RepD-mediated recruitment of PcrA helicase at the *Staphylococcus aureus* pC221 plasmid replication origin, *oriD*

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ABSTRACT

Plasmid encoded replication initiation (Rep) proteins recruit host helicases to plasmid replication origins. Previously, we showed that RepD recruits directionally the PcrA helicase to the pC221 *oriD*, remains associated with it, and increases its processivity during plasmid unwinding. Here we show that RepD forms a complex extending upstream and downstream of the core *oriD*. Binding of RepD causes remodelling of a region upstream from the core *oriD* forming a ‘landing pad’ for the PcrA. PcrA is recruited by this extended RepD–DNA complex via an interaction with RepD at this upstream site. PcrA appears to have weak affinity for this region even in the absence of RepD. Upon binding of ADPNP (non-hydrolysable analogue of ATP), by PcrA, a conformational rearrangement of the RepD–PcrA–ATP initiation complex confines it strictly within the boundaries of the core *oriD*. We conclude that RepD-mediated recruitment of PcrA at *oriD* is a three step process. First, an extended RepD–*oriD* complex includes a region upstream from the core *oriD*; second, the PcrA is recruited to this upstream region and thirdly upon ATP-binding PcrA relocates within the core *oriD*.

INTRODUCTION

R-plasmids encode antimicrobial resistance genes that are a major cause for spread and establishment of antimicrobial resistance in bacteria. The *Staphylococcus aureus* plasmid pC221 is a 4.6 kb multi-copy plasmid carrying a gene conferring resistance to chloramphenicol (Cm¹). Together with pC223 and pC194 they constitute the prototype Cm¹ plasmids in this organism (1). The spread of antibiotic resistance among *S. aureus* is not confined to chloramphenicol. Plasmid mediated resistance is also found for other antibiotics such as amoxicillin and tetracycline in a high proportion of clinical isolates (2). These Cm¹ plasmids replicate via rolling circle plasmid replication. Initiation of replication is mediated by plasmid encoded replication initiation proteins known as Rep proteins (3–5). Rep proteins exhibit topoisomerase I activity, bind to their cognate plasmid origins of replication, nick one strand (known as the (+) strand) and attach themselves covalently at the 5' end of the nick via a phosphotyrosine bond utilizing an essential active site tyrosine residue (6–8). They recruit a host helicase at the origin and the Rep–helicase complex then facilitates directional unwinding of the duplex DNA during rolling-circle plasmid replication (9,10).

The pC221 plasmid encodes a dimeric RepD protein (37.5 kDa) that initiates replication from its cognate *oriD* (7) by recruiting the host PcrA helicase and stimulating its activity (10–12). PcrA is an essential enzyme found in all Gram positive bacteria. It is homologous to the UvrD and Rep helicases of Gram negative bacteria and is involved in DNA repair, and the resolution of stalled replication forks and RecFOR-mediated blocked recombination structures (13,14). Its role in rolling-circle plasmid replication was identified genetically. A *pcrA3* mutation in *S. aureus* resulted in accumulation of plasmid replication initiation complexes and a consequent reduction in plasmid copy number of pT181-related plasmids (15–17). The acronym PcrA (plasmid copy number reduction) reflects its important role in plasmid replication. Functional, genetic and direct interactions between PcrA and Rep proteins have been established. For example, suppressor mutations alleviating the effect of the *pcrA3* mutation were identified and mapped in the pT181-encoded *repC* gene (17).
The pcrA3 mutation was mapped as T61I within the PcrA3 protein (18). *Staphylococcus aureus* PerA functionally interacted with RepC to mediate pT181 plasmid unwinding (19). The Bacillus cereus and *B. anthracis* PerA helicases were able to interact with RepC and support the replication of the *S. aureus* pT181 plasmid (20), the *Streptococcus pneumoniae* PerA supported RepC-mediated unwinding of the *S. aureus* pT181 plasmid (21), whereas the *B. stearothermophilus* PerA was able to interact with RepD (encoded by *S. aureus* pC221 plasmid) and completely unwind an oriD-containing plasmid in the presence of SSB (10). Direct interactions between Rep and PerA proteins so far have been detected by pull down assays followed by western blotting using MBP-tagged Rep proteins and anti-MBP antibodies (18–20). These data show that Rep proteins can interact with heterologous PcrA helicases, a property that may have contributed to the ability of rolling-circle replication plasmids to disseminate and propagate in a broad range of Gram positive hosts.

