Interactions of the site-specific recombinases XerC and XerD with the recombination site dif

Citation for published version:
Blakely, GW & Sherratt, DJ 1994, 'Interactions of the site-specific recombinases XerC and XerD with the recombination site dif' Nucleic Acids Research, vol 22, no. 25, pp. 5613-20. DOI: 10.1093/nar/22.25.5613

Digital Object Identifier (DOI):
10.1093/nar/22.25.5613

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published In:
Nucleic Acids Research

Publisher Rights Statement:
RoMEO green

General rights
Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy
The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.
Interactions of the site-specific recombinases XerC and XerD with the recombination site dif

Garry W. Blakely and David J. Sherratt*
Microbiology Unit, Department of Biochemistry, University of Oxford, South Parks Road, Oxford OX1 3QU, UK

Received September 20, 1994; Revised and Accepted November 18, 1994

ABSTRACT

The Xer site-specific recombination system of Escherichia coli is involved in the stable inheritance of circular replicons. Multimeric replicons, produced by homologous recombination, are converted to monomers by the action of two related recombinases XerC and XerD. Site-specific recombination at a locus, dif, within the chromosomal replication terminus region is thought to convert dimeric chromosomes to monomers, which can then be segregated prior to cell division. The recombinases XerC and XerD bind cooperatively to dif, where they catalyse recombination. Chemical modification of specific bases and the phosphate–sugar backbone within dif was used to investigate the requirements for binding of the recombinases. Site-directed mutagenesis was then used to alter bases implicated in recombinase binding. Characterization of these mutants by in vitro recombinase binding and in vivo recombination, has demonstrated that the cooperative interactions between XerC and XerD can partially overcome DNA alterations that should interfere with specific recombinase–dif interactions.

INTRODUCTION

Prokaryotic cell division requires that newly replicated monomeric chromosomes are segregated to distinct cellular locations before cell division can be completed (1). Odd numbers of homologous recombination events between replicating, or newly replicated, circular chromosomes can lead to production of chromosome dimers, which must be resolved to monomers prior to nucleoid segregation. The dif site, present in the Escherichia coli K12 DNA replication terminus region, has been implicated in normal chromosome segregation through its role as a site-specific recombination locus. It has been proposed that recombination between two dif sites in a chromosome dimer converts the dimer to monomers. Although dif is dispensable, its absence produces a sub-population of filamentous cells that contain aberrant nucleoids (2, 3). We propose that the odd number of homologous exchanges that generate dimers occurs rarely, as do homologous exchanges that convert dimers to monomers. The same phenotype is demonstrated by cells that contain mutations in xerC or xerD, two genes encoding site-specific recombinases that function in recombination at dif. The protein sequences of XerC and XerD share 37% identity and show them to be members of the lambda integrase family of site-specific recombinases (3, 4).

Recombination proceeds, after recombinase binding and synapsis of sites, by activation and subsequent cleavage of specific phosphodiester bonds. The active site tyrosine of the recombinase acts as a nucleophile and cleaves the DNA to form a covalent protein–DNA intermediate. Free 5’ hydroxyl ends, generated by the initial DNA cleavage, then act as attacking nucleophiles to religate the DNA. A total of four strand cleavages and religations are required to generate recombinant products (reviewed in 5).

The XerC recombinase was initially identified by its role in resolution of ColE1 plasmid multimers (generated by homologous recombination) to monomers. This recombination is necessary for the stable inheritance of this naturally occurring high copy number plasmid and its relatives (6, 7). A second recombinase, XerD, was identified by sequence homology to XerC and is encoded in an operon with recJ and dsbC (8–10). XerC/XerD-mediated site-specific recombination in vivo at the 210 bp cer locus of ColE1 shows selectivity for intramolecular resolution, i.e. recombination only occurs between two sites in direct repeat in the same molecule (usually a dimeric plasmid) to produce two monomers. cer consists of a 30 bp core sequence to which XerC and XerD bind (Figure 1) and ~180 bp of upstream accessory sequences (11). Recombination at cer also requires two accessory proteins, ArgR and PepA. The precise function of these proteins is not known, but they and the cer accessory sequences have been implicated in resolution selectivity (12). cer-like sequences present in related, naturally occurring plasmids are also required for plasmid stability (4).

