Site-specific Relaxase Activity of a VirD2-like Protein Encoded within the tfs4 Genomic Island of Helicobacter pylori

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Background: The complement of factors involved in mobilization of the Helicobacter pylori disease-associated tfs4 genomic island are presently unknown.

Results: tfs4 encodes a VirD2-like relaxase with distinctive DNA binding and nicking activity.

Conclusion: Tfs4 VirD2 probably initiates mobilization of tfs4 by specific interaction at a chromosomal transfer origin sequence.

Significance: Tfs4 VirD2-mediated mobilization of tfs4 may increase pathogenic potential of H. pylori strains.

Four different type IV secretion systems are variably represented in the genomes of different Helicobacter pylori strains. Two of these, encoded by tfs3 and tfs4 gene clusters, are contained within self-transmissible genomic islands. Although chromosomal excision of tfs4 circular intermediates is reported to be dependent upon the function of a tfs4-encoded XerD tyrosine-like recombinase, other factors required for transfer to a recipient cell have not been demonstrated. Here, we characterize the functional activity of a putative tfs4-encoded VirD2-like relaxase protein. Tfs4 VirD2 was purified as a fusion to maltose-binding protein and demonstrated to bind and nick both supercoiled duplex DNA and oligonucleotides in vitro in a manner dependent upon the presence of Mg²⁺ but independently of any auxiliary proteins. Unusually, concentration-dependent nicking of duplex DNA appeared to require only transient protein-DNA interaction. Although phylogenetically distinct from established relaxase families, site-specific cleavage of oligonucleotides by Tfs4 VirD2 required the nick region sequence 5’-ATC-CTG-3’ common to transfer origins (oriT) recognized by MOBp conjugative relaxases. Cleavage resulted in covalent attachment of MBP-VirD2 to the 5’-cleaved end, consistent with conventional relaxase activity. Identification of an oriT-like sequence upstream of tfs4 virD2 and demonstration of VirD2 protein-protein interaction with a putative VirC1 relaxosome component indicate that transfer initiation of the tfs4 genomic island is analogous to mechanisms underlying mobilization of other integrated mobile elements, such as integrating conjugative elements, requiring site-specific targeting of relaxase activity to a cognate oriT sequence.

Helicobacter pylori is typically acquired in childhood and persistently colonizes the gastric mucosa of approximately half of the human population. It has the potential to cause a range of gastroduodenal diseases, including gastritis, peptic ulcer disease, mucosa-associated lymphoid tissue lymphoma, and gastric carcinoma (1–3). However, although infection is widespread and persistent, a complex interplay between multiple host, bacterial, and environmental factors determines that only about 20% of infected individuals will develop severe disease (3). A particular characteristic of H. pylori considered to contribute to its longevity in the host is its exceptional genetic variability, thought to be primarily a consequence of mutation and frequent intra- and intergenomic recombination events (4–6). With respect to the latter, the precise mechanisms of gene acquisition by horizontal transfer are not well defined but are considered to comprise both transformation and conjugative processes (7, 8). As a consequence of these collective mechanisms, an estimated 2–9% of the genome from any given isolate may be strain-specific, contributing to a predicted pan-genome approximately 4 times larger than the core genome (9).

Many strain-specific genes are localized in regions of genome diversity termed “plasticity zones” (PZs), which vary in number in the H. pylori chromosome and characteristically display low G + C content (10–12). Differences in PZ carriage and gene content may endow different H. pylori isolates with a selective advantage for niche colonization and increased virulence potential. Indeed, several genetic markers encoded specifically within PZs have been reported to associate with an increased risk for particular gastroduodenal diseases. These include homologues of strain J99 genes jhp0947, jhp0940, jhp0945, and jhp0917/918 (13–16). The latter is known to comprise a single reading frame in most isolates where it occurs and, through its positive association with the incidence of duodenal ulcer in several geographically distinct patient populations, has been termed “duodenal ulcer-promoting” gene (dupA) (16). dupA has also been reported to increase survival at low pH and  

2 The abbreviations used are: PZ, plasticity zone; oriT, origin of transfer; ICE, integrating conjugative element; T4SS, type IV secretion system; MBP, maltose-binding protein; DIG, digoxigenin; scDNA, supercoiled DNA.
increase the production of IL-8 from gastric epithelial cells and IL-12 from monocytes (16). Although DupA function is unknown, it probably encodes a VirB4 ATPase (16) presumably associated with the activity of a type IV secretion system. Support for this notion is provided by analysis of recently completed genome sequences in which dupA is located proximal to a complement of other vir-homologous T4SS genes.

In certain strains of H. pylori, four distinct clusters of T4SS genes have been identified (11, 12). The comB cluster, common to all H. pylori strains, encodes a minimal complement of T4SS components specialized for DNA uptake during transformation (7) and more recently has also been implicated in the transfer of plasmids between H. pylori strains (8). The cag pathogenicity island encoding a second T4SS is an important virulence factor, mediating translocation of the host-stimulatory CagA effector and peptidoglycan fragments to the gastric epithelium (17–19). The last two clusters, termed tfs3 and tfs4 are contained within mobilizable elements described as either transferable genomic islands or conjugative transposons (10–12). The tfs3 clusters in certain strain backgrounds have been reported to increase colonization fitness or up-regulate proinflammatory signaling from cultured epithelial cells, but an overarching phenotype remains elusive (11). The tfs4 cluster has a complement of genes similar to that of tfs3 and includes the disease marker dupA.

Recent work has demonstrated that large fragments of the tfs4 island can be horizontally transferred in a manner dependent upon the activity of a XerD family tyrosine recombinase also encoded within the tfs4 cluster (12). XerD excises the tfs4 element at conserved flanking 5'-AAAGAATG-3' motifs to generate a circular transfer intermediate that may subsequently be transferred to a recipient cell via the tfs4-encoded Tfs4 T4SS (12). Intermediate transfer steps are unknown; however, by analogy to conjugative mechanisms employed by both plasmids and other mobilizable genetic elements, such as integrating conjugative elements (ICEs), transfer probably also involves specific activity of an associated relaxase at a cis-acting origin of transfer (oriT) sequence comprising a nic cleavage site. Plasmid-encoded conjugative relaxases catalyze site- and strand-specific cleavage at nic, resulting in covalent attachment of the relaxase to the 5'-end of the nicked strand via a phosphotyrosyl linkage (20–23). Relaxases of both conjugal transposons and ICEs demonstrate similar activity, although few have been characterized to date (24–27). Targeting of specific relaxase activity to a cognate oriT sequence invariably requires the contribution of a varying number of auxiliary relaxosome proteins, which bind at oriT and facilitate oriT recognition and DNA processing by the relaxase (21, 28, 29). The relaxosome proteins are also integral to recruitment of the DNA-bound relaxase to a coupling protein for subsequent transfer via the membrane-embedded transfer machinery (30–32).

