Pf Filamentous Phage Requires UvrD for Replication in Pseudomonas aeruginosa

Eriel Martínez, Javier Campos-Gómez
Department of Infectious Diseases, Drug Discovery Division, Southern Research, Birmingham, Alabama, USA

ABSTRACT Pf is a lysogenic filamentous phage that promotes biofilm development in Pseudomonas aeruginosa. Pf replicates by a rolling circle replication system which depends on a phage-encoded initiator protein and host factors usually involved in chromosome replication. Rep, an accessory replicative DNA helicase, is crucial for replication of filamentous phages in Escherichia coli. In contrast, here we show that, instead of depending on Rep, Pf replication depends on UvrD, an accessory helicase implicated in DNA repair. In this study, we also identified the initiator protein of Pf and found that it shares similarities with that of Vibrio phages CTXφ and VGJφ, which also depend on UvrD for replication. A structural comparative analysis of the initiator proteins of most known filamentous phages described thus far suggested that UvrD, known as a nonreplicative helicase, is involved in rolling circle replication of filamentous phages in diverse bacteria genera. This report consolidates knowledge on the new role of UvrD in filamentous phage replication, a function previously thought to be exclusive of Rep helicase.

IMPORTANCE Biofilm development is a key component of the ability of Pseudomonas aeruginosa to evade host immune defenses and resist multiple drugs. Induction of the filamentous phage Pf, which usually is lysogenized in clinical and environmental isolates of P. aeruginosa, plays an important role in biofilm assembly, maturation, and dispersal. Despite the clinical relevance of Pf, the molecular biology of this phage is largely unknown. In this study, we found that rolling circle replication of Pf depends on UvrD, a DNA helicase normally involved in DNA repair. We also identified the initiator protein of Pf and found that it shares structural similarity with that of Vibrio cholerae phages CTXφ and VGJφ, which also use UvrD for replication. Our results reveal that, in addition to DNA repair, UvrD plays an essential role in rolling circle replication of filamentous phages among diverse bacteria genera, adding a new, previously unrecognized function of this accessory helicase.

KEYWORDS: Pseudomonas aeruginosa, Pf filamentous phage, UvrD helicase, Rep helicase, histone-like HU, rolling circle replication

Pseudomonas aeruginosa is a highly versatile opportunistic pathogen which is the leading cause of morbidity and mortality among cystic fibrosis (CF) patients and causes significant infection in other immunocompromised humans (1). The capacity of P. aeruginosa to form recalcitrant biofilms is one of the main causes of the establishment and persistence of this bacterium in chronic infection of CF patients (2). The biofilm increases the bacterium’s ability to evade host immune defenses and helps to protect the bacteria against exogenous antibiotic treatment (3). Increasing evidence suggests that the members of the family of Pf1-like filamentous bacteriophages (Pf), widely distributed among clinical and environmental strains of P. aeruginosa, decisively contribute to biofilm development (4, 5).

Filamentous phages belong to the Inovirus genus of the Inoviridae family of phages, which are long and slender proteinaceous tubes encasing a positive-sense single-stranded circular DNA (6). Pf is a member of the inoviruses that is usually integrated into
the chromosome of *P. aeruginosa* (7), but it also can replicate without integrating, as is the case with Pf1 variant in the PAK host strain (8). The integration mechanism used by Pf phage for lysogenization is unknown, but it seems to be different from those of the filamentous phages thus far described. While other filamentous phages hijack XerCD recombinases of their bacterial hosts to integrate into the *dif* site of the bacterial chromosome (9), Pf phage encodes its own integrase, which it probably uses for lysogenization.

Pf phage-carried genes are strongly upregulated in biofilm cells (10). The prophage is also induced during development of biofilms, which release phage particles into the extracellular media (5). Recently, it was described that extracellular Pf particles promote biofilm assembly and function by interacting with infected host and bacterial biopolymers to form higher-order crystal structures that enhance biofilm adhesion, desiccation survival, and antibiotic resistance (4). Interestingly, a variant of Pf formed in mature biofilms is able to kill the bacterial host, a characteristic rarely observed among filamentous phages (5). It has been reported that the extracellular DNA released by Pf-mediated bacterial lysis functions as a structural support for the biofilm architecture. In addition, Pf-mediated cell death is an important mechanism of differentiation inside microcolonies that facilitates dispersal of subpopulations of surviving cells (11). It is also interesting that the Pf variant produced in biofilm is able to infect *P. aeruginosa* even when the strain contains an integrated copy of the same phage, circumventing the phage immunity normally provided by the inserted copy of the Pf lysogen. Therefore, this variant of Pf has been named superinfective phage (SI Pf) (5).