A DNA fragment of 32 bp which contains a functional dif site is sufficient to allow Xer-mediated plasmid multimerization and dimer resolution (3). The structural organization of dif is similar to that of related lambda integrase family site-specific recombination loci, e.g. P1 loxP, and Saccharomyces cerevisiae FRT (13, 14). The core recombination site is divided into two 11 bp half-sites, which flank a 6 bp central region. The half-
sites are related by partial dyad symmetry and show homology with the core sequence of cer (Figure 1). Copper—phenanthroline footprinting demonstrated that XerC binds to the left half-site while XerD binds to the right half-site; binding of both proteins is highly cooperative. A requirement for two different recombinases appears to provide the asymmetry for ensuring correct alignment of recombining sites before the first strand exchanges occur. Neither half-site can be used to replace the other half-site and the putative active sites of both proteins are required for recombination in vivo, demonstrating the requirement and involvement of both proteins in the strand cleavage and transfer reactions (8). The novel requirement for two recombinases may enable each pair of strand exchanges to be under separate genetic control, as well as facilitating site alignment immediately after site replication in the chromosome. Based on the dyad symmetry of the half-sites and by analogy with the cleavage positions from other recombinases (13, 14), the boundaries of the central region and recombinase binding sites have been proposed to contain the bases involved in strand nicking and exchange (15). In dif the central region contains 6 bp, while in cer it consists of 8 bp; this difference may constitute a major determinant of the outcome in the recombination reaction and the requirement for accessory sequences.

The presence of limited dyad symmetry as part of the ‘inner’ sequence of each binding site suggests that the ‘outer’ sequence specifies the recognition differences between the XerC and XerD binding sites. Because of the dyad symmetry and the requirement for two related recombinases, a study of the DNA sequence and structural requirements which determine specificity for interaction between XerC, XerD and dif was undertaken. Footprinting techniques using the DNA modifying reagents dimethyl sulphate, potassium permanganate and N-ethyl-N-nitrosourea provide evidence for protein interactions with guanine and thymine bases in the major grooves, adenines in the minor grooves and phosphates in the backbone of DNA within the dif site. Selected base pairs identified within the sequence were mutagenized to determine the effect of base changes on recombinase binding and in vivo recombination.

MATERIALS AND METHODS
Plasmids, DNA fragments and Xer proteins
DNA fragments containing the functional dif site were generated from plasmid pMIN33 (2). The 67 bp HindIII-KpnI fragment was used to end-label the 3' recessed end of the top strand using the Kloney fragment of DNA polymerase I; the 73 bp EcoRI-SphI fragment was similarly used to end-label the bottom strand. XerC and XerD proteins were partially purified by fast chromatography and precipitation. Isolation and analysis of protein—DNA complexes and free DNA was as described above. Strand cleavage was performed in 1 M piperidine at 90°C for 30 min.

Ethylation interference
Labelled DNA was dissolved in 100 μl of 50 mM sodium cacodylate, pH 7.0, 1 mM EDTA and 1 μg of poly(dI—dC). 100 μl of a saturated solution of N-ethyl-N-nitrosourea in ethanol was added and incubated at 50°C for 1 h. After the modification, the DNA was precipitated with 0.3 M sodium acetate and 2 volumes of ethanol. Isolation and analysis of protein—DNA complexes and free DNA was as described above. Strand cleavage was performed in 100 mM sodium hydroxide at 90°C for 30 min (17). Samples were mixed with urea loading dye and loaded directly onto 20% sequencing gels.

Quantitation
β-Particle emission from 32P-labelled DNA fragments in sequencing gels was measured using a Molecular Dynamics PhosphorImager with ImageQuant software. Autoradiograms were scanned using a Joyce-Loesel microdensitometer.