In addition to XerD and the T4SS structural vir gene complement, the tfs4 element also encodes a putative VirD2-like relaxase, which we considered might function to initiate transfer of XerD-excised tfs4 intermediates. To address this possibility, we studied the biochemical properties of Tfs4 VirD2, demonstrating it to have a distinctive in vitro site- and strand-specific nicking activity consistent with conjugative relaxase function. We additionally identified a putative tfs4 oriT region within tfs4 and demonstrate interaction of Tfs4 VirD2 with a putative VirC1-like relaxosome protein. These studies suggest that the tfs4 PZ cluster encodes a complete complement of proteins enabling self-transmission via a conjugative mechanism analogous to other self-transmissible mobile genetic elements.

**EXPERIMENTAL PROCEDURES**

**Bacterial and Yeast Strains—**H. pylori strain AB21 (33) was minimally passaged on blood agar plates (Oxoid) in a microaerobic environment. *Escherichia coli* strains XL1-Blue (recA1 endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lacZΔ(φ80lacZΔM15) Tn10 (TetR) c, BL21 (DE3) pLysS (F-ompT hsdSB (r-b-m-b-)) gal dcm (DE3) pLysS (CmR)), and ShufflE (F- lac, pro, lacQΔ(ara-leu)7697 araD139 flpA2 lacZΔ7 T7 gene 1 (phoA)PvuII phoR hphC galE (or U) galK Lact: pNBE3-r1-cDasbC (SpecR, lacp) ΔtrxB RpsL150 (StrR) Δgor (malF3) were grown at 37 °C in Luria agar or broth supplemented with kanamycin (50 μg ml⁻¹), ampicillin (50 μg ml⁻¹), or chloramphenicol (30 μg ml⁻¹) as required. *Saccharomyces cerevisiae* strain PJ69-4A (MATα trp1-901 leu2-1312 ura3-52 his3-200 gal4Δ gal80Δ lys2Δ:GAL1-HIS3 GAL2-ADE2 met2Δ:GAL7-lacZ) was grown at 30 °C and maintained in complete synthetic complete medium supplemented with 2% glucose (w/v).

**Sequence and Phylogenetic Analyses—**Genome sequences were retrieved from the NCBI database from where PSI-BLAST searches were also performed. Sequence comparison employed the EMBOSS Needle alignment tool, and identification of palindromic sequence using the EMBOSS Palindrome program. Coiled coil predictions were performed using COILS and Paircoil2. For phylogenetic analyses, 33 relaxase sequences, comprising 2–4 sequences representative of each of the different MOB clades (34), were downloaded from the NCBI protein database. A FASTA-formatted sequence file comprising the first 300 amino acids of each sequence (N-terminal relaxase domain) was aligned using the MEGA 4 implementation of ClustalW. Phylogenetic trees were calculated by MEGA 4 (35) using the neighbor-joining method (36). Bootstrap analysis was performed with 2000 resampled data sets from evolutionary distance, based on amino acid sequence alignments.

**Cloning—**Standard techniques for DNA manipulations were used in *E. coli* strain XL1-Blue. Genomic DNA was prepared from *H. pylori* strain AB21 after growth for 48 h on plates using a genomic DNA preparation kit (Sigma). Phusion polymerase (New England Biolabs) was used to amplify *H. pylori* DNA sequences according to the manufacturer’s recommendations using primers listed in Table 1. The virD2 gene was amplified with primers virD2F1 and virD2R1 for the full-length gene or virD2R2 for the relaxase domain only (Table 1) and then cloned directly into pGEM-T-Easy or digested with BamHI and cloned into pMal-c2X (NEB) for expression with an N-terminal MBP fusion. The virC1 gene was amplified with primers virC1F and virC1R and cloned into pET28a (Novagen). A tfs4 fragment containing virD2 and upstream intergenic region was amplified with primers virD2R1 and virD4F and cloned into pGEM-T-Easy. For the yeast two-hybrid assay, tfs4 virD2, virC1, 0449, and 0450 homologous genes were amplified from gDNA prepared from strain AB21 with the primers listed in Table 1. After...
digestion with BamHI for VirD2 and EcoRI plus BamHI for the other genes, the resulting fragments were then cloned into pGAD424 and pGBT9. All constructs were verified by sequencing, and fts/4 gene sequences were deposited in GenBank™ with accession numbers KF438085 (virD2 region), KF438086 (0449), KF438087 (virC1) and KF438088 (virC2).

**Protein Purification—**MBP fusions were expressed in 500-ml cultures of _E. coli_ Shuffled (New England Biolabs) in 2xYT medium (8 g of Bacto tryptone, 5 g of yeast extract, and 5 g of NaCl per 500 ml) and induced with 1 mM isopropyl _β_ -d-thiogalactopyranoside in the presence of 0.2% glucose for 4 h at 25 °C. Bacteria were harvested and lysed by sonication in buffer A (50 mM Tris, 200 mM NaCl, 1 mM EDTA, 1 mM DTT, pH 7.5) in five 10-s bursts at an amplitude of 10%

