Helicase binding to DnaI exposes a cryptic DNA-binding site during helicase loading in Bacillus subtilis

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ABSTRACT

The Bacillus subtilis DnaI, DnaB and DnaD proteins load the replicative ring helicase DnaC onto DNA during priming of DNA replication. Here we show that DnaI consists of a C-terminal domain (Cd) with ATPase and DNA-binding activities and an N-terminal domain (Nd) that interacts with the replicative ring helicase. A Zn²⁺-binding module mediates the interaction with the helicase and C67, C70 and H84 are involved in the coordination of the Zn²⁺. DnaI binds ATP and exhibits ATPase activity that is not stimulated by ssDNA, because the DNA-binding site on Cd is masked by Nd. The ATPase activity resides on the Cd domain and when detached from the Nd domain, it becomes sensitive to stimulation by ssDNA because its cryptic DNA-binding site is exposed. Therefore, Nd acts as a molecular ‘switch’ regulating access to the ssDNA binding site on Cd, in response to binding of the helicase. DnaI is sufficient to load the replicative helicase from a complex with six DnaI molecules, so there is no requirement for a dual helicase loader system.

INTRODUCTION

Bacterial chromosome replication initiates at an origin (oriC) where the ubiquitous origin recognition protein DnaA binds to begin the recruitment of the replisome (1,2). The initial step of this process involves the coordinated assembly of a primosome to load the main replicative ring helicase and then recruit the primase (3,4). Successful assembly of the primosome allows the synthesis of primers and recruitment of the DNA polymerase III holoenzyme for elongation to begin. Occasionally replication forks collapse and different restart mechanisms reassemble the replisome at sites other than oriC, depending on the structure of the arrested fork.

In Escherichia coli the PriA/PriB/DnaT dependent mechanism restarts the replisome when a 3' end is available whilst the PriC-dependent mechanism is involved when there is a single-strand gap at the fork (5,6).

In Bacillus subtilis loading of the ring helicase DnaC (homologue of E.coli DnaB, 44% identity) is achieved by the action of three primosomal proteins DnaD, DnaB (not to be confused with the E.coli DnaB helicase) and DnaI (7–9). DnaI is homologous to E.coli DnaC (10,11), the helicase loader (12,13); it is not to be confused with the B.subtilis DnaC helicase. There are no homologues of DnaD and DnaB in E.coli but homologues of both proteins, as well as DnaI, are found in low G+C Gram-positive bacteria (7). DnaI interacts with DnaC (14,15) and together with DnaB loads DnaC onto DNA in a DnaD-dependent manner (16). The precise molecular events that underpin the function of the DnaD-DnaB-DnaI primosomal cascade are not clear but data suggest that DnaD acts early, setting the stage for the recruitment of the DnaI–DnaC complex (17,18), while DnaB may be acting together with DnaI to form a pair of helicase loaders for the recruitment of DnaC (16). Alternatively, DnaB may act as a membrane attachment protein to regulate initiation of DNA replication by regulating the recruitment of DnaD to the membrane (19,20). DnaD interacts with DnaA (17), PriA (18) and DnaB (21), disrupts the helicase–DnaI complex and exhibits a DNA architectural activity similar to the histone-like E.coli HU proteins (22–24). DnaB also exhibits a DNA remodelling activity that counteracts that observed for DnaD and the two proteins have been proposed to link nucleoid reorganization and initiation of DNA replication (22,23).

B.subtilis DnaI interacts functionally with the Bacillus stearothermophilus DnaB helicase (referred to as stearoDnaB) to distinguish it from B.subtilis DnaB), altering its ATPase activity profile and stimulating its helicase activity (11). StearoDnaB is highly homologous to the B.subtilis DnaC helicase (82% identity and 92% similarity) and is expressed in soluble form in E.coli. In the absence of DNA it forms a stable complex with DnaI with an apparent stoichiometry of 44 115 9513525; Fax: +44 115 8468002; Email: panos.soultanas@nottingham.ac.uk