RESULTS
Methylation interference of XerC and XerD binding to dif DNA in vitro
Examination of core recombination sites derived from the E.coli chromosome and from naturally occurring plasmids shows that XerD binding sites are highly conserved, while XerC binding sites are more divergent (Figure 1). What specifies XerD recognition of the right half-sites and XerC recognition of the left half-sites at these related loci? Just three nucleotides, located in the ‘outer’ sequences of each half-site, distinguish the XerC kanamycin resistance was performed after isolation of plasmid DNA from DS941. Subsequent transformation of recombination products into DS984 allowed screening for sensitivity to kanamycin; 100 transformants were tested for each reporter plasmid.

DMS methylation interference
Labelled DNA and 1 μl of poly(dI—dC) (1 mg/ml) were dissolved in 200 μl of 50 mM sodium cacodylate, pH 8.0, and 1 mM EDTA. 1 μl of DMS was added and the DNA modification reaction proceeded for 5 min at room temperature before termination by spun column chromatography through Sephadex G50 followed by precipitation. XerC and XerD extracts were then added to the modified DNA to give a final protein concentration of 3.4 μg/ml, under binding conditions previously described (8). Electrophoresis through 6% polyacrylamide gels was used to separate bound from unbound DNA, with protein—DNA complexes detected by autoradiography. After elution from gel slices, the labelled DNA was cleaved and modified positions using 1 M piperidine at 90°C for 30 min, lyophilized, resuspended in loading dye and analysed by electrophoresis through 20% sequencing gels.

Potassium permanganate interference
Labelled DNA was dissolved in 55 μl of 30 mM Tris—HCl, pH 8, followed by denaturation at 100°C for 3 min (16). Modification was carried out by adding 60 μl of 0.25 mM KMnO4 for 12.5 min at room temperature before purification by spin column chromatography and precipitation. Isolation and analysis of protein—DNA complexes and free DNA was as described above. Strand cleavage was performed in 1 M piperidine at 90°C for 30 min.
and XerD binding sites and presumably provide the differential recognition specificity for appropriate recombinase binding. Regions of dyad symmetry between the half-sites are largely confined to the 'inner' sequences of each binding site. These may be required for specific interactions with common regions of the two proteins.

Chemical modification of DNA was used to identify regions which may act as recognition sequences. Modification interference has proved a powerful technique for identification of sites in DNA which are in close proximity to binding protein in specific complexes (18). Dimethyl sulphate (DMS) methylates the N-7 of guanine and the N-3 of adenine in the major and minor grooves of double stranded B-form DNA respectively (17). The N-7 of guanine and the N-3 of adenine can donate hydrogen bonds to amino acids (19); methylation of these positions can interfere with protein–DNA complex formation where specific hydrogen bonding is required. Addition of protein to modified DNA followed by separation of bound and unbound forms allows determination of bases that interfere with binding using a methodology derived from Maxam-Gilbert DNA sequencing (20).

DNA fragments containing the dif sequence labelled at the 3' end were modified with DMS and then incubated with XerC and XerD. Bound and unbound DNA were separated using non-denaturing polyacrylamide gel electrophoresis followed by analysis on denaturing polyacrylamide gels after DNA cleavage. Modified bases which interfere with binding are underrepresented in the bound fraction of DNA and are enriched in the free fraction of DNA. These interference experiments were only informative when used with XerC and XerD combined, because of the low affinity of the individual proteins for the binding sites. Modification interference patterns were only observed when subsaturating amounts of XerC and XerD were present, suggesting that modification did not abolish binding, presumably because of the cooperative nature of XerC and XerD interactions. In general, methylation of G residues interfered with recombinase binding more strongly than A methylation. Note that piperidine-mediated cleavage of methylated guanine is more efficient than cleavage of methylated adenine (reviewed in 17).

Within the 31 bp of the dif sequence protected by XerC and XerD from attack by 1,10-phenanthroline–copper (8) there are 6 guanine residues in the top strand and 2 guanine residues in the bottom strand (Figure 1). Of the 6 G residues in the top strand, 4 are in the XerC binding site, while there is one each in the XerD binding site and the central region. The only methylated guanine in the dif top strand that interfered with formation of the XerC/XerD complex was at position 8 in the XerD binding site (Figure 2). Analysis of the bottom strand indicated that two modified G residues interfered with XerC/XerD complex formation; these were at positions −8 and −10 in the XerC binding site (Figure 2).