### TABLE 1

| Plasmids          | Relevant genotype and/or description | Reference or source         |
|-------------------|---------------------------------------|------------------------------|
| pET28a            | T7 expression vector, Km<sup>a</sup>  | Novagen                      |
| pMal-c2X          | malle fusion vector, Ap<sup>a</sup>   | New England Biolabs          |
| pGEM-T Easy       | High copy number cloning vector, Ap<sup>a</sup> | Promega                     |
| pSB14             | RP4 oriT, Km<sup>a</sup>             | Ref. 45                      |
| pGAD424           | orCol1 orCol2 LEU1 P<sub>Adr</sub>:GAL4<sup>a</sup> activator domain::MCS | Ref. 38                      |
| pGBT9             | orCol1 orCol2 TRP1 P<sub>Adr</sub>:GAL4<sup>a</sup> binding domain::MCS | Ref. 38                      |
| pRD200            | pGEM-TEasy:VirD2 fts/4 + upstream intergenic flanking sequence from strain AB21 | This study                   |
| pRD205            | pGEMEasy::virD2 fts/4 + upstream intergenic flanking sequence from strain AB21 | This study                   |
| pMal-D-2          | pMal::virD2 fts/4 (1–1911 bp)         | This study                   |
| pMal-D2(N)        | pMal::virD2 fts/4 (1–771 bp)          | This study                   |
| pET28a-C1         | pET28a:virC1 fts/4 (1–466 bp)         | This study                   |
| pGAD424-D2        | pGAD424::virD2 fts/4 (1–1911 bp)      | This study                   |
| pGAD424-C1        | pGAD424:virC1 fts/4 (1–657 bp)        | This study                   |
| pGAD424-0449      | pGAD424::0449 fts/4 (1–285 bp)        | This study                   |
| pGAD424-0450      | pGAD424::0450 fts/4 (88–1098 bp)      | This study                   |
| pGBT9-D2          | pGBT9::virD2 fts/4 (1–1911 bp)        | This study                   |
| pGBT9-C1          | pGBT9::virC1 fts/4 (1–657 bp)         | This study                   |
| pGBT9-0449        | pGBT9::0449 fts/4 (1–285 bp)          | This study                   |
| pGBT9-0450        | pGBT9::0450 fts/4 (88–1098 bp)        | This study                   |

**DNA Binding Assay—**Plasmid DNA was prepared from overnight cultures of _E. coli_ XL1-Blue using a plasmid extraction kit (Qiagen). In standard 20-μl reactions, protein and 100 ng of DNA were mixed in binding buffer (20 mM Tris, pH 7.5, 5 mM MgCl<sub>2</sub>, 100 mM NaCl) and incubated at 37 °C for 30 min. To protease-treat products, 1 μl of 0.1% SDS and 1 μl of 20 mg ml<sup>–1</sup> proteinase K (Sigma) were added, and incubation continued for an additional 30 min. Samples were subsequently mixed with loading dye (50% glycerol, 0.1% bromophenol blue) and immediately loaded onto a 0.8% agarose gel containing ethidium bromide.

**Oligonucleotide Cleavage Assay—**This method was as described previously (23) with modifications for use with digoxigenin (DIG)-labeled oligonucleotides (Sigma). Briefly, the labeled oligonucleotide (0.1 pmol) and protein were incubated in a 10-μl reaction containing buffer (20 mM Tris, pH 7.5, 5 mM MgCl<sub>2</sub>, 100 mM NaCl) for 2 h at 37 °C. Unlabeled competitor (100×) oligonucleotides C and N (10 pmol) were added where indicated. Samples were protease-treated by adding either 1 μl of 0.1% SDS plus 1 μl of proteinase K (20 mg ml<sup>–1</sup>) or 1 μl 0.1 M CaCl<sub>2</sub> plus 1 μl 1× trypsin-EDTA solution (Sigma) and incubating for a further 30 min. Immediately after incubation, 10 μl of 2× sample buffer (12% Ficoll 400, 7 μl urea, 0.1% (w/v) bromphenol blue, 0.1% (w/v) xylene cyanol in TBE) was added, and samples were denatured by heating to 70 °C for 3 min. Samples were resolved on denaturing 20% polyacrylamide, TBE 7 M urea gels run at 200 V for 100 min. DNA was then transferred to Hybond N<sup>+</sup> and cross-linked by exposure to UV light. Labeled DNA was subsequently visualized using a DIG luminescent detection kit (Roche Applied Science).

**Pull-down Assay—**Fusion proteins were separately expressed in 250-ml cultures of _E. coli_ for each pull-down experiment, harvested, and lysed by sonication in buffer A (50 mM Tris, 200 mM NaCl, 1 mM EDTA, 1 mM DTT, pH 7.5). Soluble protein lysates containing MBP or MBP fusions were clarified by centrifugation and then incubated with 0.5 ml of amylase resin in buffer A in a 2-ml Eppendorf tube for 90 min at 4 °C with mixing. The resin containing immobilized protein was subsequently washed 10 times with 1 ml of buffer A and then mixed with the soluble lysate from _E. coli_ expressing His-VirC1. Resin
**H. pylori Tfs4 VirD2 Relaxase Activity**

**RESULTS**

**Sequence Analysis of Tfs4 VirD2**—Two VirD2-like proteins can be identified within the genomes of some sequenced *H. pylori* strains based on sequence similarity in the N-terminal region of the proteins to the conserved VirD2 relaxase domain, COG3843 in the conserved domain database (E value = 1.19e-65). In strain P12, representative proteins are encoded by genes HPP12_1353 and HPP12_0451, the latter being located proximal to a complement of T4SS-encoding *vir* structural genes within the tfs4 cluster (Fig. 1A). Both proteins contain conserved N-terminal relaxase motifs (I–III) (40, 41) (Fig. 1B) with sequence characteristics most closely resembling the MOB relaxase family, which includes the well studied relaxase Trl encoded on the *E. coli* plasmid RP4 and *Agrobacterium tumefaciens* tfs3/tfs4-encoded VirD2 (34). However, overall, the proteins share minimal sequence identity; *A. tumefaciens* pTi VirD2 has 9.8% identity and 20% similarity to Tfs4 VirD2 and 11.8% identity and 21% similarity to Tfs3 VirD2, whereas Tfs3 and Tfs4 VirD2 proteins share 20.5% identity and 33.2% similarity, although there is broadly comparable secondary structure in the N-terminal relaxase portion of the proteins (data not shown). The C-terminal region of Tfs4 VirD2 is not identical to known sequences but comprises several regions with coiled-coil potential. Tfs3 VirD2 (amino acids 1–677) has a similar disposition of motifs as Tfs4 VirD2. Shown are confidently predicted coiled coil (COILS and Paircoil2) (CC) and coiled coil predicted by COILS only (cc). This figure was adapted from Ref. 41.