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is expressed in insoluble form in *E. coli* but forms a soluble complex with DnaI, with apparent stoichiometry DnaC<sub>6</sub>-DnaI<sub>6</sub> when the two proteins are co-expressed and purified in the presence of ATP (16). Purified DnaC and DnaI proteins do not re-associate to form a homogeneous DnaC<sub>6</sub>-DnaI<sub>6</sub> complex at low μM concentrations even in the presence of ATP, but form instead a variety of complexes with wide Rang- 

Structural information about bacterial helicase loaders is lacking and apart from the presence of Walker A and B motifs, nothing is known about the biochemical properties of DnaI. Here we report that DnaI is a two-domain protein with a 21 kDa C-terminal domain (Cd) that binds DNA and of DnaI. Here we report that DnaI is a two-domain protein lacking and apart from the presence of Walker A and B

**MATERIALS AND METHODS**

**Limited proteolysis**

Limited proteolysis was carried out with subtilisin (1:5000 subtilisin : DnaI molar ratio) at 50 mM Tris (pH 7.4), 1 mM EDTA, 10% v/v glycerol at 37°C. Samples were removed at time intervals and the reaction terminated by addition of loading buffer (1% SDS, 2.5% DTT, 0.1% w/v bromophenol blue and 10% w/v glycerol) prior to SDS–PAGE analysis. A protein fragment from subtilisin proteolysis was identified by N-terminal protein sequencing.

**Protein purifications**

wtDnaI. DnaI was purified from the wt dnaI gene, cloned both in pET28a and pET22b, as described before (11) but with treatment of the cell extract with benzonase.

**DnaI mutants**

The purification method for the C67A, C70A, C76A, H84A and C101A mutants was the same as for wtDnaI up to the first column, apart from the initial suspension buffer that contained 50 mM glutamate and 50 mM arginine. Mutant proteins were partially soluble (∼30%) and were loaded onto a HiTrap Blue Sepharose column, equilibrated in TD (Soulittanas, 2002), 0.1 mM EDTA, and eluted with 2 M NaCl. Fractions were pooled, diluted with TD, 0.1 μM EDTA to 6 mS and applied to a heparin column, equilibrated in TD, 0.1 μM EDTA. Proteins were eluted with a 0–500 mM NaCl gradient. Fractions were pooled, protein precipitated with ammonium sulphate, dissolved in TD, 0.1 μM EDTA, 100 mM NaCl and applied to a Superdex S75 gel filtration column, equilibrated in TD, 0.1 μM EDTA, 100 mM NaCl. Fractions were pooled and the absorbance at 280 nm was measured before being made up to 10% v/v with glycerol and freezing.

The K174A mutant was purified as for the wtDnaI except that it was expressed at 27°C overnight (60% soluble) and collected in the flow-through from the HiTrap Q column.

**Nd and Cd domains**

His-tagged Nd and Cd were purified using a 5 ml HiTrap His-tag column (Amersham Pharmacia Biotech) loaded with Ni<sup>2+</sup> or Zn<sup>2+</sup>, followed by gel filtration in a Superdex S75 column. Both proteins were finally in 50 mM Tris (pH 7.5), 0.1 mM EDTA, 100 mM NaCl, 1 mM DTT, 10% v/v glycerol. A significant fraction of Cd (∼50% as assessed by SDS–PAGE) was found in the insoluble fraction.

**StearoDnaB**

The stearoDnaB helicase was purified as described before (25).

**Circular dichroism (CD)**

The spectra were recorded on an Applied Photophysics Pi-Star-180 spectrophotometer at 25°C. The temperature was regulated using a Neslab RTE-300 circulating programmable water bath and a thermoelectric temperature controller (Melcor). The protein samples were prepared at 5 μM, in 50 mM Tris (pH 7.4), 0.1 mM EDTA, 1 mM DTT, 100 mM NaCl, 10% v/v glycerol and recorded using a 1 mm path length cuvette. A background spectrum of just the buffer was also recorded and subtracted from each protein spectrum. Each spectrum was recorded from 280 to 200 nm using a 2 nm step and 4.0 nm entrance and exit slit widths. All mutant proteins were analyzed and compared to the wtDnaI. Molar ellipticities were calculated using the equation [θ] = θ/(10 x n x c x l) were θ is ellipticity, n is the number of peptide bonds, c is the molar concentration and l is the path length of the cuvette.