Minor interference from a modified adenine was detected on the top strand at position 6. Adenines on the bottom strand which appeared to be involved in binding were observed at positions 2, 4, 5, 7 and 9; these were all detected as minor enhancements in the unbound DNA fraction. The G residues at positions 8 and −8, top and bottom strands respectively, are in equivalent positions within the limited dyad symmetry of the dif sequence (Figure 1). Most of the interference positions map in the XerD

![Figure 1](http://nar.oxfordjournals.org/)

**Figure 1.** Alignment of homologous sequences from some known Xer recombination sites. XerC binding sites are less conserved than XerD binding sites. cer is from ColE1; psi is from pSC101; cif is from CloDF13; dif is from the E.coli chromosome; the sites from plasmids ColK and ColE3 are also given (4). Base pair coordinates for dif are indicated. Sequences of the mutant dif sites used in this study are shown below the consensus. Bases that have been changed are boxed. The arrows denote the region of dyad symmetry within dif and are designated as the 'inner' sequences.

![Figure 2](http://nar.oxfordjournals.org/)

**Figure 2.** Methylation interference for both strands of dif DNA modified by DMS at N-7 of guanine and N-3 of adenine. The modified 3' labelled DNA (I) was treated with XerC and XerD and separated into bound (B) and free (F) forms. Analysis, next to a Maxam–Gilbert A + G sequencing reaction, demonstrates the sequence positions that interfere with protein binding. Interference is seen as reduction of band intensity in the bound (B) lane and an enhancement in the free (F) lane. A diagrammatic representation of dif is shown adjacent to corresponding portions of the sequencing gel. Positions of strong interference are denoted (▲), with weaker interference as (△).
KMnO₄ Interference

Top strand

Bottom strand

A + G IBF D

D central

central

C

C

-10

-6

-4

5' GGTGCGCATAA TGTATA TTATGTTAAAT ACATAT AATACAATTTA

5' GGTGCGCATAA TGTATA TTATGTTAAAT ACATAT AATACAATTTA

Figure 3. Modification of dif DNA using KMnO₄ was used to identify thymine major groove contact points important for XerC and XerD binding. Modified input DNA (I), bound complex (B) and free DNA (F) are shown, after cleavage with piperidine, adjacent to a Maxam–Gilbert A + G sequencing reaction. Both DNA strands were analysed and shown with the corresponding regions of difnext to the appropriate sequence. Positions of strong interference are denoted (△), with weaker interference as (△). Note the hypermodification of T2 in the central region and hypomodification of T−6, T4 and T5 in the dyad symmetry of the top strand.

Ethylation Interference

Top strand

Bottom strand

A + G IBFD

D central

central

C

C

-10

-6

-4

5' GGTGCGCATAA TGTATA TTATGTTAAAT ACATAT AATACAATTTA

5' GGTGCGCATAA TGTATA TTATGTTAAAT ACATAT AATACAATTTA

Figure 4. Ethylation of phosphates in the DNA backbone of dif leads to interference with XerC and XerD binding. Separation of input DNA (I) from XerC/XerD bound complex (B) and free DNA (F) allows detection after alkaline cleavage. A sample derived from a presumptive XerD bound complex (D) is also shown. The D lane shows strong interference in the right half-site. The only apparent interference positions in the left half-site were seen as enhancements at base pairs −4, −6 and −7 in the bottom strand (lane D). Lanes marked A + G are adenine and guanine Maxam–Gilbert sequencing reactions. Note the doublets produced from cleavage 3' and 5' of the modified phosphates. The strong (△) and weak (△) interference positions are indicated on the sequencing gel and the corresponding DNA sequence.

XerC and XerD binding to dif DNA modified with potassium permanganate

The non-polar methyl group of thymine at position C-5 is important for discrimination between thymine and cytosine and provides a surface for van der Waal’s contacts with amino acids (19, 21). The 5,6 double bond of thymine residues in single-stranded DNA can be selectively oxidized by potassium permanganate to produce the glycol form. Thymine glycols have been shown to prevent protein binding at specific DNA sequences, for example steroid hormone receptor interactions with promoter regions and FLP recombinase binding of FRT sites (16, 22).