**Phylogenetic Analysis and Identification of a Putative tfs4 oriT Region**—To define the relationship between *tfs3/tfs4*-encoded VirD2 proteins with established MOB relaxase families, a phylogenetic analysis was performed using the N-terminal sequence (1–300 amino acid residues) of 33 relaxases repre-
sentative of the main MOB families that share the characteristic of a single Motif I active site tyrosine residue (34). The resulting phylogeny (Fig. 2) indicates that, although Tfs3 and Tfs4 VirD2 proteins have sequence-conserved relaxase motifs strongly reminiscent of the MOBα family of relaxases, together with the MOBγ family, they are more ancestrally remote and are not obviously classified within the established MOB clusters.

Relaxases of the same MOB family and motif signature often recognize and nick within the same cognate oriT sequence (34) comprising both a highly conserved nick region sequence and associated upstream inverted repeat, the latter being more variable in sequence and containing binding sites for both relaxase and auxiliary relaxosome proteins (42) (Fig. 3A). The MOBα family A. tumefaciens VirD2 (MOBp12) and TraI of the conjugative plasmid RP4 (MOBp11) both require the core hexanucleotide sequence 5′-ATCCCTG-3′ for cleavage activity in vitro, although a consensus nick sequence can be derived that extends to additional flanking bases, 5′- (C/T)ATCCTG(C/T)-3′ (29, 40, 43). Although Tfs4 VirD2 appears phylogenetically distinct from the MOBα family, its relaxase motifs are highly conserved relative to the MOBp12/p11 subclades (Fig. 1). As such, we speculated that it might therefore have similar substrate sequence specificity and, as a self-transmissible genomic element (12), would necessarily also contain an oriT sequence for the initiation of transfer. We therefore searched for a MOBα family consensus motif within the tfs4 gene cluster of strain P12. Three such sequences were apparent, two within the coding sequence of xerD and virB10 and the other in an intergenic region immediately upstream of the coding sequence of virD2. Further examination of the intergenic sequence identified a perfect 25-bp inverted repeat immediately proximal to the putative 5′-TATCCTGC-3′ nick motif, providing this region with features characteristic of an oriT sequence (Fig. 3). Notably, an equivalent oriT-like sequence comprising an identical MOBα nick motif was also identified upstream of the virD2 in the PZ tfs3 cluster (Fig. 3). BLAST alignments determined that the 104-bp intergenic sequences incorporating the putative PZ oriTs (Fig. 3) are invariably conserved in the majority of H. pylori strains for which sequence is presently known (tfs4 sequence variant in 20 strains (5e–20) and the tfs3 sequence in 11 strains (4e–21)), further alluding to the functional significance of this region.

Expression and Purification of Tfs4 VirD2—Homologues of P12 tfs4 virD2 genes were identified in a selection of clinical isolates from our strain collection by PCR typing, and then sequences for both full-length protein (amino acids 1–637) and the N-terminal relaxase domain (amino acids 1–257) were cloned and expressed in E. coli as N-terminal maltose-binding protein (MBP) fusion proteins to enhance solubility and stability; initial efforts to express equivalent VirD2 proteins with a minimal His tag resulted in low levels of expression of unstable and almost entirely insoluble protein. Expressed MBP fusion proteins were subjected to a three-stage purification protocol in which they were first purified by affinity chromatography, fractionated by size exclusion chromatography, and finally purified in an ion exchange separation step. The latter step was required to remove co-purifying DNA from the size exclusion MBP-VirD2 fractions (Fig. 4A). Of note, both full-length VirD2 and N-terminal domain MBP fusions (MBP-VirD2 and MBP-VirD2(N), respectively) were found to elute in the void volume during size exclusion chromatography, suggesting protein aggregation, possibly due to the presence of contaminating DNA or the formation of quaternary complexes much larger than the predicted ~121-kDa (MBP-VirD2) or ~76-kDa (MBP-VirD2(N)) purified monomeric MBP-VirD2 fusion proteins observed by SDS-PAGE (Fig. 4B).

Tfs4 VirD2 Strand-specific Relaxase Activity—Several relaxases, including TrwC of plasmid R388 and TraI of F plasmids (both MOB, family), bind and nick at their cognate oriT in vitro in the absence of auxiliary factors, requiring only the presence of Mg2+ and supercoiled plasmid DNA (scDNA) for nicking activity (31, 44). To assess the activity of Tfs4 VirD2 in this context, we examined the general effects of incubating purified MBP-VirD2 with a selection of plasmid DNAs, each containing

FIGURE 2. Phylogenetic tree of relaxase families containing one active Tyr in the Motif I catalytic center. Representative relaxase sequences were selected from the MOB families defined previously (34). The MOBα family of relaxases incorporates the subclades P1–P7, P11–P14, Q1–Q3, and HEN, as indicated. The diverse MOBγ clade, of which the most populous MOBγ subclade is shown, is ancestrally related to the MOBα family. H. pylori Tfs3 (3) and Tfs4 (4) VirD2-like relaxases are shown not to be contained within established MOB clades. MOBγ subclades containing plasmid RP4 (1), endogenous H. pylori plasmids (2) and A. tumefaciens VirD2 relaxases (5) are indicated. The percentage of trees (2000 in total) supporting each node is shown.
**H. pylori Tfs4 VirD2 Relaxase Activity**

![Diagram](image)

**FIGURE 3. Comparison of the E. coli RP4 oriT with putative P2 oriT regions.** A, sequence of the well characterized RP4 oriT region highlighting the 16-bp inverted repeat (arrows) immediately proximal to the nick region comprising the conserved MOB family core nick sequence 5’-ATCCTG-3’ (position of nic cleavage site indicated by a triangle). The binding site of the RP4 TraI relaxase is shown within a box adjacent to the core conserved nick sequence (shaded). B, sequence conservation of tfs4 and tfs3 intergenic oriT regions upstream of encoded VirD2-like proteins. Perfect (tfs4) and imperfect (tfs3, one mismatch) 9-10-bp distal and proximal arms (arrows) of a 25-bp inverted repeat characteristic of oriT regions are evident immediately 5’-proximal to the putative tfs3 and 5’-ATCCTG-3’ tfs4 nick region. The tfs4 sequence shown is invariantly conserved between both P12 and AB21 strains. Shading highlights sequence identical to the tfs4 region.