**Gel shift assays**

Gel shift assays were carried out with DnaI, Nd or Cd at 0.25–28 μM, in the presence or absence of ADP•NP or ATP (1 mM) in a buffer containing 20 mM Tris (pH 7.4), 0.1 mM EDTA, 4 mM MgCl<sub>2</sub>, 1 mM DTT, 10% v/v
glycerol and radiolabelled single-strand oligonucleotides (Supplementary Figure S1) at 2.5 nM, unless otherwise stated (26). Proteins were incubated with the oligonucleotide substrate for 10 min at room temperature and then samples were resolved through an 8% w/v polyacrylamide, 5% v/v glycerol native gel, in 0.5XTBE buffer supplemented with 10 mM MgCl2, at 80 V at room temperature. Gels were dried under vacuum and visualized with a phosphorimager (Molecular Imager FX, Bio-Rad). Supershift assays were carried out in a similar manner using DnaI (8 μM) and increasing concentrations of stearoDnaB (0.25–28 μM).

**Yeast two hybrid (Y2H) experiments**

Y2H experiments were carried out using the MATCH-MAKER Two-Hybrid system 2 (Clontech). The dnaB gene was cloned as an NcoI–XhoI fragment in the same sites of pACT-2. Quantification of the interactions was carried out by β-galactosidase assays using ONPG (o-nitrophenyl β-D-galactopyranoside), as described by Clontech. The positive control is based on the p53-SV40 T antigen interaction, using the pAV3-1 plasmid carrying the GAL4 DNA-binding domain fused to murine p53 and a trp nutritional selection marker and the pTD1 plasmid carrying the GAL4 activation domain fused to the SV40 large T antigen and a leu nutritional selection marker. The negative control shows that there is no interaction between DnaB and SV40 large T antigen, using the pAS2-1-DnaB and pTD1 plasmids, described above. All plasmids were transformed into yeast by electroporation, as described elsewhere (27) and detection of positive interactions was carried out by the agarose overlay method (28) or the filter-lift method (Clontech).

**Atomic absorption spectroscopy**

The Zn content of DnaI and Nd was estimated by flame atomic absorption spectroscopy using a Perkin–Elmer atomic absorption spectrophotometer (Model 603) in the air-acetylene flame mode, which gives a lean blue flame for Zn. Measurements were standardized with standard ZnCl2 solutions in the same buffer as the protein. The wavelength of the hollow cathode lamp was set at 213.9 nm and proteins were prepared in 50 mM Tris (pH 7.5), 0.1 M NaOH/1 M NaCl. StearoDnaB, DnaI and Nd were dried under vacuum and visualized with a phosphorimager. The percentage conversion of ATP to Pi was used to determine the increase of [Pi] with time.

**The PAR assay**

The PAR (4-(2-pyridylazo)resorcinol) assay was carried out as described before (29). Purified DnaI was dialysed in 50 mM Tris (pH 7.5). PAR (100 μM) was added to the protein solution (10 μM) and different aliquots of the DnaI/PAR mixture were then prepared in the presence of increasing concentrations (0.1–1.6 mM) of p-chloromercuribenzoic acid (PMBA). The absorbance at 500 nm (A500) was measured for all the aliquots. The Zn2+ ions released from DnaI by PMBA were coordinated by PAR and the resulting PAR–Zn2+ complex absorbed light at 500 nm with an extinction coefficient of 104 M−1 cm−1. An increase of A500 indicates the release of Zn2+ ions from the protein. Increasing concentrations of EDTA were added in the aliquot with the highest concentration of PMBA and the A500 was monitored. Gradual decrease in A500 indicated the extraction of the metal from the PAR–Zn2+ complex by EDTA.