The molecular events of Rep-mediated recruitment of helicases at plasmid replication origins are poorly understood. The pC221 oriD consists of three inverted complementary repeats, ICR I-III (7). RepD covalently attaches at the 5'-end of a nick in the middle of ICR II (7) and participates in the directional recruitment of PcrA (10) and to increase its processivity (10,11), but the molecular details of their interactions at oriD during loading are not known. In an effort to understand this better, we carried out systematic exonuclease III (ExoIII) footprinting and direct imaging by atomic force microscopy (AFM) of the pC221 oriD in the presence and absence of RepD, PcrA and nucleotides. Our data suggest that binding of RepD to oriD forms an extended structure encompassing the core oriD and neighbouring regions immediately upstream and downstream from the oriD. A tighter ternary PcrA–RepD–oriD complex forms in the presence of PcrA with strong contacts extending upstream from the core oriD but limited downstream to the end of ICR III. In the presence of nucleotides the ternary complex re-organizes into a more compact structure with boundaries contracting strictly within the core oriD.

We conclude that RepD forms a complex with oriD extending upstream and downstream of the core oriD. PcrA is recruited via an interaction with RepD upstream from the core oriD. PcrA appears to have basal weak affinity for this region even in the absence of RepD. When ATP is bound, presumably by PcrA, a conformational change reorganizes the RepD–PcrA complex strictly within the boundaries of core oriD.

**MATERIALS AND METHODS**

**Protein purifications**

*Bacillus stearothermophilus* PcrA and staphylococcal RepD used in this study were purified as described elsewhere (10). RepD mutant R189K was purified using the same method as the wild-type RepD.

**Gel shift assays**

A 280 bp PCR fragment containing the core oriD sequence was amplified using pCERoriD as template and the oligonucleotides oriD(r)NdeI (5'-TTAGCTCACCTCAT ATGGCACCCTCCAGCT-3') and oriD(d)NcoI (5'-GAT GTGCCTCATGCGCATTAAGTTGG-3'), containing NdeI and NcoI restriction sites, respectively. The oriD-containing DNA fragment was gel purified and 5'-end-labelled in a reaction with T4 polynucleotide kinase 10 U (NEB) and 10 pmol γ-[32P]-ATP (3000 Ci mmol⁻¹) (Perkin Elmer). The unincorporated γ-[32P]-ATP was removed using MicroSpin™ S200 HR columns (GE Healthcare). Binding reactions were carried out with RepD, PcrA and RepD plus PcrA (concentrations are indicated in figure legends) in 15 μl binding buffer (50 mM Tris–HCl pH 7.5, 200 mM KCl), in the presence of 0.1 nM radio-labelled oriD-containing DNA fragment, and in the presence or absence of 0.1 μg polydIdC non-specific competitor DNA (Sigma). When indicated, 2 mM of ADP or ADPNP and 5 mM MgCl₂ were included. Binding reactions were incubated at 30°C for 15 min and samples were applied to a 6% non-denaturing polyacrylamide gel for electrophoresis in 1×TBE (Tris Borate EDTA) buffer. When nucleotides and MgCl₂ were present EDTA was omitted from the electrophoresis buffer. Gels were dried and imaged using a Molecular Imager FX and associated software (BioRad).

**DNasel footprinting**

DNasel footprinting experiments were carried out as described elsewhere (22). Purified RepD and/or PcrA proteins were incubated with 0.37 pmol supercoiled pCERoriD in 50 μl binding buffer for 1 min at 30°C. Then 50 μl of DNasel buffer were added to the reaction (40 mM Tris–HCl pH 7.9, 10 mM NaCl, 6 mM MgCl₂, 1 mM CaCl₂) and the mixture was incubated for another 1 min at 37°C, before addition of 10 U DNasel (Roche). Reactions were incubated at 37°C for 3 min and stopped by addition of 100 μl stop buffer (SDS 1% v/v, 200 mM NaCl, 20 mM EDTA). The digested fragments were purified by phenol:chloroform (1:1) extraction and ethanol precipitation, after addition of 20 μg/μl glycogen as DNA carrier. DNA was suspended and quantified using a Nanodrop prior to primer extension analysis. The following control reactions were included: DNA untreated with DNasel, RepD or PcrA, DNA treated with DNasel in the absence of RepD and/or PcrA and DNA incubated with RepD or PcrA, without DNasel.