Pf replicates using a rolling circle replication (RCR) mechanism, which produces the single-stranded DNA genome of the phage (6). Replication starts with the binding of the phage-encoded initiator protein (IP) at a specific site in the replicative form of the phage, the *ori* (+) (6). The IP introduces a nick, creating a 5'-phosphotyrosine intermediate and a free 3'-OH at the *ori* (+). The rest of the process is driven by host factors that are usually essential for replication of the bacterial chromosome together with the IP forming the phage replisome. The replisome starts polymerizing at the free 3'-OH, and when it makes a complete round, the IP circularizes the original positive DNA strand that was displaced by the *de novo* synthesized DNA, and a new replication cycle then follows. Instead of DnaB, the bacterial helicase essential for chromosomal replication, filamentous phage replication depends on the replicative Rep helicase in *Escherichia coli* (12). Rep is an accessory helicase normally involved in chromosomal replication that directly interacts with DnaB and helps advance the replisome by removing nucleoprotein complexes in front of the replication fork (13, 14). In contrast, we recently reported that replication of *Vibrio cholerae* filamentous phages CTXφ and VGJφ depends on another accessory helicase, the DNA repair UvrD helicase (12). UvrD is well known for its role in UvrABC-dependent nucleotide excision repair (15) and MutHLS-dependent mismatch DNA repair (16). The role of UvrD in bacterial chromosome replication seems to be more limited than the role of Rep. UvrD can promote the movement of the replisome along protein-bound DNA and participates in the restart of replication forks (14), but deletion of the uvrD gene does not directly affect replication fork progression in *E. coli* (13).

Here we report for the first time that replication of Pf phage depends on UvrD helicase. UvrD is encoded by the open reading frame (ORF) PA5443 (a homologue of *E. coli* UvrD) in *P. aeruginosa*, and we show here that it is a fully functional homologue of UvrD of *E. coli*. We also found that, as with the CTXφ and VGJφ phages, histone-like protein HU is a host factor implicated in Pf replication. Additionally, we demonstrated that PA0727, an ORF localized upstream of the putative phage integrase, encodes the initiator protein of Pf. Although the amino acid sequence of the IP of Pf has no homology with that of any other described IP, an analysis revealed that it shares structural similarities with the IPs of *Vibrio* phages relying on UvrD for replication and with the IPs of many filamentous phages of other bacterial species. These findings consolidate information concerning the new function for UvrD helicase in filamentous phage replication, making UvrD a more versatile helicase than previously thought.
**RESULTS**

**Pf phage is spontaneously produced in a MutS-deficient genetic background.** In the PAO1 model strain, a superinfective variant of Pf (SI Pf) is normally exported to the extracellular media during the dispersal phase of biofilms (5). Previous studies have reported some physiological and genetic host factors involved in the formation of SI Pf (17). It was reported that a mismatch repair (MMR)-deficient strain with a mutS deletion resulted in the early appearance and increased numbers of SI-Pf in biofilms of *P. aeruginosa* (17). Here, we show that a deletion of the mutS gene (Table 1) induces spontaneous production of SI Pf even under planktonic conditions of growth. SI Pf can be detected because it forms plaques on lawns of *P. aeruginosa*. Numerous plaques generated by SI Pf were spontaneously formed in lawns of the /H9004 mutS mutant but not in strain PAO1 (Fig. 1A). The quantity of SI Pf produced by the ΔmutS mutant was on the order of 10^5 particles/ml in an overnight culture (with titers determined using PAO1 as host strain), while no SI-PF particles were detected in the supernatant of the wt PAO1 parental strain grown under the same conditions (Fig. 1B).

**TABLE 1** Bacterial strains used in this study

<table>
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<tr>
<th>Strain</th>
<th>Genotype/phenotype</th>
<th>Reference or source</th>
</tr>
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</tr>
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<tr>
<td>EMP1</td>
<td>PAO1, ΔmutS, deletion from aa 188 to 501 of 806 aa</td>
<td>This study</td>
</tr>
<tr>
<td>EMP2</td>
<td>PAO1, ΔuvrD, deletion from aa 16 to 717 of 731 aa</td>
<td>This study</td>
</tr>
<tr>
<td>EMP3</td>
<td>PAO1, Δrep, deletion from aa 10 to 646 of 669 aa</td>
<td>This study</td>
</tr>
<tr>
<td>EMP4</td>
<td>PAO1, ΔmutS ΔuvrD (same as above for each gene)</td>
<td>This study</td>
</tr>
<tr>
<td>EMP5</td>
<td>PAO1, ΔPA0727, deletion from aa 16 to 392 of 431 aa</td>
<td>This study</td>
</tr>
<tr>
<td>EMP6</td>
<td>PAO1, ΔmutS ΔPA0727 (same as above for each gene)</td>
<td>This study</td>
</tr>
<tr>
<td>EMP7</td>
<td>PAO1, PA0727 Y → F</td>
<td>This study</td>
</tr>
<tr>
<td>EMP8</td>
<td>PAO1, ΔmutS, PA0727 Y → F</td>
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<td>PAO1 hupA::SlacZ/hah</td>
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<tr>
<td>PW4171</td>
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<td>Tp' Sm' recA thi pro hsdR&quot;-λnλPc::Mud::km Tn7 λpir</td>
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*a*aa, amino acid; *Sm*, streptomycin resistance; *Tp*, trimethoprim resistance.

