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Symbiosis

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Many organisms contain specialized cells and organs that house a microbial symbiont. Genomic signatures of host–symbiont interactions can be detected by comparing gene expression patterns within these specialized structures to those within tissue from other parts of the body. Belcaid et al. 2018 and Hansen & Moran 2011 are two studies that aim to characterize the host-microbe interactions in two different invertebrate species. Belcaid used the newly sequenced squid genome to understand the processes that influence the origin of specialized symbiotic organs. Hansen used the fully sequenced genomes of the pea aphid and bacterial symbiont *Buchnera* to observe coordination of host gene expression with bacterial metabolic pathways. While the objectives of these two studies differ, similar genomic techniques were used to further analyze the underlying mechanisms of these host-microbe interactions.

*Objectives*

The main objective of the Belcaid study was to define elements of genome structure and function that are critical for symbiosis and the evolution of cephalopods. A key result of this study was the most comprehensive assembly of the squid genome to date, which revealed the highly repetitive nature of the genome. Doing so allowed them to identify genomic transitions from the noncephalopod bilaterian architecture to the cephalopod architecture. They also included the genome of an octopus species, which is also highly repetitive, but with a higher proportion of short interspersed nuclear elements compared to long elements. However, the octopus does not have the same symbiotic organs as the squid, which allowed them to compare these two genomes. They determined that major genomic reorganization happened in a cephalopod ancestor because microsyntenic patterns conserved in many noncephalopod bilaterian genomes were disrupted in both the squid and octopus. They also found linkages of genes expressed in developed organ systems and symbiotic organs that were shared between these two cephalopod species.

The main objective of the Hansen & Moran study was to identify the coordination of gene expression between an aphid species and its bacterial endosymbiont as the capabilities of these two organisms have fused into a single integrated metabolism. As opposed to the other study, the aphid and *Buchnera* were previously annotated, so time was not spent exploring the nature of each genome. Instead, Hansen & Moran took advantage of these fully sequenced genomes to identify genes involved in amino acid biosynthesis.

*Symbiotic organs*

In the case of the squid, multiple specialized organs exist that house the microbial symbiont. Belcaid extracted RNA from the squid’s light organ (LO) and accessory nidamental gland (ANG) and compared genomic signatures of genes in these organs to those in nonsymbiotic organs. From these comparisons, they identified an evolutionary link between the light organ and the eye. In the aphid, their endosymbiont is located in the cytosol of specialized insect cells called bacteriocytes, so Hansen & Moran compared gene expression between these specialized cells and other body tissues.

*Sequencing*

Both studies used RNASeq to compare gene expression between symbiotic and nonsymbiotic tissue of the host. Belcaid profiled protein-coding transcripts against the NCBI data and then classified the transcripts as either squid-specific or shared within larger taxonomic groupings. Doing so revealed that these two symbiotic organs likely have two different patterns of genomic innovation. In the Hansen & Moran study, RNASeq data were mapped to the aphid genome, as it had been previously sequenced. In addition to RNA sequencing, Belcaid also used PacBio IsoSeq to identify and count unique isoforms across different functional categories in several adult tissues.

*Main Takeaways*

By assembling the squid genome, Belcaid was able to identify a unique genomic architecture that may have contributed to the innovations in the general cephalopod body plan. This genomic architecture is due to the highly repetitive nature of the cephalopod genome and the major reorganization compared to noncephalopod bilaterian ancestors. Comparing genetic signatures of the symbiotic and nonsymbiotic organs revealed relatively recent innovations of the ANG and LO within the squid lineage through gene duplication. They found a prevalence of functional novelty through gene duplication in the LO compared with taxon-specific genes in the ANG, which suggests that these two organs evolved by different means, potentially due to unique selection pressures.

Hansen & Moran observed gene expression of the symbiotic bacteriocyte cell, which revealed that the aphid and its bacterial endosymbiont “work together” to synthesize the amino acids required by both species. *Buchnera* synthesizes the essential amino acids that are deficient in the phloem-feeding insects by using complementary aphid-encoded enzymes. Nonessential amino acids that are not synthesized by *Buchnera* are synthesized by the bacteriocyte in the aphid.

While both studies focused on the underlying mechanisms of symbiotic interactions, Belcaid worked towards determining the evolutionary origin of symbiotic organs while Hansen & Moran were more interested in understanding the integration of host and symbiont capabilities in an important pathway.

**References**

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