Highlight: Tiniest of the Tiny—A New Low for Genome Size

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The cells of sap-feeding insects house a unique partnership—symbiotic bacteria provide essential amino acids to sap-sucking insects in exchange for a place to live and, in some cases, basic cellular housekeeping. Symbionts evolve at the mercy of genetic drift. Routinely, they loose pathways and genes other bacteria couldn't cope without: the genetic material required for cellular regulation, DNA repair, or cellular envelope biosynthesis.

In the past several years, a pattern has emerged: the genomes of symbiotic bacteria are startlingly small. "When we first began looking at these back in 2000, we realized their genomes are doing something kind of crazy," says Nancy Moran, an evolutionary biologist at the University of Texas. "It seemed impossible that something could live with less than 200 genes."

In her most recent work, Moran and Gordon Bennett, a postdoctoral fellow in Moran's lab, examine the genomes of two obligate symbionts living within the aster leafhopper (*Macrosteles quadrilineatus*), a bug that feeds on the sugar-rich phloem fruits, vegetables, and other plants. One of them, *Nasuia deltocephalinicola*, sets a new record for tininess. At just 0.112 million bases, it's the smallest bacterial genome ever sequenced. They report their findings in a new article in *Genome Biology and Evolution* (Bennet and Moran 2013).

How small bacterial genomes can possibly go is an open question (*Escherichia coli* appears bloated in comparison at 4.6 million bases). Some studies in the future may find even smaller genomes. But, for some researchers, the question of size is not the most fascinating issue.

"What's interesting in this series of papers," says Dr. Martha Hunter, an entomologist and evolutionary biologist at the University of Arizona not involved in this work, "is not the discovery of the 'minimal gene set' .... It is instead a process of illumination of the pathways lost, the pathways kept, and the integration of these obligate symbionts in the environment of a host and other bacterial symbionts that complement the missing genes of the focal bacterium."

The diminutively genomed *Nausia* still has genes for DNA replication, transcription, and translation, and genes to synthesize 2 of the 10 essential amino acids its host needs. However, *Nausia* and its co-symbiont *Sulcia muelleri* (0.190 million bases), responsible for the other eight amino acids, have both lost genes for producing energy. ATP demands are probably reduced in these bacteria, write the authors, because both symbionts have lost basic cellular functions. But numerous pathways that they do retain require ATP, begging the question: where is their energy from?

Bennet and Moran suggest the answer lies in host diet. Leafhoppers feed on sugary, energy-abundant phloem. It's possible their host takes care of their energy needs, and Bennet and Moran speculate that the host exchanges intermediate metabolites needed for carbohydrate metabolism directly. (Xylem-feeding insect symbionts, on the other hand, survive primarily on a water diet and retain a more complete oxidative phosphorylation pathway and, likely, larger genomes overall.) Or, it's also possible that phloem-feeding hosts can supply their symbionts directly with ATP or that the needed (but absent) oxidative phosphorylation enzymes come from one of the symbiotic partners.

If this is true, it raises the question of just how far the codependence between obligate symbionts and host can go. "In some ways, they're a lot like organelles," says Moran. Even though these bacteria live without much of the "usual" genetic material, they, unlike mitochondria or chloroplasts, are found only in certain cells in the body. They aren't present in the germ line cells and so far there is no evidence that the host handles protein synthesis.

The finding, that host lineage may fundamentally affect the genomic architecture of symbionts, is something that some researchers, such as Hunter, plan to look for as they study other symbionts. As she investigates the facultative symbiont *Cardinum*, "we will be looking for host associated signatures in the genome," she says.

What is clear, however, is that both host and symbiont are made for each other. Phylogenetic analysis by Moran and others indicates that the insects and their hosts have been co-evolving for at least 200 million years, when leafhoppers and spittlebugs first emerged, and possibly longer than that. Acquiring these symbionts allowed these bugs to specialize on nutrient-poor plant sap and turned the Hemipterans into a species-rich order found around the world.

Moran proposes no specific applications from this current line of work. But one could be down the road. "Leafhoppers are major pest species," she says. "You could imagine finding the Achilles heel of the [host-bacterial] symbiosis that could be used to control the pest. If that happened, I'd be pleased."

Literature Cited

Bennet G, Moran N. 2013. Small, smaller, smallest: the origins and evolution of ancient dual symbioses in a phloem-feeding insect. Genome Biol Evol. Advance Access published August 5, 2013, doi:10.1093/gbe/evt118.