

Transfer of photosynthesis genes to and from Prochlorococcus viruses.

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Abstract

Comparative genomics gives us a new window into phage-host interactions and their evolutionary implications. Here we report the presence of genes central to oxygenic photosynthesis in the genomes of three phages from two viral families (Myoviridae and Podoviridae) that infect the marine cyanobacterium *Prochlorococcus*. The genes that encode the photosystem II core reaction center protein D1 (psbA), and a high-light-inducible protein (HLIP) (hli) are present in all three genomes.

Both myoviruses contain additional hli gene types, and one of them encodes the second photosystem II core reaction center protein D2 (psbD), whereas the other encodes the photosynthetic electron transport proteins plastocyanin (petE) and ferredoxin (petF). These uninterrupted, full-length genes are conserved in their amino acid sequence, suggesting that they encode functional proteins that may help maintain photosynthetic activity during infection. Phylogenetic analyses show that phage D1, D2, and HLIP proteins cluster with those from *Prochlorococcus*, indicating that they are of cyanobacterial origin.

Their distribution among several *Prochlorococcus* clades further suggests that the genes encoding these proteins were transferred from host to phage multiple times.

Phage HLIPs cluster with multicopy types found exclusively in *Prochlorococcus*, suggesting that phage may be mediating the expansion of the hli gene family by transferring these genes back to their hosts after a period of evolution in the phage. These gene transfers are likely to play a role in the fitness landscape of hosts and phages in the surface oceans.