GENOME WATCH

Honey, I shrunk the mimiviral genome

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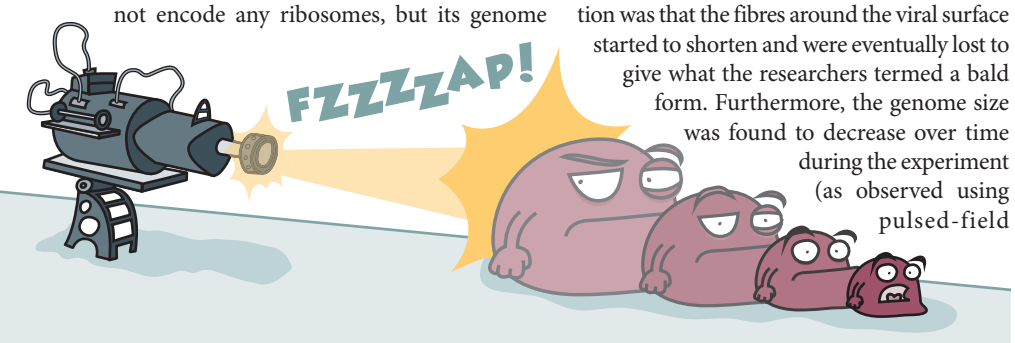
This month's Genome Watch describes how the large size of the mimiviral genome is a result of the sympatric lifestyle of mimivirus in host amoebae.

Viruses are typically small in physical size as well as genome size (ranging from a few kilobases to a few hundred kilobases), making the discovery of the mimivirus, a nucleocytoplasmic large DNA virus (NCLDV) found replicating in amoebae, something of a shock to virologists and evolutionary biologists. Mimivirus (so named for its mimicry of a microorganism) is currently the largest known virus both in terms of its particle size (750 nm in diameter) and its genome size. It is also the only virus for which distinct particles are visible under a conventional light microscope.

The genome of mimivirus was first sequenced in 2004 and found to be ~1.2 Mb in size[1], which is 2.4 times the size of the smallest sequenced microbial genome — that of *Nanoarchaeum equitans*. Using high-throughput whole transcriptome shotgun sequencing (RNA-seq), two recent studies have annotated the total gene count in the mimiviral genome as 1,018 (REFS 2,3). This is more than double the gene content of the next-largest published viral genome, that of a coccolithovirus that infects *Emiliania huxleyi*, which trails far behind with a genome size of 407 kb and only 472 predicted genes[4]. Like all viruses, mimivirus does not encode any ribosomes, but its genome does contain the genes for components that allow translation competence, such as genes encoding four aminoacyl-tRNA synthetases. The genome also contains genes (for example, those encoding topoisomerase IA, IB and IIA) that are suggestive of alternative mechanisms of DNA repair which are not seen in other viruses. Thus, mimivirus exhibits greater genetic complexity than many intracellular bacterial parasites, leading many to rethink the traditional assumptions that are made when defining a virus.

Mimivirus has a sympatric lifestyle, sharing its amoebal niche with many other species of microorganism. Although the vast majority of mimiviral genes have no cellular homologues, there is evidence of various origins for some genes, with ~15% originating through lateral gene transfer from the amoebal host, bacteria and virophages[5]. Only 5% of mimiviral genes were classified as NCLDV core genes. Gene acquisition from a range of sources is probably a consequence of the lifestyle of this virus, as intra-amoebal organisms exchange genes with each other and tend to have chimeric genomes.

To further investigate this idea, Boyer and colleagues[6] cultivated wild-type mimivirus in pure cultures of *Acanthamoeba polyphaga* (that is, lacking the other microorganisms that are usually found in amoebae). During 150 passages, the first noticeable effect of the selection was that the fibres around the viral surface started to shorten and were eventually lost to give what the researchers termed a bald form. Furthermore, the genome size was found to decrease over time during the experiment (as observed using pulsed-field gel electrophoresis). The team isolated the bald form of the virus and sequenced its genome, finding that it had lost 17% of the wild-type mimiviral genome, corresponding to 155 genes, through deletions. It was revealed that more than one-third of the total genes involved in intracellular host–virus interactions were lost. By comparing the proteomes of the wild-type mimivirus and the bald form, the complete lack of fibre was attributed to the loss of two (L829 and R135) of the three proteins that form the fibres. Interestingly, the loss of fibres makes mimivirus more resistant to the virophage Sputnik, which was thought to attach itself to the fibres as a means of penetrating the amoeba.



This work shows that a change in lifestyle can induce major reduction of the mimiviral genome by deleting unnecessary genes that are required for competition in its natural niche. Furthermore, the interplay between genome dynamics and the environment that was demonstrated in this study brings new insight to the origin of mimivirus and the consequences of a sympatric lifestyle on genome evolution.

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Competing interests statement
The author declares no competing financial interests.