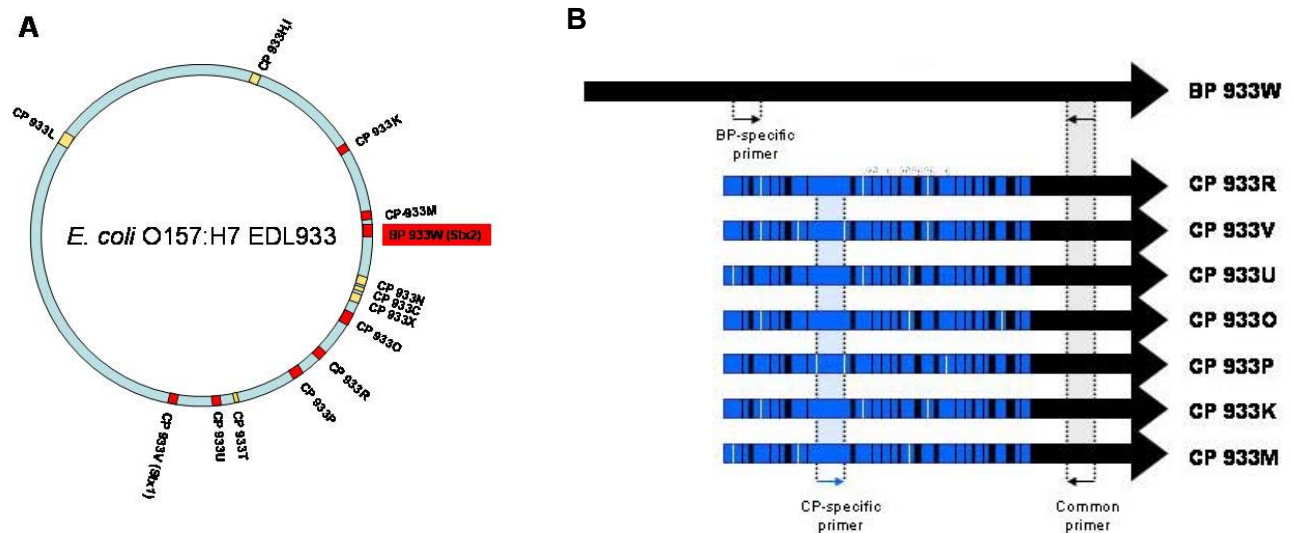


“All the World’s a Phage”
The Role of Bacterial Viruses in Microbial Diversity and Virulence

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Bacterial viruses, or bacteriophages, play several important roles in microbial communities. Results from environmental sampling of bacteriophages over the past decade or so suggests that there are probably on the order of 10^{31} bacteriophages in the biosphere, making them by far the most abundant organism on the planet. Not surprisingly, bacteriophages are found associated with bacteria in all environmental niches. Marine ecologists believe that bacteriophages kill between 5% and 40% of marine prokaryotes daily by viral lysis, which gives them a key role in planetary carbon cycling. Bacteriophages provide one of the major mechanisms for horizontal gene transfer among different strains of bacteria, which drives bacterial evolution. Temperate bacteriophages, i.e. those that can form stable lysogens rather than killing the bacterial host, carry novel genes that confer new properties upon the host bacterium. A number of toxins, including those responsible for diphtheria, cholera, botulism and scarlet fever, are actually encoded on bacteriophage genomes within the bacteria that cause these diseases. In my laboratory, we are carrying out a variety of studies that involve comparative genomic analysis and targeted mutagenesis to investigate the contributions of specific genes carried by temperate bacteriophages. These studies allow us to make testable predictions about bacteriophage biology and the nature of the interactions between these bacteriophages and their bacterial hosts, and identify bacteriophage-encoded genes that contribute to bacterial virulence and other interesting phenotypes.



(A) Schematic map of the genome of enterohemorrhagic *E. coli* strain EDL933, showing the locations of the Shiga toxin 2-encoding bacteriophage BP933W and 13 cryptic prophages (CP). The 7 cryptic prophages designated by red boxes carry genes with homology to the putative tail fiber gene L0121 of BP933W. (B) Schematic of the sequence similarities between the tail fiber gene of BP933W and those of the cryptic prophages. Black corresponds to nucleotides shared between BP933W and the cryptic prophages; blue corresponds to sequences present among the cryptic prophage but not BP933W. Regions chosen for sequence-specific primers to distinguish the tail fiber genes of BP933W and the cryptic prophages by PCR are also illustrated.