PHAGES OF *PSEUDOMONAS*

Tetsuya Hayashi and Keisuke Nakayama

Department of Microbiology, Miyazaki Medical College
5200 Kiyotake, Miyazaki 889-1692, Japan

1. INTRODUCTION

A large number of bacteriophages have been isolated and analyzed in *Pseudomonas*. Many of them have been used as tools for epidemiological studies (phage typing) and for genetic analysis by transduction. Some have been developed as molecular biological tools for *Pseudomonas*; for example, the D3112 transposable phage-derived cloning system, φCTX-derived integration-proficient vectors, and the D3 phage-derived cosmid vector. Furthermore, infections of some temperate phages have been demonstrated to confer new phenotypes to the host strains (lysogenic or phage conversion), and thus played important roles in generating the genetic and phenotypic diversity of *Pseudomonas*. From the clinical point of view, virulent phages have been regarded as potential therapeutic tools for *Pseudomonas* infections, the treatment of which are often very difficult because of their high resistance to antibiotics. Despite such importance of bacteriophages in various aspects, only limited knowledge about the biological and genetic features of *Pseudomonas* phages were available, though several RNA phages and filamentous phages have been extensively studied as model systems, for replication, gene regulation, morphogenesis, and structural biology of the macromolecules. However, by the recent progress in sequencing technology, it is now easy to obtain the whole genome sequence information of bacteriophages, which has considerably expanded our knowledge on the biological features of *Pseudomonas* phages.
Although the genome sequences of several *Pseudomonas* phages with small genome sizes, such as a filamentous phage Pf3, were determined very early\(^6^7\), the progress in the genomic analyses of *Pseudomonas* phages was relatively slow compared to enterobacterial phages. In 1999, however, the genome sequence of φCTX was determined for the first time as a tailed double-stranded DNA phage of *Pseudomonas*\(^8^0\). After that, three more tailed double-stranded DNA phages each belonging to different phage family have been determined. Furthermore, the presence of several prophage or phage-related elements that are integrated into the chromosomes of *P. aeruginosa* strain PAO1 and *P. putida* strain KT2440 were identified by whole genome sequencing\(^8^2, 10^2\).

In this chapter, we first briefly summarize the genomic features of *Pseudomonas* phages with small single-stranded RNA, double-stranded RNA, and single-stranded DNA genomes. Then, genomic features of recently sequenced tailed double-stranded DNA phages will be described in more details. Finally, genomic features of prophages on the two sequenced *Pseudomonas* genomes, including those of the genes for phage-tail like bacteriocins (R-type and F-type pyocins), are summarized. Many transposable phages have also been isolated and analyzed in *Pseudomonas*. In particular, bacteriophage D3112, which has a 38-kb linear double-stranded DNA genome and possesses a genetic organization similar to a transposable coliphage Mu, has been extensively examined\(^4^3, 5^4\). However, we do not include D3112 in this chapter, since only a part of its genome sequence has been determined so far\(^4, 10^8\).

2. SINGLE-STRANDED RNA PHAGES

Bacteriophages of the *Leviviridae* family are small phages that possess positive, single-stranded RNA genome\(^10^9\). They infect a wide range of Gram-negative bacteria that express F or polar pili on the cell surface. Initially, these bacteriophages were isolated from *Escherichia coli*, but were found soon after in *Pseudomonas* as well\(^8, 2^4, 11^6\). Since then, many single-stranded RNA phages have been isolated from various bacteria. Single-stranded RNA phages have a common genomic organization and a high degree of similarity in the replication and translational control mechanisms. Based on the different physical and serological properties, they are categorized into four groups (I–IV), each represented by coliphages MS2, GA, Qβ, and SP. Because of the simple structure, these phages have been studied as model systems for replication and translation. In particular, their coat proteins serve as excellent model systems for studying protein–RNA interaction and the role of secondary structure in gene regulation.

Among the *Pseudomonas* single-stranded RNA phages isolated so far, only PP7, which was originally isolated in 1966 by Bradley\(^8\), has been sequenced\(^8^7\). PP7 is not male-specific, but instead adsorbs on the sides of polar