**FIG 1** The *P. aeruginosa* ΔmutS mutant spontaneously produces superinfective Pf particles. (A) The wild-type PAO1 strain (wt) and the ΔmutS mutant were plated to confluency on LB agar plates; only the ΔmutS mutant produced clearly visible phage plaques spontaneously on the bacterial lawn. (B) Overnight cultures of the ΔmutS mutant spontaneously produced more than 10^5 SI-PF particles/ml, while the wt strain did not produce detectable amounts of Pf. The PAO1 strain was used for titration of the phage. Data represent means and standard deviations of the results of 3 independent experiments.
UvrD promotes UvrABC-dependent nucleotide excision repair in *P. aeruginosa*. The genome of the PAO1 strain encodes a homologue of *E. coli* UvrD (PA5443); however, UvrD has not been fully characterized in *P. aeruginosa*. It was previously reported that a *P. aeruginosa* isolate with a mutated PA5443 gene, which produces a variant of UvrD with 3 amino acid substitutions within the conserved ATP binding site, showed defective MMR activity (18). Unexpectedly, the strain showed the same UV sensitivity as the wt strain, casting doubts on the role of the PA5443 product in UvrABC-dependent nucleotide excision repair (NER) (18). To ascertain that the product of PA5443 encodes a functional homologue of *E. coli* UvrD helicase, we deleted the PA5443 gene from the PAO1 strain (Table 1). Consistent with a role of PA5443 product in MMR, the ΔPA5443 mutant showed a hypermutagenic phenotype. This mutant generated approximately 40-fold and 29-fold more spontaneous rifampin-resistant (Rifr) colonies than a rep deletion mutant (Table 1) and the wild-type strain, respectively (Fig. 2A). Subsequently, the role of the PA5443 product in NER was revealed by the increased sensitivity of the ΔPA5443 mutant to UV radiation. The ΔPA5443 mutant was 4 orders of magnitude more sensitive to UV radiation than a Rep mutant and the wt PAO1 strain (Fig. 2B). A Rep mutant was included as a control, since it is a helicase of the same family (SF1) as UvrD, which is normally involved in replication but not in DNA repair. Our results indicate that the PA5443 gene encodes a *P. aeruginosa* functional homologue of *E. coli* UvrD helicase.

**Pf replication depends on UvrD.** We recently reported that RCR of two filamentous phages of *V. cholerae*, CTXφ and VGJφ, depends on UvrD helicase (12). In contrast, RCR of TLCφ, a defective phage of *V. cholerae*, as well as *E. coli* filamentous phages Ff and Ike depends on the replicative accessory helicase Rep (19). This finding raised the issue of whether the role of UvrD in phage replication is an exception for *V. cholerae* or whether it is an additional function of UvrD extended among bacteria. Thus, we tested the role of UvrD in the replication of *P. aeruginosa* phage Pf. We observed that deletion of uvrD gene in a ΔmutS genetic background completely arrested spontaneous SI Pf production. In contrast, deletion of the rep gene from the ΔmutS mutant had no effect on SI Pf production (Fig. 3A). Additionally, we exposed a single mutant ΔuvrD strain to a concentrated suspension of SI Pf isolated from the supernatant of the ΔmutS strain (~10⁶ particles/ml). As expected, the ΔuvrD mutant was refractory to infection with SI-Pf whereas strain PAO1 and the Δrep strain were highly susceptible (Fig. 3B). The reinsertion of a wt uvrD copy into the ΔuvrD strain reestablished the susceptibility to SI Pf infection (Fig. 3B). These results demonstrated that UvrD plays an essential role in Pf phage replication.
The histone-like HU protein contributes to Pf replication. We previously found that, in addition to UvrD, HU is a host factor involved on CTX/H9272 and VGJ/H9272 replication in V. cholerae (12). In order to test whether the similarity between Pf and V. cholerae phage is not limited to UvrD-mediated replication but also includes the use of other host factors in the replication process, we tested the role of HU in Pf replication. HU/H9251 and HU/H9252 transposon insertion mutants from the University of Washington mutant collection (20) were used for this purpose. SI Pf was able to generate plaques on lawns of both HU/H9251-deficient and HU/H9252-deficient strains. However, the plaques observed on lawns of the HU/H9252 strain were visibly smaller than those formed on lawns of HU/H9251, which at the same time were smaller than the plaques formed by the parental strain (0.75 versus 1.70 versus 2.50 mm in diameter, respectively) (Fig. 4A). This observation suggests that replication of Pf, as in the case of CTX/H9272, is partially affected by the lack of HU/H9252 and to a lesser extent by the lack of HU/H9251.