A different putative nick region using an electrophoretic mobility shift assay. Plasmids, prepared by conventional alkaline lysis, included the H. pylori shuttle vector pSB14 containing a cloned RP4 oriT (45) and two pGEMT-based vectors, one containing cloned tfs4 virD2 plus the putative upstream intergenic oriT sequence (pRD205) and the other containing just tfs4 virD2 (pRD200). In all cases, incubation of plasmid (100 ng) with increasing amounts of MBP-VirD2 (0.05–0.5 pmol) resulted in a concentration-dependent conversion of scDNA to both the open circle, nicked form and a non-migrating species retarded in the gel loading wells (Fig. 4C, lanes 2–6). Subsequent treatment with detergent and protease (Fig. 4C, lane 7) released plasmid from wells as both supercoiled and nicked species, confirming the non-migrating plasmid to be in the nucleoprotein complex. Effects were most prominently observed with pRD205 containing the putative tfs4 oriT, and notably, whereas a small and broadly constant amount of linear product was observed in all incubations regardless of MBP-VirD2 concentration, pRD205 was the only plasmid in which linear product was no longer evident following protease treatment and release from VirD2 binding (Fig. 4C, ii). This suggests that in complex with linear plasmid containing a particular oriT, an excess of VirD2 can mediate an end-joining reaction in vitro, resulting in resealing of the phosphodiester backbone. All effects required the presence of MgCl\(_2\) and were not observed when plasmid was incubated with MBP alone (data not shown). Collectively, these results demonstrate that, in limiting concentration, tfs4 VirD2 can reversibly bind scDNA independently of other factors in vitro and catalyze a strand-specific nicking reaction that is dependent upon the presence of Mg\(^{2+}\). An excess of protein, however, results in seemingly irreversible formation of large nucleoprotein complexes or aggregates requiring protein denaturation for plasmid release.

**Sequence-specific Cleavage of Oligonucleotides by Tfs4 VirD2**—The sequence specificity for Tfs4 VirD2 binding and nicking activity could not be determined from the previous experiments because all plasmids contain the 5’-ATCCTG-3’ hexanucleotide in their backbone sequence in addition to the putative nick motifs within the cloned oriT regions. Therefore, to more clearly demonstrate nicking activity of Tfs4 VirD2 and to determine its target sequence requirements, two 30-base substrate oligonucleotides were designed for use in single-stranded DNA cleavage assays. The first was based on the putative tfs4 oriT nick sequence (“Tfs4”) invariantly conserved in unrelated H. pylori strains AB21 and P12, and a second was based on the RP4 oriT sequence (“RP4”) identical to the cloned fragment within pSB14 (45). Because relaxase activity is strictly a component of the N-terminal relaxase domain (46–48), we employed an MBP fusion to N-terminal VirD2, MBP-VirD2(N), in these assays to confine observations to this region of the protein. Subsequent cleavage products resulting from incubation of MBP-VirD2(N) with DIG-labeled oligonucleotides were separated in denaturing polyacrylamide gels and analyzed by Southern blotting.

Incubation of MBP-VirD2(N) with 5’ DIG-labeled Tfs4 oriT oligonucleotide resulted in cleavage of the 30-mer oligonucleotide to a marginally smaller product, indicating loss of a small (<10 nucleotides) 3’-unlabeled fragment. That mobility of the large 5’-labeled fragment was not retarded in the gel indicates that VirD2 does not bind to the 3’-cleaved end and further, given the large size of this product, that cleavage occurs either within or immediately 3’ of the 5’-ATCCTG-3’ sequence (Fig. 5, blot 1), located 9 nucleotides from the 3’-end of the Tfs4 oligonucleotide (Table 2).

Conversely, incubation with the identical 3’ DIG-labeled 30-mer oligonucleotide resulted in a non-migrating product observed in the gel well, corresponding to the 3’-cleavage fragment attached at its 5’-end to MBP-VirD2(N) protein. Subsequent treatment of the retarded nucleoprotein complex with proteases liberated the small (~9-mer) 3’-oligonucleotide cleavage product, the gel mobility of which differed according to the size of the trypsin or proteinase K-proteolyzed peptide fragment of VirD2 remaining attached (Fig. 5, blot 2, lanes 3 and 4). In competition experiments, both VirD2 binding to and nicking of the labeled substrate could be inhibited by adding a 100-fold excess of unlabeled competing Tfs4 oligonucleotide but was not affected by the presence of excess unlabeled random sequence oligonucleotide, confirming nick sequence specificity of the Tfs4 VirD2 active site to sequence within the Tfs4 oligonucleotide (Fig. 5, blot 2, lanes 5 and 6). Binding and nicking activity was subsequently determined to be specifically dependent upon the 5’-ATCCTG-3’ hexanucleotide sequence by lack of discernable VirD2 activity toward a DIG-labeled Tfs4 oligonucleotide with a 6-position base-substituted 5’-ATCCTG-3’ sequence (Fig. 5, mut/blot 3a). Finally, an oligonucleotide containing the RP4 oriT nick region (RP4), comprising the MOB family consensus motif in an entirely different flanking sequence context, was also nicked by Tfs4 VirD2. RP4 and Tfs4...
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Prevalence of the Tfs4 VirD2 Nick Sequence
—The collective
results of the cleavage assays determine that Tfs4 VirD2 specif-
ically recognizes the conserved hexanucleotide nick motif
5’-ATCCTG-3’ in vitro. Because certain ICEs have been demon-
strated to mobilize chromosomal DNA, plasmids, and other
GIs that lack machinery for self-mobilization (27, 49), we con-
sidered whether there might be additional cognate nick sites
outside of the tfs4 PZ cluster that might be subject to Tfs4
VirD2 activity. To investigate this, the consensus sequence
(C/T)ATCCTG(C/T), incorporating the sequence context of
PZ relaxase activity. To investigate this, the consensus sequence
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VirD2(N) (lane 2) resolved by 10% SDS-PAGE. C, MBP-VirD2 DNA
binding activity. Incubation of MBP-VirD2 with 100 ng of pSB14 (containing
cloned
oriT
(lane 1) is efficiently removed in a subsequent ion exchange step (lane 2). B
three-stage purification of MBP-VirD2. *, purified MBP-Tfs4 VirD2 (lane 1) and
MBP-Tfs4 VirD2(N) (lane 2) resolved by 10% SDS-PAGE. C, MBP-VirD2 DNA
binding activity. Incubation of MBP-VirD2 with 100 ng of pSB14 (containing
cloned
oriT
(i), pRD205 (pGEM-TEasy containing cloned tfs4 virD2 and
upstream intergenic sequence) (ii), or pRD200 (pGEM-TEasy containing
cloned tfs4 virD2 only) (iii) results in a decrease in supercoiled plasmid and
concomitant increase in both open circle (nicked) forms and loading well-
retarded nucleoprotein complexes (black arrow) as protein concentration
increases. Effects are most pronounced with plasmid pRD205. Notably, linear
plasmid is also absent from the pRD205 sample following protease K treat-
ment. Lanes 1–6, 0, 0.05, 0.1, 0.15, 0.3, and 0.5 pmol of MBP-VirD2; lane 7, 0.5
pmol of MBP-VirD2 treated with protease K; lane 8, linear plasmid generated
by restriction enzyme digest. All reactions were performed at 37 °C in the
presence of MgCl2. OC, open circle (nicked); SC, supercoiled, L, linear.
oligonucleotide cleavage products appeared identical, indicat-
ing cleavage at the same position within the RP4 nick sequence,
5’-TATCCTGC-3’, common to both Tfs4 and RP4 oligonu-
cleotides. Tfs4 VirD2 is therefore indicated to have sequence-
specific nicking activity, which, similar to a subset of non-
MOBp family relaxases, is independent of auxiliary factors in
vitro, and a nick sequence specificity that conforms to that of
the MOBp family consensus motif, consistent with the charac-
ter of its signature relaxase motifs.

