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The marine cyanobacterium *Prochlorococcus* fixes carbon into biomass by photosynthesis. *Prochlorococcus* spp. are responsible for a substantial fraction of global primary production, so the evolution of the genome of this microorganism, mediated by interactions with viruses (phages), could affect the global carbon cycle. Reporting in *Nature*, Debbie Lindell, Sallie Chisholm and colleagues analysed the evolutionary interactions between *Prochlorococcus* MED4 and the lytic cyanophage P-SSP7 (a T7-like podovirus), using a global 'omics' approach.

Gene expression was probed over the course of infection of *Prochlorococcus* MED4 with P-SSP7 using a custom-designed microarray. The main features of the P-SSP7 life cycle are surprisingly reminiscent of lytic phage T7, which infects the resident gut species *Escherichia coli*. Both T7 and P-SSP7 have three main gene-expression clusters (clusters 1–3), which comprise similar genes that are expressed at similar times during the infection of their extremely different bacterial hosts. However, one striking difference between the phages was the presence of bacterial-like photosynthesis and stress-response

genes in cluster 2 of P-SSP7. The authors propose that these bacterial-like genes enable P-SSP7 to generate the energy and deoxyribonucleotide triphosphates that are required for maximum phage-DNA replication in the nutrient-poor oceans.

According to previous studies, host genes are rarely upregulated in phage infection systems, so the upregulation of 41 *Prochlorococcus* genes in response to P-SSP7 infection was a surprising finding. More than a third of the upregulated host genes are present in genome islands and some of them have homologues in cyanophages. This led the authors to propose that genes which are expressed by a host in response to infection are recruited by the phage through random incorporation and natural selection. That is, if the genes confer a selective advantage they become fixed into the phage genome. As an agent of horizontal gene transfer, the phage might later deliver these genes back into the host. This dynamic interchange of genes could be a mechanism for the co-evolution of host and phage.

Phages are the most abundant forms of life on the Earth. Consequently, understanding the evolutionary processes that involve these mobile genetic elements is of fundamental importance, not only to global carbon cycling but also all processes that involve bacteria and archaea.

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ORIGINAL RESEARCH PAPER Lindell, D. et al. Genome-wide dynamics of a marine virus and host reveal features of co-evolution. *Nature* 6 Sept 2007 (doi10.1038/nature06130)