To quantitate the impact of HU on Pf replication, we measured the capacity of HUα-deficient and HUβ-deficient strains to produce Pf in overnight lysogeny broth (LB) cultures. We first discarded the idea of a possible role of HU in Pf internalization that could affect the phage propagation. HUα and HUβ exposed to SI Pf at a low multiplicity of infection (~10^-4) showed susceptibility to the phage equal to that seen with the wt PA01 strain (Fig. 4B). Then, we measured the ability of the infected HUα, HUβ, and PA01 strains to produce SI Pf particles during overnight cultures. HUβ produced around 5 orders of magnitude less SI Pf than the wt and 3 orders less than HUα (Fig. 4C). These results indicate that, as seen with CTXφ, HU plays an important role in Pf replication. Also, similarly to the case of CTXφ, the contribution of HUβ is more important than that of HUα.

The PA0727 ORF encodes the Pf initiator protein. A comparative analysis of the DNA sequences of the Pf genome did not reveal any obvious ORF encoding an initiator protein with homology to those of other filamentous phages. In addition, Pf does not have a genome organization similar to those of other filamentous phages which may help to identify the IP-encoding gene by its conserved position inside the phage genome (Fig. 5A). In the region where we expected to find the gene encoding the IP, Pf contains several small ORFs with unidentified functions (Fig. 5A). However,
analysis of the protein encoded by PA0727, an ORF localized upstream of the putative Pf integrase, revealed that it contains a Pfam02486 domain and a catalytic module, SIYNK, which is also present in the IPs of CTXφ and VGJφ (Fig. 5B). To test a possible role of the PA0727 product in Pf replication, we deleted the PA0727 gene (Table 1) of the Pf-integrated copy in a ΔmutS background. Deletion of the PA0727 gene completely abolished production of SI Pf in the ΔmutS mutant (Fig. 5C). To discard any collateral effect of the PA0727 deletion on the Pf life cycle besides replication, we introduced a direct mutation replacing the putative catalytic tyrosine at position 223 of the PA2077 product (PA2077 Y → F). Consistent with a role of the PA0727 product in Pf replication, the 223 Y → F substitution completely abolished production of SI Pf particles in the ΔmutS background (Fig. 5C). These results, taken together, indicate that PA0727 is the IP of Pf and that the tyrosine at position 223 catalyzes the initial nick at the origin of replication during RCR.

FIG 4 Quantification of contribution of HUα and HUβ to Pf replication. (A) Plaques produced after infection of strains HUα and HUβ with Pf are smaller than plaques formed by wt PAO1. The left panels show pictures of representative plaques of each strain, and the graphic to the right shows the average diameter of plaques for each strain. (B) Graphic of the susceptibility of strains HUα and HUβ after they were exposed to SI Pf particles at a multiplicity of infection (MOI) of 10^-4 phages/cell. Both strains showed levels of susceptibility to Pf similar to those seen with the wt PAO1 strain. (C) Pf-infected PAO1, HUα, and HUβ cells were allowed to produce Pf particles overnight, and the amounts of particles produced in the medium were measured by titration. As shown in the graph, the level of particles produced by the HUβ strain was 5 orders of magnitude lower than that seen with the PAO1 strain, while the level of particles produced by the HUα strain was 1 order of magnitude lower. Data represent means and standard deviations of the results of 3 independent experiments.
Dependence on UvrD for filamentous phage replication may be extensive among bacteria. As mentioned above, the IPs of CTXφ, VGJφ, and Pf, which rely on UvrD and HU for replication, have structural similarities in the same way that the IPs of TLCφ, Ff, and Ike, which replicate independently of HU and depend on the Rep helicase activity, also share structural similarities. This observation revealed a correlation between the phage IP structure and host factors mediating phage replication. Taking this into account, we made an extended analysis of the IPs from most of the filamentous phages described so far to predict potential host factors involved in filamentous phage replication in other bacteria. We found that a Pfam02486-like domain which is conserved in the IP structure of CTXφ, VGJφ, and Pf is also present in the IPs of several filamentous phages of diverse bacterial species (Table 2). However, IPs containing a Pfam05144 or Pfam05155 domain seem to be confined to the prototypical filamentous phages of E. coli and TLCφ of V. cholerae. This observation suggests that the role of UvrD in filamentous phage replication is more extensive in bacteria than we had previously thought. The analysis also revealed the existence of a third group of filamentous phages containing a Pfam1446-like domain. Those proteins harbor a highly conserved catalytic module, VGYVAKY (Table 2). Interestingly, the Pfam1446 domain is also found