End-labelled dif DNA was denatured and treated with KMnO₄ at a concentration appropriate for glycolization. After reannealing, the modified DNA was incubated with subsaturating amounts of KMnO₄ before separation on non-denaturing polyacrylamide gels. Bound and free DNA were analysed on sequencing gels after cleavage with piperidine.

Analysis showed that modification of thymines within the dif sequence, in both top and bottom strands, interfered with binding of XerC and XerD. The top strand of dif showed four positions of interference when thymines were modified at positions −12, −4, 9 and 10 (Figure 3). Not all thymines in the sequence were oxidized equally. Bases between the regions of dyad symmetry were always undermodified in comparison to sequences which constitute the rest of the binding site. The thymine at position 2 in the central region was hypermodified. The reproducibility of this modification pattern suggests it is a function of the DNA sequence and may be a consequence of secondary structure, e.g. a hairpin loop occurring during the modification procedure.

Similar anomalies have been reported for KMnO₄ modification of certain thymine residues in FRT DNA, where the protein binding sites are almost perfectly symmetrical. Secondary
structure in single-stranded DNA may lead to ambiguous assignment of binding interference for particular bases (22). An aberrant cleavage product which ran between bases A3 and T4 may have been a result of the hypermodification of bases between the regions of dyad symmetry.

Modification of the dif bottom strand produced seven thymine residues that interfered with binding; T at positions -5, -4, 1, 6, 11, 12 and 13 (Figure 3). Hypermethylation of T1 in the central region of the bottom strand was also observed. Thymines at positions 9 and 10 in the top strand and 11, 12 and 13 in the bottom strand could therefore define the sequence which XerD recognizes as an appropriate binding site.

Interference of XerC and XerD binding by phosphate ethylation of the DNA backbone

Hydrogen bonding to DNA phosphodiester can be important for positioning of specific protein structures, such as alignment of α-helices to allow ionic interactions with appropriate base pairs in adjacent major grooves (19). DNA conformation is also sequence-dependent, so proteins could indirectly recognize a specific DNA site by the arrangement of the phosphate—sugar backbone (reviewed in 23). Interactions between proteins and the DNA backbone can be studied by modifying phosphates with the addition of an ethyl group donated from N-ethyl-N-nitrosourea. The ethyl group may sterically interfere with the protein or may inhibit binding by altering the charge on the DNA backbone (24).

The alkaline cleavage chemistry for ethylated DNA produces two products from a single modification; the products being dependent on whether the cleavage occurs at the 5' or 3' side of the phosphate (24). The resultant products migrate with an apparent difference of half a base pair on the sequencing gels used in these studies, therefore each cleavage produces a doublet.

Analysis shows that ethylation of 3 phosphates interfered strongly with binding, while ethylation of another 5 interfered weakly. The strong interference positions corresponded to 3' phosphates at bases A6, T7 and G8 in the XerD binding site of dif (Figure 4). The weaker positions corresponded to phosphates 3' to bases T2, A3, T4, T5 and A12. The bottom strand ethylation pattern was analogous to the top strand pattern: strong interference was observed by ethylation of 4 phosphates in the right half-site, 3' to base pairs at positions 4, 5, 7 and 14; weak interference was observed by ethylation of 3 phosphates in the left half-site, 3' to base pairs -4, -6 and -7. The evidence for interference in the left half-site was from enhancement of cleavage products present in a weak XerD complex isolated from the gel shift. This complex showed strong interference in the right half-site, so may have been derived from a portion of modified DNA to which XerC could not bind.

Site-directed mutagenesis of dif

To determine if bases detected by the modification interference analysis were of significance to protein binding and site function, site-directed mutants of dif were constructed. Three bases
(positions C-8, T4 and G8) assigned importance as potential contact positions were changed. One base (A-7) that did not appear to interfere with protein binding when modified was changed as a control (Figure 1). Bases were changed to sequences which did not occur in other known natural recombination sites. The mutant produced for base T4, which was within the region of hypomodification by KMnO4 on the top strand, would also allow confirmation of its role in protein binding. The effects of these four mutations on in vivo Xer-mediated plasmid recombination and in vitro protein binding were studied.