**Site-directed mutagenesis**

All point mutants were constructed with the QuikChange site-directed mutagenesis kit (Stratagene) using the wild-type dnaI gene cloned in pET22B, according to the manufacturer’s instructions. The mutagenic oligonucleotides used are shown in Supplementary Figure S1. All mutant genes were sequenced to verify the correct mutation.

**Fluorescence studies**

Binding of ATP to DnaI and Cd was investigated using N-methylanthraniloyl ATP (MANT-ATP), a fluorescent analogue of ATP. Binding reactions were carried out at different concentrations of DnaI (1–50 μM) or Cd and MANT-ATP (90–500 nM) in binding buffer (20 mM Tris (pH 7.5), 5 mM MgCl2, 1 mM EDTA and 10% v/v glycerol), using Starna fluorimeter special optical cells (3 mm path and 315 μl volume) in a total volume of 300 μl. The excitation wavelength was set at 356 nm and fluorescence changes were measured at 440 nm. All binding reactions were carried out in triplicate and each reaction was scanned 10 times to obtain a final average for analysis. Binding stoichiometries were measured by continuous variation binding analysis (30). Both [MANT-ATP] and [DnaI] were varied for a fixed and constant summed concentration of 1.1 μM at room temperature.

**Thin layer chromatography (TLC)—based ATPase assays**

ATPase activity was assayed by monitoring the 32Pi produced during hydrolysis of [γ-32P]ATP (3000 Ci/mmol) using TLC with TEI plates, under conditions of excess DnaI over ATP. All reactions were carried out at 37°C in triplicate, with different concentrations of [γ-32P]ATP (1.66, 3.33, 8.32, 16.65, 25 and 33.3 nM), 8 μM protein (DnaI, Cd, Nd and K174A) in binding buffer and in the presence or absence of 0.48 mM 33mer single-strand oligonucleotide. Samples were removed at time intervals (0–120 min) and reactions were terminated with the addition of 20 mM EDTA. Small samples (1.2 μl) were spotted onto TLC plates that were then developed in 1 M formic acid, 0.5 M LiCl2 and analysed using a phosphorimager. The percentage conversion of ATP to Pi was used to determine the increase of [Pi] with time.

**SPR experiments**

Experiments were carried out at 20°C in a BIAcore 2000 at 5 μl/min with HBSEP buffer (Biacore) supplemented with 1 mM DTT as running buffer, essentially as described previously (31). A solution (100 nM) of 3’-biotinylated (dT)35 in running buffer was injected over a streptavidin-coated chip surface (Biacore SA chip) to yield an increase of 300 RU (1 min) on one flow cell. Another flow cell was unmodified and served as a control. The binding buffer was HBSEP (Biacore) supplemented with 10 mM MgCl2 and 2.7 mM ATP. When required to remove tightly-bound proteins, regeneration of the flow cells was achieved with 1 min injection of 50 mM NaOH/1 M NaCl. StearoDnaB, DnaI and Nd were
diluted in binding buffer and injected in combinations or individually during 1 or 2 min, followed by dissociation in running buffer. The binding buffer was selected because it gave the strongest binding of stearoDnaB-DnaI onto ssDNA. Use of the running buffer (without Mg\(^{2+}\)/ATP and with 3 mM EDTA) during the dissociation phase resulted in a fast dissociation of DnaI from the loaded complex, allowing the observation of the subsequent slow dissociation of stearoDnaB from the ssDNA. When the binding buffer was used throughout, the same biphasic dissociation was observed, but with a slower DnaI dissociation phase, making it difficult to determine the stoichiometry of the complex.