![Image of a diagram showing the genomic organization and catalytic sites of IPs from CTXφ, VGJφ, and Pf phages.](http://msphere.asm.org/)

**FIG 5** Identification of the gene encoding the rolling circle initiator protein of Pf. (A) Genomic organization of Pf phage compared with that of CTXφ and VGJφ phages. The linear maps of CTXφ, VGJφ, and Pf phages were aligned using the structural (deep blue) and assembly (cerulean blue) gene modules, which conserve the same genome organization in the three phages. The replication initiator protein (IP) genes (in orange) conserved their relative positions in CTXφ and VGJφ phages but not in Pf, where its relative positions shifted. A conserved domain of the family Rep-trans 024286 inside the IP genes is shown with a yellow bar. Other notable genes, such as those encoding repressors (in black), single-stranded DNA (ssDNA) binding proteins (dark blue), cholera toxin in CTXφ phage (pale gray), and Pf integrase (dark gray), are shown. Other genes of unknown function are represented in white. The site of site-specific recombination with the bacterial chromosome (attP) is also shown. A fragment of the Pf genome (represented by a dashed segment) was omitted to simplify the scheme. (B) Alignment of the catalytic sites of IPs from CTXφ, VGJφ, and Pf phages. Identical amino acids in the three phages are highlighted in yellow, where the catalytic tyrosine residue is shown in red. (C) Graph showing the suppression of Pf phage production after deletion of the PA0727 ORF from the ΔmutS strain and after changing of the catalytic tyrosine residue of PA0727 to a phenylalanine in the ΔmutS strain (PA0727Y→F). Data represent means and standard deviations of the results of 3 independent experiments.
in the IP structure of the $\varphi$X174 lytic phage of *E. coli*. This phage replicates by a similar RCR mechanism using the Rep helicase. This suggests that this third group of filamentous phages may depend on Rep helicase too.

## DISCUSSION

Prototypical filamentous phages of *E. coli* use the replicative accessory helicase Rep for rolling circle replication (19). However, here we report for the first time that replication of Pf filamentous phage of *P. aeruginosa* depends on the DNA repair UvrD helicase. Rep and UvrD are two members of the SF1 family of helicases and share approximately 40% amino acid sequence similarity (21). However, despite their similarities, the physiological roles of UvrD and Rep are not interchangeable (22, 23). Rep directly interacts with the bacterial DnaB helicase in *E. coli* and provides a second motor which helps the replisome progress along highly transcribed regions of the chromosome (13, 14). Rep is also involved in the restart of stalled replication forks after replication has been interrupted (24). Consistently, deletion of Rep in *E. coli*, as well as in *V. cholerae*, has been shown to significantly reduce the rate of chromosome replication and consequently the growth rate (22, 23). On the other hand, UvrD plays a pivotal role in MutHLS-dependent mismatch DNA repair (MMR) (16) and UvrABC-dependent nucleotide excision repair (NER) in *E. coli* (15). The role of UvrD in NER in *P. aeruginosa* has not been determined. Oliver et al. reported that a strain harboring an UvrD variant with a substitution of 3 amino acids in the ATP binding site showed a deficient MMR phenotype but UV sensitivity equal to that of the wild type (18). In contrast, here we show that deletion of the PA5443 gene leads to a UV-sensitive phenotype, indicating that, in *P. aeruginosa*, UvrD is also involved in the UvrABC-dependent nucleotide excision repair pathway in a manner similar to that seen with *E. coli* (Fig. 1A and B). This result suggests that the UvrD variant isolated by Oliver et al. does not completely arrest the ATP hydrolysis activity of UvrD but that it is affected in a way that mainly impairs the MMR function and retains the NER activity. Thus, the active role of *P. aeruginosa* UvrD in both MMR and NER reveals for the first time that the PA5443 gene encodes a fully functional homologue of *E. coli* UvrD in *P. aeruginosa*.

