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Genomic analysis of bacteriophages

Roger Hendrix

University of Pittsburgh, USA

Abstract

The majority of organisms on planet Earth are bacteriophages. The most easily identified phages, and possibly the most abundant, are the dsDNA tailed phages. There are estimated to be 10^{31} individuals of this type of virus in the global population, or enough to reach 200 million light years into intergalactic space if they were laid end-to-end. To date only a little over 1000 complete genome sequences of these phages have been determined, but analysis of these genomes has already yielded significant information about the remarkable diversity of the group, about the evolutionary mechanisms by which this group has changed over the past ~3 billion years, and about how different members of the population are related to each other and to other viruses.

Analysis of the genomic data benefits greatly from the availability of the tremendous body of knowledge about phages and how they work accumulated over the past 70 years of research on phages. Interpreting genome sequences in the context of this knowledge can lead to novel insights into topics like mechanisms of translation and gene expression, and population dynamics and evolution. Examples will be given.

Biography

Roger Hendrix started working on bacteriophages as an undergraduate at Caltech, he completed his PhD at Harvard University and did a postdoc at Stanford University School of Medicine before coming to the University of Pittsburgh. He has roughly 130 published peer-reviewed papers primarily describing bacteriophages and cellular components they interact with, with emphases on virion assembly and genome evolution. He is an accomplished clarinetist.