera Symbiosis. *PLoS Biol* 1(1): e21. https://doi.org/10.1371/journal.pbio.0000021

Hansen, A.K. & Moran, N.A., 2011. Aphid genome expression reveals host-symbiont cooperation in the production of amino acids. *Proceedings of the National Academy of Sciences*, 108(7), pp.2849–2854.