In *E. coli*, UvrD also promotes the movement of the replisome along regions of protein-DNA complexes and participates in the restart of replication forks after a stall caused by encountering protein-bound DNA (14). However, the role of UvrD in chromosome replication seems to be more limited than the role of the replicative Rep

### TABLE 2 Initiator proteins of filamentous phages

<table>
<thead>
<tr>
<th>Phage(s)</th>
<th>Host</th>
<th>Predicted IP domain(s)</th>
<th>Catalytic module</th>
<th>Reference(s)</th>
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*This is a complete list of the described filamentous phages but includes most of those with identified IPs. X. campesrnis, Xanthomonas campesrnis.
*Undetermined, the IP sequence did not reveal a conserved catalytic module. Predicted catalytic tyrosines are underlined and highlighted in bold.
helicase. While a Rep deletion mutant seriously impairs growth, a deletion mutant of
uvrD exhibited a normal growth phenotype (13). Nevertheless, a previous study dem-
onstrated that the UvrD activity, as in the case of Rep, can promote progression of
replisomes. Some heterologous RCR plasmids, most of them isolated from Gram-
positive bacteria, can replicate in E. coli using UvrD (25). Replication of these plasmids
in the original bacteria depends on the unique accessory helicase PcrA (26). More
recently, we described a role for UvrD in RCR under natural conditions. UvrD assists
replication of the filamentous phages CTXφ and VGJφ in V. cholerae (12).

The implication of Rep helicase in RCR of filamentous phages was reported in the
early 1970s, when the molecular biology of the Ff family of phages was extensively
studied in E. coli (19). This function of Rep is consistent with its role on chromosome
replication. More recently, many other filamentous phages were identified in several
bacteria, aided by the advent of the deep sequencing technologies. Association of Rep
helicase with replication of filamentous phages was probably assumed from its role in
replication of filamentous phage of E. coli. However, the findings on the role of UvrD in
CTXφ and VGJφ replication revealed that the function of Rep in filamentous phage
replication was not a paradigm. This finding raised the issue of whether the role of UvrD
in RCR of filamentous phages was restricted to V. cholerae bacteria or whether it is a
more generalized function of UvrD among bacteria. Thus, we examined the capacities
of UvrD versus Rep to support rolling circle replication of the clinically relevant
P. aeruginosa filamentous phage Pf.

P. aeruginosa is evolutionarily distant from V. cholerae and E. coli. Accordingly,
filamentous phages of P. aeruginosa show remarkable differences from those of V. chol-
erae and E. coli. The evolutionary distance of Pf is especially notable by the lack of an
orthodox genomic modular organization, which is conserved among most of the
filamentous phages described to date (Fig. 1A). In terms of the biological cycle, Pf is also
remarkably different from other filamentous phages. While most of them exploit XerCD
recombinases for integration in the dif site of the bacterial chromosome (9), Pf
integrates in the tRNA-gly gene, probably using its own encoded integrase. Addition-
ally, under certain conditions Pf is induced and forms a superinfecrive variant of the
phage (SI Pf), which is able to infect P. aeruginosa even when it contains a copy of Pf
integrated into the chromosome. This process is called superinfection because it
circumvents the phage immunity normally provided by a resident lysogenized phage
(27). Even more interesting, the SI-Pf variant, unlike previous described filamentous
phages, can kill the host bacteria by an unknown mechanism (5).

From this study, we report that Pf is continually produced in the supernatant of a
ΔmutS strain. The mechanism by which Pf is induced in the ΔmutS strain remains
unclear. However, the fact that deletion of mutS completely arrests the MMR system
and leads to a hypermutagenic phenotype suggests that some mutation in the genome
of the phage derepresses the excision and replicative functions of Pf. This idea is
supported by a study that revealed a high frequency of mutation in the Pf genome in
biofilms, where SI Pf is normally produced (28). We found that deletion of uvrD gene
completely abolished production of SI Pf variants in a ΔmutS genetic background. This
finding suggested that Pf replication depends on the activity of the UvrD helicase.
Accordingly, deletion of uvrD rendered a strain fully resistant to SI-Pf (Fig. 3). Complement-
mentation of the ΔuvrD strain with a wt copy of uvrD reestablished the susceptibility to
SI Pf infection (Fig. 3). Altogether, these results revealed that UvrD is essential for Pf
replication.