**Primer extension analysis**

The same oligonucleotides oriD(r)NdeI and oriD(d)NcoI that were used to amplify the oriD-containing fragment for gel shift assays were also used in primer extension reactions. They were designed to anneal to the (+) and (−) strands, respectively, outside the oriD region in pCERoriD. The DNasel digested fragments were probed by primer extension using the fmol DNA cycle sequencing system from Promega, according to the manufacturer’s instructions. Primer extension reactions contained...
Exonuclease III footprinting

Exonuclease III footprinting experiments were carried out as described elsewhere (23,24). A 280 bp 5'0 Exonuclease III footprinting software (BioRad). imaged using a Molecular Imager FX and associated polyacrylamide sequencing gel. Gels were dried and 0.05% (w/v) bromophenol blue, 0.05% (w/v) xylene stop solution (10 mM NaOH, 95% (v/v) formamide, Reactions were stopped by addition of sequencing stop solution (10 mM NaOH, 95% (v/v) formamide, 0.05% (w/v) xylene cyanol) and then resolved through a urea-denaturing 6% polyacrylamide sequencing gel. Gels were dried and imaged using a Molecular Imager FX and associated software (BioRad).

Analytical ultracentrifugation

The DNA substrate used in analytical ultracentrifugation (AUC) experiments was prepared by PCR using the same oligonucleotides as in the gel shift assay. Fluorescein labels were attached at the 5'-end of both oriD(r)NdeI and oriD(d)NcoI oligonucleotides to obtain the fluorescently labeled oriD-containing DNA fragment. The DNA–protein complexes were magnified using the Multimode Nanoscope IIIa Atomic force microscopy (AFM) (Veeco, Santa Barbara, CA, USA) in Tapping Mode™. Rectangular silicon cantilevers (Olympus, Japan) with integrated tips were used with a typical spring constant of 42 N/m and a resonant frequency around 300 kHz. The cantilevers were driven at their resonant frequency and the scan line frequency was 2 Hz at 512 × 512 pixel resolution. Typical scan sizes were 2 × 2 µm from which DNA–protein complexes were magnified using the Nanoscope software (version 5.13r3, Veeco) to generate 300 × 300 nm images. The total number of images in each case, n, is given in the ‘Results’ section. Contour lengths and bend angles were measured using the section analysis and angle tools, respectively, of the same software.

RESULTS

ExoIII probing at the front of oriD

The 5'-end of the (−) strand of the oriD containing DNA fragment was radioactively labelled and ExoIII digestion was carried out in the presence and absence of RepD and PcrA, as shown in Figure 1. In the absence of proteins, ExoIII was able to digest the (−) strand through the oriD (see control lane 3 in Figure 1A–D), whereas in the presence of RepD an initial protection point from
ExoIII digestion was located ~74–80 bp upstream from the ICR I site (Figure 1A). Further resistance points were detected just in front of the ICR I site and in the first half of the ICR II site. In the presence of RepD and PcrA, the first resistance point ~74–80 bp upstream from the ICR I site, became considerably stronger as the ExoIII was unable to pass this point even after 10 min digestion (Figure 1C).

Interestingly, in the presence of only PcrA three resistance points were evident on the (~) strand as the ExoIII approached the ICR I site. One strong resistance point at ~35 bp upstream from the ICR I site, and two weak resistance points within the first halves of the ICR I and ICR II
sites (Figure 1B). These data indicate that even in the absence of RepD, PcrA appears to bind to this DNA fragment, targeting the area upstream from the ICR I site (see gel shift data later on).

In the presence of ADPNP, a non-hydrolysable analogue of ATP, the ExoIII footprint of the ternary complex on the (−) strand changed drastically. As the ExoIII approached the ICR I site, the strong resistance at ~74–80bp upstream from ICR I and the second resistance just in front of ICR I disappeared, whereas the resistance point within the first half of ICR II strengthened with ExoIII being unable to pass this point even after 10min digestion (compare the ExoIII digestion patterns of RepD + PcrA in the absence and presence of ADPNP in Figure 1C and D, respectively).