Prevalence of the Tfs4 VirD2 Nick Sequence—The collective
results of the cleavage assays determine that Tfs4 VirD2 specif-
ically recognizes the conserved hexanucleotide nick motif
5’-ATCCTG-3’ in vitro. Because certain ICEs have been demon-
strated to mobilize chromosomal DNA, plasmids, and other
GIs that lack machinery for self-mobilization (27, 49), we con-
sidered whether there might be additional cognate nick sites
outside of the pTi
PZ cluster that might be subject to Tfs4
VirD2 activity. To investigate this, the consensus sequence
(C/T)ATCCTG(C/T), incorporating the sequence context of
both the putative tfs4/tfs3 oriT nick sequence and known nick
regions of MOBp family relaxases, was used as a search thread
to interrogate the genome sequence of strain P12. Accounting
for both strands, 69 sites in total were identified, 24 of these
comprising the conserved 8-bp 5’-TATCCTG(C/T)-3’ sequence of
the putative tfs4 oriT nick motif (supplemental Table 1).
Next, to define these regions as candidate oriT regions spec-
ifying for
in vivo relaxase activity, the first 50-bp sequence
upstream of each putative nick motif was assessed for the pres-
ence of inverted repeats using the EMBOSS Palindrome pro-
gram set to detect palindromes of 8 bp or more with one per-
missible mismatch. Using this criterion, which reflects the
sequence and motif disposition of RP4, A. tumefaciens pTi, and
the putative tfs4 oriT regions, seven sequence regions were
identified. However, of these, only tfs4 and tfs3 oriT regions
were intergenic, suggesting that PZ relaxase activity
in vivo may be restricted to these specific chromosomal regions, at least in
strain P12. Interestingly, the 8-bp tfs4 nick motif was also evi-
dent in the endogenous pHPP12 plasmid and also conserved in
several other H. pylori plasmids (supplemental Table 1). How-
ever, it was not present in all H. pylori plasmids and was con-
tained within coding sequence, and the inverted repeat was

FIGURE 4. Purification and DNA binding activity of Tfs4 VirD2. A, DNA
cr-factionating in the MBP-VirD2 size exclusion chromatography fraction
(lane 1) is efficiently removed in a subsequent ion exchange step (lane 2). B
three-stage purification of MBP-VirD2. *, purified MBP-Tfs4 VirD2 (lane 1) and
MBP-Tfs4 VirD2(N) (lane 2) resolved by 10% SDS-PAGE. C, MBP-VirD2 DNA
binding activity. Incubation of MBP-VirD2 with 100 ng of pSB14 (containing
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(i), pRD205 (pGEM-TEasy containing cloned tfs4 virD2 and
upstream intergenic sequence) (ii), or pRD200 (pGEM-TEasy containing
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5’-TATCCTGC-3’, common to both Tfs4 and RP4 oligonu-
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specific nicking activity, which, similar to a subset of non-
MOBp family relaxases, is independent of auxiliary factors in
vitro, and a nick sequence specificity that conforms to that of
the MOBp family consensus motif, consistent with the charac-
ter of its signature relaxase motifs.

Prevalence of the Tfs4 VirD2 Nick Sequence—The collective
results of the cleavage assays determine that Tfs4 VirD2 specif-
present in the immediate 3'- rather than 5'-proximal flanking sequence.

Identification of a Putative VirC1 Protein and Interaction with VirD2—Elaboration of relaxase function in vivo occurs in the context of the relaxosome of complex auxotrophic proteins, which both assist relaxase-mediated cleavage at the cognate oriT and recruitment of relaxase-bound transfer intermediates to the membrane-localized secretion machinery (21, 28, 30–32). In Agrobacterium, the relaxosome comprises VirD1, VirD2, VirC1, and VirC2 (32). Of these, the ParA/Mind-like ATPase protein, VirC1 mediates relaxosome formation at the oriT-like border sequences and coordinates transfer of nucleo-protein complexes to the secretion channel (32).

In H. pylori tfs4, a virC1 homologue (gene 0448) can be identified as the first of three contiguous genes convergent with virD2 (Fig. 6A). The encoded protein shares 22.8% identity and 39.8% similarity with A. tumefacians VirC1 and has the conserved domain structure and ATPase motifs characteristic of the ParA, VirC1, and RP4 TraL family (50). The two other genes comprising the putative virC1 operon (homologues of genes 0449 and 0450 in the P12 genome) are of unknown function, appearing unique to H. pylori tfs3/tfs4 clusters.