Here we also report that the histone-like HU protein promotes Pf replication. HU
is a major component of the bacterial nucleoid (29). It is a small protein composed
of two closely related subunits, HUα and HUβ. HU binds duplex DNA with low
affinity and without specificity but recognizes defined DNA structures and repair
intermediates with high affinity (30, 31). Although the main form of HU in bacteria
is the heterodimer HUαβ, both homodimers (HU2α and HU2β) have been detected
(32). We previously developed a screening method which revealed that V. cholerae
HU is involved in CTXφ phage replication (12). Here we show that HU from
P. aeruginosa participates in Pf replication. Interestingly, the role of HUβ was more relevant than that of HUα in both cases, suggesting a common mechanism by which HU promotes rolling circle replication in both phages. A previous report noted that HU specifically binds to the origin of an RCR plasmid, pKYM, and enhances binding of the initiator protein (33). A similar role of HU in RCR of filamentous phages is highly probable. Interestingly, E. coli filamentous phages and V. cholerae TLCφ, which use Rep helicase for replication, replicate independently of HU. Thus, it is tempting to speculate that these two groups of phages harbor two well-defined families of IPs which differ not only in the nature of the interaction with other copartners, as the accessory helicases, but also in the way that they recognize the replication origin in the replicative form of the phage.

Additionally, we identified the initiator protein of Pf; the protein is encoded by the PA0727 gene of the PAO1 strain. It contains a predicted Pfam02486 domain and a catalytic module, SIYNK, conserved in the IPs of CTXφ and VGJφ. We tested the function of the tyrosine contained in the SIYNK module by replacing it with a phenylalanine and demonstrated that it is essential for the establishment and production of Pf phage. Interestingly, our analysis of the predicted domain structures of most of the IPs described so far revealed that the Pfam08426 domain is widely distributed among filamentous phages of different bacterial species. In contrast, the Pfam05144 and Pfam05145 domains, conserved in the IPs of filamentous phages that depend on Rep for replication, seem to be limited to the prototypical filamentous phages of E. coli and the TLCφ satellite phage of V. cholerae. Taken together, our results allow the classification of filamentous phages into at least two groups on the basis of the identity of helicase used for replication: those using UvrD and those using Rep (Fig. 6).

In conclusion, we demonstrated for the first time that UvrD of P. aeruginosa, which possesses fully functional MMR and NER activities, also assists rolling circle replication of Pf filamentous phage. Additionally, we provide evidence indicating that UvrD protein plays a general role in assisting rolling circle replication of filamentous phages hosted by such diverse bacterial species as V. cholerae, V. parahaemolyticus, P. aeruginosa, and Ralstonia solanacearum. This expanded role of UvrD, previously known as a nonreplicative helicase, concerns not only scientists interested in the molecular biology of inoviruses but also those involved in the study of helicases and their role in DNA replication and repair.

**MATERIALS AND METHODS**

**Strains and culture conditions.** Strains, plasmids, and oligonucleotides used in this study are described in Table 1, Table 3, and Table 4, respectively. All strains were grown in LB medium, to which agar was added when solid medium was required. LB agar without NaCl plus 15% sucrose was used to segregate suicide plasmid from merodiploids during construction of mutants by allelic exchange. Antibiotics were added, when necessary, at the following concentrations: ampicillin (Amp), 100 μg/ml; carbenicillin (Cb), 300 μg/ml; spectinomycin (Sp), 100 μg/ml; chloramphenicol (Cm), 34 μg/ml for E. coli and 200 μg/ml for P. aeruginosa; kanamycin (Kn), 50 μg/ml; and rifampin (Rif), 300 μg/ml.

**DNA isolation and manipulation.** P. aeruginosa total DNA was prepared using a GenElute bacterial genomic DNA kit (Sigma). Plasmid DNA was prepared using a QiAprep Spin Miniprep kit (Qiagen), which was used also to purify the replicative form of PF phage. DNA fragments were purified from agarose gel using a QIAquick gel extraction kit (Qiagen). Restriction and modification enzymes were used according to the manufacturer’s instructions (NE Biolabs). The DNA was electrophoresed on 0.8% (wt/vol) agarose gels and was visualized with ethidium bromide (1 μg/ml).

**PF identification.** The genome of Pf was sequenced for confirmatory purposes when needed. The replicative form of PF was digested with restriction enzymes BamHI and HindIII, and the generated DNA fragments were inserted into the pUC19 vector. The resultant constructs were sequenced using universal M13 Fw and Rev primers.

**Construction of P. aeruginosa mutants.** All mutant strains were constructed by allelic exchange using suicide vector pEX100Tlink (34). The mutants were confirmed by PCR and sequencing. Complementation of the mutants was performed by replacing the mutated allele with the original copy from the parental strain PAO1, also through allelic exchange. E. coli DH5α was the host for plasmid constructions, and E. coli S17-1 Apir was used as the donor for conjugative transfer of the suicide vector pEX100Tlink-based constructs into P. aeruginosa.