ExoIII probing at the back of oriD

In this series of experiments, the 5′-end of the (+) strand was radioactively labelled and the DNA digested with ExoIII in the presence and absence of RepD (Figure 2A) and PcrA (Figure 2B). In the absence of proteins, ExoIII was able to digest through the ICR III and ICR II sites but then encountered strong resistance in a stretch of thymines in the middle of ICR I (see lane 3 in Figure 2A, B and lane 1 in Figure 2C and D). This was
specific for the (+) strand as it was not observed on the
(−) strand when the ExoIII approached from the front of
the ICR I site (see control lane 3 in Figure 1A–C and lane
1 in Figure 1D). The possibility of a secondary DNA
structure inhibiting ExoIII was investigated by creating
mutant oriD fragments with mutations in ICR I (oriDI),
ICR II (oriDII) and ICR III (oriDIII), but all mutant oriD
fragments exhibited the same resistance point upon
ExoIII digestion, albeit slightly weaker in the oriDI case
(Supplementary Figure 1s). This resistance appears to be
specific to oriD as a non-specific DNA fragment amplified
from the empty pCER19 vector with the same oligo-
nucleotides used to amplify oriD did not exhibit resistance
to ExoIII digestion (Supplementary Figure 1s).

In the presence of RepD, protection from ExoIII was
extended ~46–50 bp downstream from the ICR III site
(Figure 2A). At longer digestions ExoIII was able to
pass this point but then encountered several more resis-
tance points starting at the end of ICR III and extending
all through the ICR II and ICR I sites (compare the 5, 10
and 15 min digestions in the presence of RepD alone in
Figure 2A). With PcrA alone ExoIII digested through the
oriD containing DNA fragment but a strong resistance
point was detected about 30–35 nucleotides past the
ICR II and ICR I sites (Figure 2C; point marked by an asterisk).
A second minor resistance point was apparent in the
middle of ICR II.

In the presence of RepD and PcrA, the first resistance
point ~46–50 bp downstream from the ICR III site on the
(+) strand, remained the same as in the absence of PcrA.
However, the resistance points at the end of ICR III
became considerably stronger in the presence of PcrA.
Even after 15 min digestion, the ExoIII was halted at the
end of ICR III and could not progress into the ICR II and
ICR I sites (compare the 5, 10 and 15 min digestions in the presence of RepD alone in
Figure 2A). With PcrA alone ExoIII digested through the
oriD containing DNA fragment but a strong resistance
point was detected about 30–35 nucleotides past the
ICR I site (Figure 2B the band marked by an asterisk)
which coincides with the same strong resistance point
detected in the equivalent experiment in Figure 1B.
A second minor resistance point was apparent in the
middle of ICR II.

Newly seen ADPNP-induced changes when we
probed the (−) strand with ExoIII (see above). Similar
changes were also apparent at the other end of the oriD
on the (+) strand as the ExoIII approached the ICR III site
(Figure 2D). In the presence of ADPNP, the first resist-
tance point ~46–50 bp downstream from the ICR III site
on the (+) strand became weaker (compare the gels in
Figure 2C and D), the resistance points at the end of
ICR III also became weaker and the ExoIII was able to
progress beyond ICR III into the ICR II site (compare the
ExoIII digestion patterns of RepD+PcrA in the presence
and absence of ADPNP in Figure 2C and D).

DNaseI probing of oriD

DNaseI footprinting was carried out with the
supercoiled oriD-containing pCERoriD in the presence
and absence of RepD and PcrA. This technique ensures
that any supercoiling-dependent features of the system are
preserved. Both (+) and (−) strands can be probed sepa-
ately using the appropriate complementary radiolabelled
oligonucleotide. DNaseI footprinting analysis of the (−)
strand revealed a clear footprint in the presence of RepD
encompassing the core oriD that includes the ICR I–III
sites (Figure 3A). This footprint did not change in the
presence of PcrA (Figure 3B).

By comparison, DNaseI footprinting of the (+) strand
revealed a clear footprint for RepD in oriD and an addi-
tional hypersensitive site at ~55–61 bp upstream from
ICR I (Figure 4A–D). In the presence of PcrA, the foot-
print in oriD remained the same but the hypersensitive site
upstream from ICR I disappeared and two other hyper-
sensitive sites in the region extending further upstream
~62–90 bp from ICR I appeared (Figure 4E and F). The
presence of ADPNP did not change the footprinting
pattern of the ternary complex (Figure 4C and D).