Reporter plasmids containing each mutant site as direct repeats, flanking a kanamycin resistance gene, were constructed and transformed into a Xer+ strain. Recombination products were analysed by agarose gel electrophoresis after ~ 30 generations. Xer-mediated intramolecular recombination between dif sites within the reporter plasmid produces a plasmid equivalent in size to pMIN33 (Figure 5a, lane 3), while intramolecular fusion of the reporter plasmid and its resolved products produces a complex ladder of multimeric forms (Figure 5a, lanes 4-8). Sites difC-8A, difT4G and difG8T were all capable of inter- and intramolecular recombination (lanes 5, 7 and 8), but appeared not to be as proficient in Xer-mediated recombination as wild-type dif; for example, compare the amounts of monomer and dimer product in lanes 5, 7 and 8 to lane 4. In contrast, plasmid DNA containing the site difA-7C gave a pattern of recombinant products indistinguishable from wild-type dif (lane 6).

A genetic test was used to quantify the relative in vivo intramolecular recombination proficiency of each of the mutant dif sites. Total plasmid DNA from Xer+ strains containing reporter plasmids was scored for loss of kanamycin resistance by subsequent transformation into a Xer- strain. After ~50 generations, the reporter plasmid containing the wild-type dif site showed 99% resolution, while the site difA-7C, which appeared to have wild-type recombinational characteristics, showed 76% resolution. The other mutant sites which had shown reduced resolution by gel electrophoresis produced a lower percentage of phenotypic loss; difC-8A 20%, difT4G 5% and difG8T 1% resolution, confirming their reduced proficiency in recombination.

To analyse the in vitro binding of the recombinases to each mutant site, band shift assays were carried out. A DNA fragment containing wild-type dif binds either XerC or XerD weakly as judged by the amount of protein-DNA complex at a given recombinase concentration (8). The same concentrations of XerC and XerD when added together converted most of the input DNA to recombinase-DNA complexes, demonstrating the highly cooperative nature of recombinase binding to dif (Figure 5b, panel 1). Site difC-8A, containing a mutation in the XerC binding site, did not produce a detectable XerC complex and showed less than 50% of the total DNA in a complex with XerC and XerD, suggestive of a reduced overall affinity of XerC and XerD for this site, presumably arising as a consequence of reduced XerC binding (Figure 5b, panel 4; note that in this gel the XerD complex is barely visible; we do not believe this is a consequence of reduced XerD binding to this mutant site since in other band shift experiments the XerD complex was evident). Sites difT4G and difG8T, which both contained mutations in the right half-site, were able to form XerC complexes but there was no evidence for the formation of stable XerD complexes (Figure 5b, panels 2 and 3). Although both of these sites could be bound by XerC and XerD, the overall apparent affinity for the DNA was reduced, presumably because of reduced XerD binding (Figure 5b, panel 2). The control site for this mutagenesis, difA-7C, demonstrated binding patterns which were similar to the wild-type dif sequence (Figure 5b, panel 5).

The in vivo recombination results demonstrate that mutation of nucleotides implicated in protein binding, determined from interference analysis, reduced but did not abolish function of the recombination site. In parallel, XerC and XerD binding was reduced but not abolished at these mutant sites. This data also demonstrated that the assignment of position T4 as a potential contact point was correct.

DISCUSSION

This study has identified potential points of interaction between XerC/XerD and dif DNA, and is the first to examine molecular interactions in a two recombinase system. XerC and XerD can bind to many related natural recombination sites from plasmid DNA and the E. coli chromosome (4). These recombination sites contain limited dyad symmetry of 4-5 bp, yet XerC only binds to the left-half site and XerD binds to the right half-site under standard in vitro binding assays (8). What features of the recombination locus enable these related proteins to differentiate between the half-sites?