**Isolation of a superinfective variant of Pf.** A MutS-deficient strain which spontaneously produces superinfective PF (SI Pf) viral particles was used as the SI Pf donor. The strain was grown in 5 ml of LB for
20 h with shaking (240 rpm) at 37°C. One milliliter of the culture was spun down, and the supernatant was serially filtered through 0.45- and 0.22-μm-pore-size filters (sartorius). Cell-free supernatants containing Pf particles were stored at 4°C until use. When concentrated phage preparations were required, the phage particles were precipitated from the filtered supernatant by adding sodium chloride and polyethylene glycol to give final concentrations of 3% and 5% (wt/vol), respectively. The mixture was incubated on ice for 30 min and centrifuged at 12,000 g for 20 min. The supernatant was discarded, and the phage-containing pellet was resuspended in a desired volume of phosphate-buffered saline (PBS). The concentrated suspension was stored at 4°C until use. Identity of the phage was confirmed by sequencing as described above.

**Phage titration.** Titers of SI Pf were routinely determined by dropping serial dilutions of filtered culture supernatants of phage-producing cells onto soft LB agar (0.4%) plates containing the PAO1 strain. The numbers of plaques were determined after overnight incubation at 37°C. Isolated plaques were used to isolate monoclonal SI Pf when required.

![Proposed models for rolling circle replication dependent on Rep or UvrD proteins. (A) The IP of Rep-dependent filamentous phages recognizes the origin of replication, ori(+), independently of HU and recruits DNA polymerase III (Pol III) and Rep helicase to form the replisome. The IP introduces a nick at the ori(+) position in the positive DNA strand, which remains attached to the IP by the 5' end. The replisome starts DNA polymerization by extending the 3' end of the nick, while Rep helicase opens DNA strands. (B) The IP of phages depending on UvrD requires HU to recognize ori(+). Subsequently, the IP recruits polymerase III (Pol III) and UvrD helicase in this case to form the replisome. Replication starts and continues as described for panel A. In both cases, the positive DNA strand is represented in dark blue, the negative strand in cerulean blue, and the de novo synthesized DNA in red. RF, replicative form.](FIG 6)

**TABLE 3** Relevant plasmids used in this study

<table>
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<tr>
<th>Plasmid</th>
<th>Genotype</th>
<th>Reference or source</th>
</tr>
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<tbody>
<tr>
<td>pUC19</td>
<td>Cloning vector Ap&lt;sup&gt;a&lt;/sup&gt;</td>
<td>56</td>
</tr>
<tr>
<td>pEX100Tlink</td>
<td><em>E. coli</em>-P. aeruginosa shuttle suicide vector</td>
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<td>pMG002</td>
<td>pEX100T::mutS</td>
<td>This study</td>
</tr>
<tr>
<td>pMG003</td>
<td>pEX100T::uvrD</td>
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</tr>
<tr>
<td>pMG004</td>
<td>pEX100T::PA0727</td>
<td>This study</td>
</tr>
<tr>
<td>pMG005</td>
<td>pEX100T::ΔPA0727</td>
<td>This study</td>
</tr>
<tr>
<td>pMG006</td>
<td>pEX100T::PA0727 Y → F</td>
<td>This study</td>
</tr>
<tr>
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<td>pEX100T::ΔmutS</td>
<td>This study</td>
</tr>
<tr>
<td>pMG008</td>
<td>pEX100T::rep</td>
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</tr>
<tr>
<td>pMG009</td>
<td>pEX100T::Δrep</td>
<td>This study</td>
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</table>

<sup>a</sup>Amp, ampicillin resistance.
Infection assay. A 10-μl volume of the cell-free supernatants containing Pf particles was mixed with 20 μl of recipient strains cultured in LB to an optical density (OD) of 0.5. Mixtures were incubated 20 min at room temperature to allow infection and then plated on LB. Infection events were determined by counting the plaques formed on soft LB agar over PAO1 lawns.

Phage production quantitation. To quantify the capacity of strains to produce Pf virions, infected cells were spun down and the supernatant was discarded to avoid counting unabsorbed virions already present in the suspension used for infecting the cells. Cells were suspended in PBS, and the OD of the suspensions was adjusted to 0.5. Bacterial colonies after 36 h of incubation at 37°C. All experiments were performed in triplicate and the mean value and standard deviation calculated.

References


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| Oligonucleotide | Use | Sequence (5’→3’)
<table>
<thead>
<tr>
<th></th>
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<td>Deletion of mutS</td>
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<td>EM57</td>
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</tr>
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</table>

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