Similar results were obtained with the mutant R189K
version of RepD that nicks and attaches itself on the
5′-end of the nick but fails to religate the nick
(unpublished data). ExoIII and DNaseI footprints of the
(+ and (−) strands were identical to those obtained with
native RepD (data not shown). An example of DNaseI
footprints obtained with R189K on the (+) strand is shown in Figure 4C.

ATP-binding affects the PcrA–RepD–oriD
ternary complex

Our ExoIII experiments described above revealed that
ADPNP binding presumably by PcrA, since RepD is
not known to bind ATP, somewhat affects the ternary
complex (Figures 1 and 2), although this effect was not
detected by DNaseI fingerprinting (Figure 4). In order to
first verify the formation of a ternary PcrA–RepD–oriD
complex and then the effects of ADPNP binding on the
complex, we carried out gel shift assays using the same
oriD-containing fragment that was used in ExoIII experi-
ments described above.

First, we established that RepD binds to this DNA even
in the presence of competitor polydIdC, as at increasing
concentrations an initial shift followed by a second
supershift at high RepD concentrations were observed
(Figure 5A; gel on the left). Then we established the
formation of a ternary PcrA–RepD–oriD complex by
keeping the RepD concentration constant at 0.5 μM
(a concentration at which all of the DNA substrate was
shifted by RepD) and introducing increasing concentra-
tions of PcrA. A distinct supershift was detected as the
PcrA concentration increased indicating the forma-
tion of the ternary complex (Figure 5A; gel on the
right). Addition of ADPNP or ADP nucleotides in the
binding mixture reduced ternary complex formation
(Figure 5B).

PcrA has weak affinity for oriD

During ExoIII probing in the presence of PcrA we
detected two resistance sites at the front of oriD.
A stronger site at ~35 bp upstream from the ICR I site
(within the pCER19 vector sequence) and a weaker site
within the first half of the ICR I site (Figure 1B).
Therefore, even in the absence of RepD, PcrA appears
to bind upstream of oriD. PcrA is not known to have
affinity for any specific dsDNA sequence. It does,
however, bind dsDNA apparently with weak affinity,
since binding was detected using a classical gel shift
assay only in the absence of competitor DNA (Figure 5C). There is no higher affinity for oriD because shifts observed with oriD-containing and a non-specific fragments were comparable (data not shown).

The stoichiometry of the RepD–oriD complex

The formation of the initiation complex was studied by velocity sedimentation AUC experiments to obtain information of the stoichiometry of the RepD–oriD and PcrA–RepD–oriD complexes (Figure 6). Incubation of 5 nM of the same oriD-containing DNA fragment (fluorescein labelled at the 5’-ends of both strands) as the one used in our gel shift assays with increasing concentrations of RepD resulted in the formation of complexes with increasing sedimentation coefficients (Figure 6A). A plot of the sedimentation coefficients versus [RepD] produced a biphasic curve, with a steep increase in the first phase up to a RepD concentration of ~60–80 nM and a shallow increase in the second phase up to a RepD concentration of 7.375 μM (Figure 6A). We interpret these data as follows. The first phase shows the formation of the specific oriD–RepD complex and the second phase shows the formation of a non-specific oriD–RepD complex consistent with our gel shift assays shown in Figure 5A. Considering oriD as a single RepD-binding site and fitting the first phase (0–1.25 μM RepD) to a single site binding hyperbola, using GraphPad Prism, produced a good fit ($R^2 = 0.961$) with an apparent $K_d$ of 124 nM and a stoichiometry of approximately 1 DNA: 10 RepD (Figure 6A). This apparent stoichiometry should be considered with caution as binding of RepD to oriD appears to be rather weak and thus a mixture of free and complexed DNA would be present both of which have different buoyancy. Present methods are unable to distinguish between such species. Another complication is that there are potentially three RepD-binding sites (ICR I–III) within oriD with potential cooperativity at play that complicate theoretical binding models. Complications also arise from the effect of shape changes. Free DNA would be quite flexible in solution adopting a number of conformations. As RepD binds the DNA would become more rigid and any additional RepD-induced changes such as bending (see below) would complicate buoyancy comparisons.