The sequences of XerD binding sites are highly conserved, while the XerC binding sites show much greater heterogeneity. A sequence comparison of recombinase binding sites suggests that only 3 positions within the left half-site contain base pairs which do not appear in equivalent positions in the right half-site. For example, position -10 is always a G-C pair but never an A-T pair, while position 10 is always A-T (Figure 6). These base pairs must at least be part of the sequence recognition determinants for each of the recombinases. When the positions of modification interference for top and bottom strands are mapped on aligned sequences it is clear that the 3 conserved positions at base pairs 10, 11 and 13 are important for specific recognition and binding by XerD. The XerC binding site produced fewer modification interference positions, possibly because of its ability to bind DNA less specifically. One of the detected positions corresponded to base pair -10, which is part of the unique left half-site sequence. The other interference positions are primarily within the region of dyad symmetry and
in equivalent positions within each half-site, at positions T4, T-4, G8 and G-8; though note that G at position -8 is not invariant for Xer sites. Base pairs A-12 and A12 in the ‘outer’ sequences appear to be invariant, these equivalent positions also appear to be protein contact positions. The Xer recombinases would not be unusual in their use of a 3–4 bp recognition sequence; many DNA binding proteins use short DNA sequences for specific bond interactions between protein structures and base pairs, for example helix 3 of the POU domain from Oct-1 makes all its hydrogen bonds with the 5'-ATGC subsite (26). Binding of the 434 repressor is also specified by a 4 bp sequence at the end of the operator, 5'-ACAA, while the remainder of the 14 bp site may modulate affinity (27).

The pattern of potential base–protein interactions at dif is suggestive of a bipartite binding function, where each recombinase may recognize the appropriate ‘outer’ unique sequence from the recombination site and use the ‘inner’ dyad symmetry as the determinant for interaction with a common protein structure. The most similar region of XerC and XerD (73% identity) is the putative catalytic domain II, which provides the tyrosine nucleophile and is thought to be involved in phosphodiester activation and cleavage. Thymines at positions -4, -5, 4 and 6 could interact, via the major groove, with the conserved domain II. An analogous DNA structural arrangement has been proposed for the inverted repeats of IS903. The sequence recognition determinants for the transposase may be contained within the last 9 bp of 18 bp repeats and the outer sequences may be required for an additional function (28). Dissection of the related recombinase FLP, from Saccharomyces cerevisiae, has identified various regions of the protein required for different parts of the recombination reaction. The presence of an ∼200 amino acid proteolytic cleavage product (P21) that can bind DNA but which has little effect on DNA bending and no other function (29) may support the possibility of separate protein segments interacting with different DNA domains in each half-site.

When the positions of interference for modified bases and backbone phosphates are superimposed on a projection of B-form helical DNA (Figure 7), the pattern is suggestive of XerD binding on both faces of the helix. XerD interactions with both major and minor groove residues were detected. For example, the minor groove contact at position A3 is accessible from the back of the helix, while contact at position A7 is from the front of the helix (Figure 7). Major groove contacts extend along the whole sequence of the right half-site. The proposed model for these proteins binding to dif would involve a ‘head-to-head’ disposition of protomers along the helical axis with the proteins reaching around the helix at the cleavage position. In contrast, many characterized DNA binding proteins only bind on one face of the helix, as described for interactions between RNA polymerase–T7 promoters and AraC–ara/ complexes (24, 30). The type of binding exhibited by Hin invertase may provide a model for these DNA binding proteins use short DNA sequences for specific bond interactions between protein structures and base pairs, for example helix 3 of the POU domain from Oct-1 makes all its hydrogen bonds with the 5'-ATGC subsite (26). Binding of the 434 repressor is also specified by a 4 bp sequence at the end of the operator, 5'-ACAA, while the remainder of the 14 bp site may modulate affinity (27).

The need to use both recombinases in the interference assays, along with their highly cooperative interactions, may have reduced the sensitivity of our analysis. Nevertheless, the site-directed mutagenesis of dif clearly demonstrates that the interpretation of the interference analysis was correct. Although all the mutant sites were capable of in vivo recombination, the amount of resolution as observed by genetic testing appears to relate to the extent of interference. Mutant difG8T produced less resolution in comparison to the other mutant sites; this base also produced the strongest reproducible interference signal of any base in the dif sequence. It therefore appears that the cooperative binding of XerC and XerD can partially overcome the reduced binding affinity for a particular mutant half-site, allowing the formation of a protein–DNA complex that can give rise to a productive synapse. Reduced stability of such a complex may explain the reduced recombination rates observed.

REFERENCES