

Ribonucleotide Reductases as Indices of Diversity in Unknown Marine Viruses



Significance:

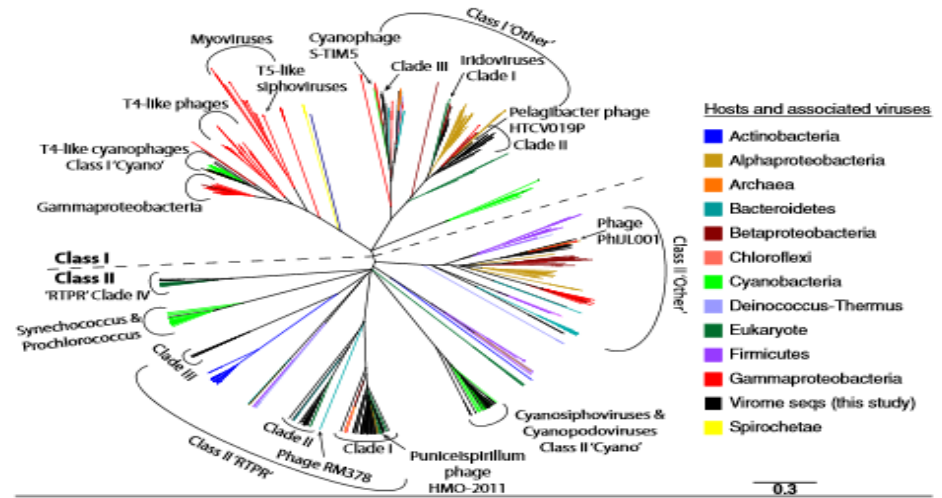
- Within aquatic ecosystems viruses facilitate horizontal gene transfer, biogeochemical cycling, and energy transfer by infecting and lysing microbial host cells.
- Despite their critical role in ecosystem function very little is known of the biological, ecological, and evolutionary features of most viruses in nature.
- Ribonucleotide reductase (RNR) genes encode ancient enzymes that reduce ribonucleotides to deoxyribonucleotides, priming DNA synthesis, and were identified as superior markers of viral diversity, which are distributed over a broad range of viruses, >90% in ds virioplanktons.
- Frequency distributions of RNR clades within viral metagenome sequence libraries support predictions made by the “kill the winner” hypothesis, indicating that specialist podoviruses specifically adapted to infecting abundant heterotrophic bacterioplankton predominate within the viroplankton.
- RNR polymorphism provides a means of connecting the biological and ecological features of viroplankton populations

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Ribonucleotide reductases reveal novel viral diversity and predict biological and ecological features of unknown marine viruses

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Diversity of putative viroplankton RNR sequences. Viral reference RNR sequences are colored the same as their hosts. Major groups of RNR sequences identified in this study were class I Other and class I Cyano and class II Other, class II RTPR, and class II Cyano. Aligned region corresponds to residues N437 to S645 in the *E. coli* class I alpha RNR peptide. Scale bar represents amino acid substitutions per site.