To investigate binding of PcrA to the oriD–RepD complex, we incubated 5 nM oriD–DNA with 600 nM
RepD to allow the formation of the oriD–RepD complex and then added increasing concentrations of PcrA (Figure 6B). The excess of RepD was used to ensure that all of the oriD–DNA was sequestered at all times in the RepD–oriD complex. A plot of sedimentation coefficients versus PcrA concentration produced a curve with two phases. An initial increase followed by a plateau up to 2 μM PcrA followed by a further increase up to 8.25 μM...
of PcrA with the oriD–PcrA complex. The combined AUC data are entirely consistent with our gel shift data shown in Figure 5. Fitting of the first phase to a single site binding hyperbola produced a fit with $R^2 = 0.903$ and an apparent $K_D$ of 98.5 nM for binding of PcrA to the oriD–RepD complex. The apparent stoichiometry of PcrA relative to RepD is 1:10 but deconvoluting the precise stoichiometry of the ternary complex with this method is not possible for reasons explained above.

**RepD bends oriD**

A 353 bp DNA fragment containing oriD was imaged by AFM in the presence of RepD or R189K with PcrA and ADPNP, as appropriate (Figure 7). To ensure preservation of supercoiling effects and efficient covalent linkage of RepD or R189K to oriD we first assembled all complexes on supercoiled pCERoriD, then excised an oriD-containing 353 bp DNA fragment by PvuII digestion before imaging. In the absence of proteins, typical images were observed with no high or globular features ($n = 50$) (Figure 7A, a1–a4). There was considerable flexibility in the molecules observed and many displayed an asymmetrically located bend (such as Figure 7A, a3). In the 353 bp fragment used, oriD is also located asymmetrically, the nick site at the centre of the oriD sequence being 213 bp from the 5′-end of the molecule. Although the orientation of the DNA fibre is unknown, in one of two scenarios this observation is in agreement with electrophoretic mobility shift experiments which demonstrated the presence of an intrinsic bend in the closely related oriC sequence in the absence of any protein (26). For the 50 naked DNA molecules imaged by AFM, the average contour length was 109.8 ± 8.9 nm, slightly shorter than 115.4 nm predicted for B-form DNA with 10.4 base pairs per turn and a pitch of 3.4 nm. Yields of the 353 bp fragment on the mica surface in the absence of any protein were low because the spermidine buffer used favored the binding of DNA–protein complexes.

In the presence of RepD, a high, globular feature was seen on the DNA, which was localized at the bend in the DNA fibre (Figure 7A, b1–b4). This was also seen for the active site mutant R189K, which does not relativate the nicked oriD sequence, forming a more stable covalent DNA–protein complex than the wild-type RepD. From 100 images of each complex the contour lengths of the DNA arms extending from the globular feature were measured (Supplementary Table 1). The average total length of DNA for all complexes was marginally shorter than for free DNA (108.0 ± 9.4 nm for RepD, 101.1 ± 9.9 nm for R189K), although some variation in individual length was noted. From the relative lengths of the DNA arms extending from the globular feature, the latter is placed at 65% along the length of the fragment. This corresponds to the 5′ side of ICR III (27) and therefore in agreement with previous work on binding of RepD with oriD as well as studies of RepC bound to oriC (26).

The angle between the DNA arms at the globular feature was measured for each image. Histograms depicting the bend angles (Figure 8) suggest two principal types of complex, one characterized by a bend angle of...
around 90° and another with a broader distribution about 140–150°. Complexes were thus classified into one of two types depending on whether the bend was acute or obtuse. The two types were named ‘sharp’ and ‘shallow’ if the bend was less or greater than 110° relative to the axis of the DNA backbone, respectively. The sharp-angled complexes comprised 39% and 35% of the imaged populations for complexes containing RepD and R189K, respectively. These populations also had a slightly smaller contour length than their shallow-angled counterparts (Supplementary Table S1).

**RepD-mediated recruitment of PcrA induces additional oriD bending**

In the presence of PcrA with RepD or R189K (Figure 7A, c1–c4), the proportion of sharply bent DNA fragments observed increased to 60% and 57%, respectively, for 100 images of each complex. The distribution of bend angles (Figure 8) was also seen to focus about the principal angles for each complex upon the addition of PcrA, suggesting that complexes of intermediate angle were more likely to be resolved to the sharp-angled classification in the RepD:PcrA complex. As before, the average contour length of each sharply-angled population was slightly smaller than that of the shallow-angled molecules.

