

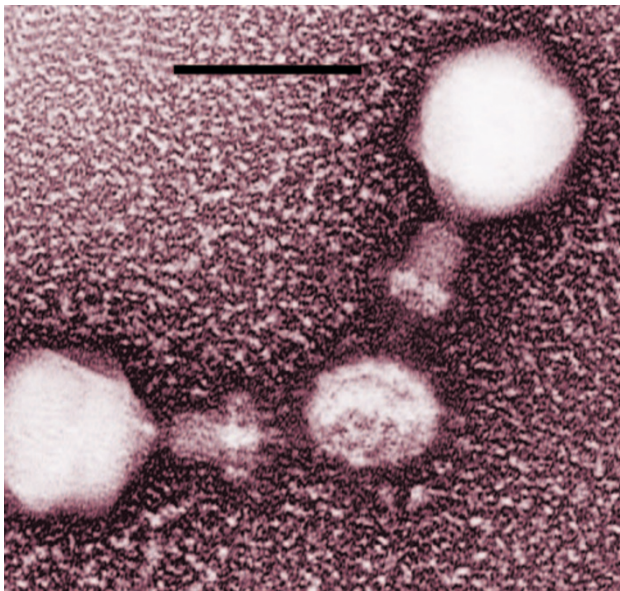
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VIRAL GENOMICS

Small is beautiful

The recent characterization of the genomes of three bacteriophages that are capable of infecting *Prochlorococcus* strains has provided an intriguing glimpse into the potential roles of these entities in global oceanic processes.

Marine unicellular cyanobacteria, including the genera *Synechococcus* and *Prochlorococcus*,



constitute a major component of the prokaryotic population of the oceans and make an important contribution to the overall productivity of this environment through their photosynthetic capabilities. Because of the crucial importance of these microorganisms to the ocean environment, any agent that influences their population dynamics and evolutionary pathways has the potential to have a considerable impact on global oceanic cycles — cyanophage, the group of viruses that have the ability to infect cyanobacteria, are no exception and probably play an important part in mediating cyanobacterial population size, as well as contributing to their extensive microdiversity. Reporting in the latest issue of *PLoS Biology*, Matthew Sullivan, Sallie Chisholm and colleagues describe the genomic analysis of a podovirus and two myoviruses that infect *Prochlorococcus* strains. A key feature of all three genomes is that, in addition to encoding genes typical of phage, they also encode genes of which the closest homologues are found in their host cyanobacteria. The authors speculate that many of these genes represent ‘signature’ cyanophage genes. These include core photosynthetic reaction centre genes and an aldolase-family gene that might help the bacterial host maintain photosynthesis and provide alternative routes of carbon metabolism, respectively, during infection. Family-specific

‘signature’ genes include those that could function in nutrient acquisition in these nutrient-poor oceanic environments.

Whether the potential proteins encoded by these genes provide any benefit for the phage and their interaction with the bacterial host remains to be elucidated, as do their roles in phage ecology and host range. However, the absence of these genes in terrestrial phage supports the idea that these marine phage have evolved unique adaptive mechanisms in response to the low-nutrient oceanic environment of their photosynthetic hosts.

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References and links

ORIGINAL RESEARCH PAPER Sullivan, M. B. *et al.* Three *Prochlorococcus* cyanophage genomes: signature features and ecological interpretations. *PLoS Biol.* **3**, e144 (2005)

FURTHER READING Edwards, R. A. & Rohwer, F. Viral metagenomics. *Nature Rev. Microbiol.* **3**, 504–510 (2005)