Because VirC1 proteins are demonstrated to interact with VirD2 and other relaxosome components, we first employed the yeast two-hybrid assay to investigate the possibility of equivalent interactions between the Tfs4 VirD2 and VirC1-like proteins. Because genes encoded within the same operon often function in the same biological context, we also included 0449 and 0450 in our yeast two-hybrid screens as additional candidate components of a Tfs4 relaxosome. The four sequences were cloned into yeast two-hybrid vectors pGAD424 (GAL4 activation domain fusion/prey vector) and pGBT9 (GAL4 binding domain fusion/bait), and all heterologous bait/prey pairwise combinations were co-transformed into S. cerevisiae strain PJ69-4A (38). Positive interactions were indicated by activation of reporter combinations (HIS3, ADE2, and lacZ), enabling direct assessment of the yeast two-hybrid phenotype by the color of transformant colonies growing on minimal selective medium, and subsequently also by a β-galactosidase assay.

None of the fusions were found to self-activate yeast reporters in control transformations. Pairwise interaction screens indicated reciprocal VirD2-VirD2 and VirD2-VirC1 interactions both by stringent growth selection and a β-galactosidase assay (Table 3). No other interactions were strongly predicted, although non-reciprocal activation of two reporters suggested possible weak or transient interaction between VirD2–0449 and VirD2–0450 (Table 3).

To provide biochemical evidence in support of the VirD2-VirC1 interaction, we analyzed binding of VirC1, expressed as a soluble His6-tagged protein in E. coli, to either MBP or MBP-VirD2 and MBP-VirD2(N) fusions immobilized on amylase
**H. pylori Tfs4 VirD2 Relaxase Activity**

**TABLE 3**

|                      | VirD2<sup>a</sup> | VirC1<sup>b</sup> | 0449<sup>c</sup> | 0450<sup>d</sup> | VirD2<sup>e</sup> | VirC1<sup>f</sup> | 0449<sup>g</sup> | 0450<sup>h</sup> | VirD2<sup>i</sup> | VirC1<sup>j</sup> | 0449<sup>k</sup> | 0450<sup<l</sup>
|----------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|
| −His/<sup>e</sup> Ade<sup>e</sup> | +                 | −                 | −                | −                | +                 | −                 | −                | −                | +                 | −                 | −                | −                |
| −His<sup>e</sup> | +                 | +                 | +                | +                | +                 | +                 | +                | +                | +                 | +                 | +                | +                |
| lacZ<sup>e</sup> | +                 | +                 | −                | −                | +                 | −                 | +                | +                | +                 | +                 | +                | +                |

<sup>a</sup> Prey fusions were constructed in the pGADT7 vector.
<sup>b</sup> Bait fusions were constructed in the pGBK9 vector.
<sup>c</sup> YMM plates were supplemented with Met and uracil and lacked either His or both His and Ade, as indicated.
<sup>d</sup> lacZ reporter activity was assessed both by blue colony color on 5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside plates and subsequently by a β-galactosidase assay.

**Discussion**

Relaxase proteins are key essential components in the processing and mobilization of bacterial DNA via conjugative mechanisms. Commonly, they mediate the transfer of endogenous plasmids between strains but are also integral to the dissemination of self-transmissible mobile genetic elements, such as conjugative transposons and ICEs (51). The tfs4 PZ gene cluster is described as a self-transmissible genomic island/conjugative transposon (11, 12), although its function and clinical relevance remains unclear, particularly because it appears to be inactive in many strain backgrounds due to either fragmentation or inactivating mutation. However, interstrain transfer of large fragments of the tfs4 gene cluster has recently been demonstrated (12), suggesting a mechanism for rapid reconstitution of inactive T4SSs and alluding to a significant, but perhaps sporadic, benefit for maintenance of Tfs4 T4SS capability within the *H. pylori* population. Because relaxase activity would probably be critical for this process, we sought to examine the functional activity and biochemical properties of a VirD2-like relaxase encoded within the tfs4 cluster.

As noted for a homologous protein (HP1004) in an early in silico analysis of reference strain 26695 (41), the protein we define here as Tfs4 VirD2 comprises a well defined N-terminal relaxase domain with relaxase sequence motifs (I–III; Fig. 1) similar to the well characterized conjugative RP4 TraI and *A. tumefaciens* VirD2 proteins of the MOB<sub>p</sub> superfamily. Surprisingly, however, despite an evident ancestral relationship to these proteins, Tfs4 VirD2, together with Tfs3 VirD2, appear phylogenetically distinct and are not clearly assigned to any of the established MOB families. In this respect, the PZ VirD2 proteins are quite atypical because distinct clades and even subclasses within the same MOB relaxase family invariably develop different patterns of signature sequence conservation within component relaxase motifs (34).

Nevertheless, consistent with the sequence specificity of many MOB<sub>p</sub> family relaxases for the consensus 5′-(C/T)ATC-CTG(C/T)-3′ oriT nick sequence, Tfs4 VirD2 also demonstrates classical metal ion (Mg<sup>2+</sup>)-dependent relaxase activity at this core motif; following cleavage, the protein becomes tightly attached to the 5′ terminus of the nicked fragment and remains attached as a peptide fragment following proteolytic digest. Conventionally, this interaction is mediated by a phosphotyrosyl linkage between the relaxase Motif I active site tyrosine residue and the 5′ DNA terminus at the nic cleavage site (20–23) and appears consistent with our observations for Tfs4 VirD2. Indeed, the ability of purified Tfs4 VirD2 to specifically nick DNA in vitro in the absence of any other factors is a clear demonstration that it contains the active site required for phosphodiester bond cleavage at the nic site.

Cleavage of oligonucleotides containing an appropriate nick region in the absence of other relaxosome proteins is a commonly reported in vitro activity of purified relaxase proteins. However, nicking of duplex plasmid DNA containing equivalent nick sequences invariably requires the additional presence of one or several auxiliary relaxosome proteins and protease treatment to observe conversion of supercoiled plasmid to nicked forms (29). Tfs4 VirD2 differs somewhat in these respects; although all Tfs4 VirD2 nicking activity requires Mg<sup>2+</sup> and supercoiled plasmid, conforming to requirements of other relaxases (20–23, 29, 44), nicking is observed entirely independently of other proteins and, more unusually, protein denaturant. This latter observation indicates that at low concentrations, the association of Tfs4 VirD2 with duplex DNA is more transient than observed for other relaxases, allowing for release of protein-free nicked intermediate following single strand cleavage.