When ADPNP was included with RepD and PcrA or R189K and PcrA (Figure 7A, d1–d4) the number of sharply bent DNA fragments decreased to 41% and 46%, respectively, again for 100 images of each complex. The histograms (Figure 8) show that the focus about each principal angle is reduced once more, with an increase in the number of
intermediate-angled molecules suggesting that the remodelled protein–DNA complex is more flexible. Summarizing the AFM data (Figure 7B), we conclude that the naked DNA is able to adopt a variety of conformations, including the presence of an asymmetric bend within oriD. Binding of Rep results in a bend at a defined position along the length of the DNA which is consistent with the location of oriD within the DNA fragment, and recruitment of PcrA biases the population towards one with a sharper bend angle. However, when PcrA binds ADPNP this population is once again reduced.

**DISCUSSION**

*RepD forms an extended loose complex with oriD*

Mapping the boundaries of the RepD–oriD complex by ExoIII footprinting revealed that protection from ExoIII in the presence of RepD was extended ~74–80 bp upstream from the ICR I site and 46–50 bp downstream from the ICR III site. The downstream protection site was somewhat weaker than the upstream site, as it was reduced more readily by ExoIII digestion for 15 min. In both cases, as the ExoIII approached the oriD on the (−) strand from the ICR I site or the (+) strand from...
the ICR III site, there were strong protection points at the beginning of ICR I and end of ICR III, respectively, indicating strong interactions of bound RepD molecules with the core oriD sequence. After digestion of the (−) strand for 15 min the ExoIII managed to pass the resistance point at the beginning of ICR I but then halted at a second strong resistance point within the first half of the ICR II site. By comparison, on the (+) strand after 15 min digestion as the ExoIII approached from the ICR III site it encountered several additional resistance points beyond the ICR III end boundary and within the ICR I, ICR II and ICR III sites. By comparison, DNaseI footprinting did not reveal protection outside the core oriD boundaries but did reveal an additional hypersensitive site 55–61 bp upstream from ICR I. This is probably because in the extended RepD–DNA complex the DNA outside the core oriD is still accessible to DNaseI. These data are consistent with an extended, loose RepD–oriD complex with strong interactions of RepD within the core oriD including the ICR I–III sites and additional weak interactions extending upstream and downstream beyond oriD. An oriD–RepD complex of five RepD dimers bound to oriD based upon the apparent stoichiometry from the AUC data is shown in the model of Figure 9.

**PcrA is recruited upstream from the ICR I site**

In the presence of RepD and PcrA, the resistance point 74–80 bp upstream from the ICR I site on the (−) strand became considerably stronger, whereas the resistance point 46–50 bp downstream from the ICR III site on the (+) strand remained the same in the presence or absence of PcrA. However, the second resistance point at the end of ICR III on the (+) strand became much stronger in the presence of PcrA. Even after 15 min digestion in the presence of PcrA the ExoIII was halted at the end of ICR III and could not progress into the rest of the oriD. These data indicate that when PcrA is recruited the ternary complex reorganizes somewhat differently than the binary RepD–oriD complex forming strong contacts at the end boundary of ICR III and outside the core oriD ~74–80 bp upstream from the ICR I site (Figure 9).

DNaseI footprinting experiments with supercoiled pCERoriD revealed footprints of RepD on the (+) and (−) strands within oriD, consistent with binding of RepD
molecules in the ICR I-III sites. However, an additional DNaseI hypersensitive site appeared to form at 55–61 bp upstream from ICR I site on the (+) strand when RepD was bound to oriD. In the presence of RepD and PcrA, this DNaseI hypersensitive site disappeared, whilst two other hypersensitive sites appeared nearby in the region extending further upstream 62–90 bp from ICR I. This is consistent with a reorganization of the binary RepD-DNA complex when PcrA is also bound. The area where these effects were observed coincided broadly with the ExoIII resistance point 74–80 bp upstream from the ICR I site. The combined data reinforce the notion that initial RepD binding to oriD forms an extended loose complex that recruits PcrA upstream from the ICR I site (Figure 9).

**ATP binding induces re-modelling of the PcrA–RepD–oriD ternary complex**

Upon binding of ATP by PcrA the ternary complex changes drastically, as indicated by the differences in the ExoIII footprinting patterns in the presence and absence of ADPNP. On the (−) strand as the ExoIII approached the ICR I site, the upstream resistance point outside the oriD and the second resistant point at the front of ICR I disappeared, whereas the resistance point within the first half of ICR I strengthened. Similar changes were also apparent at the other end of oriD on the (+) strands as the ExoIII approached the ICR III. In the presence of ADPNP, the resistance point at the end of ICR III weakened and ExoIII progressed beyond ICR III into ICR II. The effect of ATP binding on the ternary complex was also detected by gel shift assays. In the presence of ADPNP or ADP, the initial extended ternary complex was reduced. The combined data indicate that ATP binding by PcrA induces remodelling of the ternary complex, perhaps setting up PcrA to start the translocation process upon ATP hydrolysis (Figure 9).