RESULTS

DnaI is a two-domain protein

DnaI was sensitive to subtilisin and a cleavage site was identified by N-terminal protein sequencing (data not shown). Subtilisin treatment and N-terminal sequencing identified a domain boundary at the sequence QVDI, separating two domains; Nd 16644 and Cd 21619 Da. Both Nd and Cd were tagged with hexahistidine tags at their C-termini. Nd was over-expressed as soluble protein but Cd was 50% soluble (data not shown). Nd was purified using a 5 ml HiTrap-Ni\(^{2+}\)-chelating column and gel filtration through Superdex S75. Attempts to fully solubilize Cd at different temperatures and/or expression inductions at different isopropyl-\(\beta\)-D-thiogalactopyranoside (IPTG) concentrations were unsuccessful (data not shown). Repositioning of the hexahistidine tag at the N-terminus of Cd did not improve solubility. N-terminally tagged Cd was consistently 50% soluble upon expression in large scale cultures (data not shown). It was purified from the soluble fraction in good quantities to carry out its biochemical characterization.

Nd interacts with stearoDnaB

DnaI interacts with stearoDnaB [(11) and Figure 1A] and *B. subtilis* DnaC (16), forming stable complexes that can be isolated by gel filtration. StearoDnaB eluted at \(\sim 9.8\) ml and DnaI at 14.5 ml. The precise elution volume depends on the actual gel matrix and the size of the particular column, but the resolution power of the Superdex S200 column is not sufficient to clearly separate complexes above 200 kDa in size. However, the clear shift of some DnaI into the earlier peak in the presence of stearoDnaB indicates the formation of a complex (Figure 1A). An interaction between Nd and stearoDnaB could also be detected by gel filtration (Figure 1B). While Nd eluted at \(\sim 18.2\) ml in the presence of stearoDnaB some Nd appeared in the earlier peak indicating the formation of a complex. The interactions of DnaI and Nd with stearoDnaB were also verified by yeast two hybrid experiments (Figure 2A). By comparison, Cd exhibited a very weak interaction in these experiments (Figure 2B and C) and no complexes with stearoDnaB or Nd were detected by gel filtration (data not shown). These data were confirmed with quantitative ONPG assays (Figure 2B). Several yeast clones carrying Cd were tested and although none exhibited significant DnaI-interactions, weak signals just above the background were detectable (Figure 2B and C).

DnaI binds Zn\(^{2+}\)

The C67, C70, C76, H84 and C101 residues in Nd are part of the sequence CX\(_3\)CX\(_3\)CX\(_3\)HX\(_{16}\)C that could potentially coordinate Zn\(^{2+}\). The Zn\(^{2+}\) contents of DnaI and Nd were investigated by atomic absorption spectroscopy. Four different DnaI preparations, at different concentrations (2.8 and 4.2 \(\mu M\)) were used using standard solutions of Zn\(^{2+}\) and the presence of the metal was confirmed (Table 1). The Zn\(^{2+}\) molar contents were measured at 1:1 and 1:1.6 relative to the protein. Similar experiments were carried out with Nd but our initial data revealed that it contained less Zn\(^{2+}\) than expected, estimated at 1:25.3 relative to the protein (Table 1). One explanation for the poor Zn\(^{2+}\) content of Nd could be that the Ni\(^{2+}\) column used in our first purification step of the His-tagged Nd may have competed off the Zn\(^{2+}\). We investigated this using a Zn\(^{2+}\)-loaded column and a preparation of Nd purified in this manner was assayed for Zn\(^{2+}\).
The data confirmed the presence of Zn\(^{2+}\) in 1:1 molar ratio (Table 1). The involvement of cysteines in Zn\(^{2+}\) coordination was established directly using the PAR assay (Supplementary Figure S2). The gradual increase of the absorbance at 500 nm, as \(p\)-hydroxymercuribenzoic acid was titrated into a solution of DnaI and PAR, indicated the release of Zn\(^{2+}\) from cysteines and the formation of the PAR–Zn\(^{2+}\) complex. Subsequent titration of increasing concentrations of EDTA resulted in decreasing absorbance indicating the release of Zn\(^{2+}\) from PAR and its chelation by EDTA.

