Large Freshwater Phages with the Potential to Augment Aerobic Methane Oxidation

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There is growing evidence that phages with unusually large genomes are common across various natural and human microbiomes, but little is known about their potential ecosystem impacts. Here, we reconstructed large phage genomes from freshwater lakes known to contain bacteria that oxidize methane. Twenty-two manually curated genomes with 159-527 kbp in length were found to encode the *pmoC* gene, an enzymatically critical subunit of the particulate methane monooxygenase, the predominant methane oxidation catalyst in nature. The phage-associated PmoC show > 90% similarity and affiliate phylogenetically with those of coexisting bacterial methanotrophs, and their abundance patterns correlate with the abundances of these bacteria, supporting host-phage relationships. We suggest that phage PmoC has similar functions to additional copies of PmoC encoded in bacterial genomes, thus contribute to growth on methane. Transcriptomics data from one system showed that some phage-associated *pmoC* genes are actively expressed *in situ*. Augmentation of bacterial methane oxidation by pmoC-phages during infection could modulate the efflux of this powerful greenhouse gas into the environment.