Characteristically, relaxases that function to mobilize plasmids exhibit a long half-life in DNA complex (52). Although the shorter half-life of the Tfs4 VirD2-DNA interaction seen here is clearly a component of protein concentration, the fact that it is observed at limiting concentrations of VirD2 suggests it to be functionally significant. At higher concentrations, plasmid is seen to be increasingly bound in more stable, if not irreversible, nucleoprotein complex (Fig. 4C, ii), which, as suggested by size exclusion chromatography, may be explained by a tendency toward VirD2 aggregation or multimerization at higher protein concentrations in vitro. Although nicked plasmid is clearly evident at low VirD2 concentrations in the absence of denaturants, that protease treatment of nucleoprotein complexes recovers both nicked and more topologically constrained (supercoiled) forms suggests that when in complex with Tfs4 VirD2, plasmid is in equilibrium between nicked and ligated states, as proposed previously (29). Resealing of the phosphodiester backbone is a complementary activity of relaxase function necessary for termination of DNA strand transfer and, in the
case of relaxases with a single active site tyrosine, usually requires relaxase dimerization (53). Consistently, the yeast two-hybrid analyses indicate that Tf4 VirD2 may also dimerize, although a propensity for homomultimerization of purified protein in vitro is also observed. Interestingly, we also observed linearization of plasmid upon incubation with even the lowest concentration of Tf4 VirD2. Cleavage of both DNA strands may reflect nonspecific activity, as similarly observed for the BmpH Mob protein of the Tn5520 mobilizable transposon (54) and for the Orf20 relaxase of the conjugative transposon Tn916 when incubated with DNA in the absence of an auxiliary specificity protein (24). A similar requirement may contribute to the residual in vitro activity of Tf4 VirD2 seen here. More remarkably, whereas the linear species appeared to diminish at higher VirD2 concentrations, it was entirely absent from protease-treated VirD2-pRD205 complexes (Fig. 4C, ii), suggesting that when in nucleoprotein complex, in vitro at least, VirD2 also has a capacity for rejoining of both single and double DNA strands. Whether these observations represent novel catalytic activity of Tfs4 VirD2 or, more simply, artificial in vitro activity resulting from a saturating concentration of fusion protein in high molecular weight nucleoprotein complex remains to be determined. With respect to the latter possibility, nonspecific cleavage of duplex DNA in vitro appears to be most notably associated with transposon mobilization proteins (24, 54), and it may therefore be the case that the observed atypical Tf4 VirD2 activities are reflective of subtle functional differences, prominent in vitro, of a non-plasmid class of relaxase.

Although Tfs4 VirD2 bound and nicked all plasmids in this study, it appeared to have the most pronounced effect on supercoiled pRD205, comprising the putative tfs4 oriT, within the comparable concentration range used. Because the 5′-ATC-CTG-3′ motif was present in all templates, we consider that the enhanced activity toward pRD205 was specifically a component of the broader sequence context of the cloned tfs4 oriT. Although in vitro, the nick-region proximal inverted repeat probably offers optimal tight positional binding for Tfs4 VirD2 nicking, a previous observation that an N-terminal fragment of Tfs4 VirD2 (termed Rlx2) expressed in trans could not be demonstrated to nick the cloned Rlx2 oriT in pSB14 by a primer extension assay (45) suggests involvement of other factors for nick region targeting in vivo. In this respect, we also demonstrated direct interaction between Tfs4 VirD2 and a putative tfs4-encoded VirC1 homologue. In the T-DNA transfer system of A. tumefaciens, the VirC1 ATPase protein nucleates relaxosome formation at oriT by directly interacting with VirD2 and other relaxosomal proteins and has a further role in recruitment of transfer intermediates to the T4SS channel-associated coupling protein (32). By analogy, we speculate that the Tfs4 VirC1 homologue may fulfill similar functions at the tfs4 oriT, possibly in association with additional yet-to-be-confirmed relaxosome components.

As potential specificity determinants for Tfs4 VirD2 activity, both auxiliary proteins and cognate oriT would conventionally function to selectively target relaxase activity to one specific nick sequence of the many identical or similar sequences encoded within the genome. Consistently, we found a modest distribution of candidate orITs within the H. pylori genome, suggesting that activity of the PZ-encoded relaxases is specifically targeted to the tfs3 and tfs4 clusters and that they most likely function in mobilization of these regions. Because both PZ clusters and endogenous plasmids each encode an associated relaxase and sequence diverse oriT sequences, albeit with the same conserved nick region, we speculate that reciprocal relaxase activity at even these similar oriT sequences may not be permissible in vivo. In this respect, mobilization of endogenous plasmids by PZ T4SSs has not been demonstrated (8, 12).

Transfer of segments of the tfs4 cluster has been shown to be dependent upon the function of the tfs6-encoded XerD tyrosine-like recombinase for chromosomal excision (12). Our data indicate that the VirD2-like relaxase will also be integral to this process and, via activity at oriT, may initiate transfer of PZ genes in a manner similar to ICE mobilization. Ices typically also encode a relaxase, and a T4SS required for ICE transfer via the T4SS generated mating pore (51). Following integrase-mediated ICE excision, the resulting extrachromosomal single-stranded circular ICE intermediate is nicked by the relaxase at an intergenic cis-acting oriT locus. The relaxase attached to the 5′-end of the single-stranded DNA is subsequently recruited to the coupling protein component of the mating pore and then transferred in a T4SS-dependent manner to a recipient cell (51). By close analogy, tfs3 and tfs4 circular intermediates generated by activity of the associated PZ XerD recombinase (12) can be predicted to follow a similar pathway mediated by the respective PZ relaxase acting at its cognate oriT within the excised PZ clusters. That PZ tfs3 and tfs4 clusters additionally encode a complement of Vir-homologous T4SS structural proteins, including a putative VirD4 coupling protein, indicates that these regions similarly comprise all of the elements required for self-transmissibility.

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