GENOME WATCH

Voyage to the bottom of the 'seaquence'

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This month's Genome Watch highlights the use of deep sequencing metagenomics to identify bacteriophages that carry sulphur-oxidizing genes in deep-sea hydrothermal vent plumes.

Deep-sea hydrothermal vents are extraordinary environments that have high levels of toxic hydrogen sulphide and extreme temperature gradients of up to 450 °C. Although they are relatively unexplored, it is known that they harbour active and diverse ecosystems and contain large numbers of microorganisms that have evolved to derive energy from inorganic compounds, such as sulphur. One of the most active and common groups of bacteria in these ecosystems is the sulphur-oxidizing Gammaproteobacteria SUP05. These chemolithoautotrophs contain several genes that encode components of the reverse dissimilatory sulphite reductase (Rdsr) complex[1]. This enzymatic complex is crucial for converting elemental sulphur to sulphite (SO_3^{2-}), both of which are important substrates in sulphur-oxidation pathways[2]. A recent study by Anantharaman *et al.* now shows that, in addition to SUP05, bacteriophages that putatively infect this lineage also encode sulphur-oxidizing-like genes of the Rdsr complex[1].

The authors collected samples from hydrothermal vent plumes in the Pacific Ocean Lau Basin and the Gulf of California Guaymas Basin[1] and generated *de novo* whole-genome assemblies using shotgun metagenomic sequencing. By examining phylogeny, synteny and protein similarity with known phages, they constructed 18 viral genome sequences that represented three different marine viral families of the orders Podoviridae, Siphoviridae and Myoviridae. Importantly, 15 of the viral genomes encoded the α-subunit (*rdsrA* gene) and the γ-subunit (*rdsrC* gene) of the Rdsr complex, which suggests that these phages originally obtained the genes from their sulphur-oxidizing hosts.

No genomic similarity between the flanking regions of SUP05 *rdsr* bacterial genes and viral *rdsr* genes was found, which rules out any recent homologous recombination events between the bacteriophages and their hosts. However, phylogenetic analysis showed a tight clustering of viral *rdsrA* with *rdsrA* from two separate lineages of SUP05 bacteria, suggesting that the genes were obtained from these hosts via horizontal transfer.

On the basis of these findings, the authors proposed that the acquisition of *rdsr* genes provides a selective advantage for the phage: following infection, viral *rdsr* genes supplement the sulphur-oxidation pathway in SUP05 bacteria to sustain or increase sulphur oxidation. Furthermore, phage genomes also contained genes that had high sequence identity to other SUP05 genes, including genes encoding proteins that are involved in metabolic pathways, such as cytochromes, iron–sulphur cluster proteins and sulphur relay proteins. This supports the specificity of SUP05 bacteria as hosts for the bacteriophages and further suggests that viral genes may maintain or assist host metabolism during infection, thereby ensuring an abundant production of viral progeny. In addition, the viral genetic pool might increase the genetic diversity of bacterial sulphur-oxidizing enzymes.

Previous metagenomic analyses have shown that genetic exchange between phages and their bacterial hosts does occur; for example, many phages that infect photosynthetic bacteria contain host-like metabolic genes[3]. Although these viral auxiliary genes share sequence similarities with host genes, they have their own distinct evolutionary history[4], with differing evolutionary rates and selection pressures. The study by Anantharaman *et al.*[1] is the first report of a comparable phenomenon in the chemosynthetic system of deep-sea waters. However, the species of SUP05 bacteria that the phages infect were not identified. To facilitate host identification, another recent study used 'viral tagging' to screen 10^7 fluorescently labelled marine cyanophages, which were mixed with host *Synechococcus* sp. WH7803 that contained isotopically labelled heavy DNA[5]. Infected cells were collected using flow cytometry, followed by separation of isotopically light viral DNA from host DNA. Subsequent deep sequencing facilitated the identification of previously unknown phages that specifically infected this bacterial species. Thus, where culturing is possible, viral tagging could be used to link viruses to specific host species in deep-sea hydrothermal vent plumes and other marine environments.

These studies have improved our understanding of host–virus interactions in marine environments and have provided insights into their role in deep-sea ecosystems. The abundance of viruses in deep-sea waters and the discovery of viral sulphur-oxidizing genes make them key players in global biogeochemical sulphur cycles.

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1. Anantharaman, K. *et al.* Sulfur oxidation genes in diverse deep-dea viruses. *Science* **344**, 757–760 (2014).
2. Anantharaman, K. *et al.* Evidence for hydrogen oxidation and metabolic plasticity in widespread deep-sea sulfur-oxidizing bacteria. *Proc. Natl Acad. Sci. USA* **110**, 330–335 (2013).
3. Mann, N. H. *et al.* Marine ecosystems: bacterial photosynthesis genes in a virus. *Nature* **424**, 741 (2003).
4. Zeidner, G. *et al.* Potential photosynthesis gene recombination between *Prochlorococcus* and *Synechococcus* via viral intermediates. *Environ. Microbiol.* **7**, 1505–1513 (2005).
5. Deng, L. *et al.* Viral tagging reveals discrete populations in *Synechococcus* viral genome sequence space. *Nature* http://dx.doi.org/10.1038/nature13459 (2014).

Competing interests statement
The authors declare no competing interests.