Subtle rearrangements have also been observed within the replication origin of the filamentous phage f1. Progressive binding of the replication initiator protein gpII at the three repeated sequences β, γ and δ produces an extended complex that bends and locally melts the DNA for nicking to occur (28). The PcrA–RepD–oriD system may be organized in an analogous manner through progressive binding of RepD, PcrA and ATP to set up a complex competent for processive unwinding. In our model for RepD-mediated loading of PcrA at oriD we propose that there is an ATP-induced hand-over event of PcrA from the RepD dimer bound to ICR I, which presumably initially recruits PcrA, to the RepD dimer bound to ICR II (Figure 9). This is consistent with the loss of the ExoIII resistance point within ICR I and the strengthening of the resistance point within ICR II observed in the presence of ADPNP (Figure 1). Our ExoIII footprinting and gel shift experiments cannot confirm unequivocally that PcrA remains bound in a ternary complex in the presence of ADPNP or ADP. Our data are equally consistent with a scenario whereby PcrA dissociates from the ternary complex in the presence of nucleotides. However, this is an unlikely scenario since RepD and PcrA have been shown to remain associated in a processive tight active complex coupling ATP hydrolysis to DNA unwinding (10,12,29). Further evidence, albeit indirect, that PcrA is still associated with the ternary complex is offered by our DNaseI footprinting of the (+) strand shown in Figure 4B. The DNaseI footprinting patterns of the ternary complex in the presence and absence of ADPNP are identical and different than that of RepD alone. If PcrA were to dissociate from the complex in the presence of ADPNP then one would expect the DNaseI footprinting patterns of the ternary complex in the presence and absence of ADPNP to be different, which is not the case. Therefore, PcrA must
remain bound in the complex even in the presence of ADPNP or ADP.

Recruitment of PcrA by RepD results in a visible change in DNA conformation

The model proposed above is consistent with our AFM imaging data. AFM images of protein–DNA complexes fell in two categories depending on the severity of the protein induced bend (sharp or shallow). It is possible that wild-type RepD may nick at oriD but religate the DNA during the course of sample preparation, resulting in a mixed population of nicked and religated DNA. For this reason, the RepD mutant R189K was also studied, as it is severely compromised with respect to DNA religation and thus yields a population of nicked DNA covalently attached to oriD. As both population types were observed for both Rep proteins, we conclude that they do not correspond to separate populations of nicked and religated DNA.

When PcrA was incubated with RepD and R189K, the proportion of sharply bent DNA fragments increased significantly in comparison with DNA bound to Rep proteins alone, and the contour lengths of those sharply bent fragments were slightly less than their shallow-angled counterparts. Bending of the closely related RepC–oriC system has been documented before (26), however this is the first time that further induced bending by the recruitment of the PcrA helicase has been shown. The contraction in contour length of the sharply bent DNA suggests a rearrangement of oriD, with possibly a looping of the DNA around the Rep–PcrA complex. When ADPNP was added, the sharply bent protein–DNA complex was further rearranged, and the increased distribution of bend angles suggests a more flexible DNA molecule in this remodelled complex.

Different functions of the ICR I–III sites

Sequence comparisons of several contiguous plasmid replication origins revealed that sequence conservation is highest in ICR II and in ICR I, whilst ICR III exhibited the greatest sequence diversity (7). Such sequence conservation patterns may be indicative of a functional division of labour between the three ICR sites. ICR III confers specificity on the Rep–ori interaction resulting in plasmid specific replication in vivo (7). ICR II is highly conserved as it is the site of the cleavage reaction and participates in the termination of replication (6,7,30,31). ICR I is also well conserved in terms of sequence and our data suggest that its role is to participate in the initial recruitment of the host helicase at the plasmid ori. Overall we conclude that RepD-mediated recruitment of PcrA at oriD is a three step process. Initially, an extended RepD–oriD complex includes a region upstream from the core oriD. PcrA is recruited to this upstream region and finally upon ATP-binding PcrA relocates within the core oriD.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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