### A Zn\(^{2+}\)-binding module mediates the interaction with the helicase

The C67A, C70A, C76A, H84A and C101A mutants of DnaI were constructed to identify the residues involved in metal coordination. Mutant proteins, when expressed in \(E.coli\) were partially soluble (~30% soluble; data not shown) and were purified in good quantities for biochemical investigations. Atomic absorption experiments revealed that the C67A, C70A and H84A mutants contained no Zn\(^{2+}\), whereas C76A still bound Zn\(^{2+}\) (Table 1). The C101A mutant gave mixed results. In one preparation Zn\(^{2+}\) was undetectable but in another Zn\(^{2+}\) was detected. We conclude that residues C67, C70 and H84 are involved in Zn\(^{2+}\)-binding whereas C76 is not. The status of C101 could not be confirmed unequivocally (see Discussion for an explanation). Notably, all the mutant proteins were partially soluble after sonication of the cells only in the presence of 50 mM glutamate and 50 mM arginine, indicating that these mutations alter somewhat the solubility properties of the protein (32). This is not the result of misfolding as the CD spectra of all mutant proteins were identical to the wtDnaI, indicating similar overall folds (Supplementary Figure S3). In addition, all the mutant proteins eluted at the same point as the wtDnaI through the Superdex S200 gel filtration column indicating proper globular folding.

![Figure 2](image)

**Figure 2.** Investigation of the DnaI–stearoDnaB interaction by yeast two hybrid. (A) Yeast two hybrid experiments revealed strong interactions between DnaI and stearoDnaB, as well as Nd and stearoDnaB. An interaction between Cd and stearoDnaB could not be detected. (B) The Nd–stearoDnaB interaction was verified by ONPG assays. Assays with two different clones each of Nd and Cd are shown. Cd did not reveal an interaction with DnaB. (C) Weak interactions between Cd and stearoDnaB were revealed by yeast two hybrid. Six different clones of Cd were tested and they all exhibited weak and variable interactions with stearoDnaB.

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Nd\(_a\) indicates Nd purified through a Ni-loaded His-tag column. Nd\(_b\) indicates Nd purified through a Zn-loaded His-tag column.

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unable to bind Zn$^{2+}$, whereas the C76A protein was able to bind Zn$^{2+}$ and the C101A protein gave mixed results (Table 1).

**DnaI binds MANT-ATP in 1:1 stoichiometry**

Binding of ATP to DnaI was investigated by fluorescence using MANT-ATP. The binding stoichiometry was determined using the continuous variation analysis from Job plots and the fitted lines gave an intersection at the stoichiometry 1:1 (Figure 4A). Binding was examined at four different [MANT-ATP] (90, 200, 300 and 500 nM) while the [DnaI] was varied and the fluorescence change was plotted as function of [DnaI], (Figure 4B). The binding curves were fitted to an one site binding hyperbola using GraphPad Prism programme to obtain $K_D$ values for each set of data. The dissociation constant is $K_D = 0.9 \, \mu$M.

**DnaI exhibits limited ATPase activity**

Although DnaI has Walker A and B motifs and binds ATP, no ATPase activity has been demonstrated to date. The DnaI ATPase activity was demonstrated by TLC assays under conditions of excess protein over ATP, and was found to be unaffected by ssDNA (Figure 5). Since the Walker A and B motifs reside in the Cd domain, its ATPase activity was also examined under the same conditions. Cd exhibited poorer ATPase activity compared to the full-length protein but in the presence of ssDNA, the activity was stimulated to the same level as that of DnaI (Figure 5). By comparison, Nd exhibited no detectable ATPase activity (data not shown), and the Walker A K174A mutant exhibited reduced ATPase activity (Supplementary Figure S4).

Under conditions of excess ATP over protein, DnaI failed to fully hydrolyse all the ATP even after 2 h, indicating that the enzyme does not turn over ATP (Supplementary Figure S5). These data imply that once DnaI hydrolyses ATP it is then locked into an inactive ADP-bound conformation. We also observed that at a fixed ATP concentration (50 $\mu$M) all DnaI molecules turn over ATP once (0.1 $\mu$M DnaI hydrolyses...
but as the concentration of DnaI is increased the relative fraction of DnaI molecules that hydrolyses ATP is decreased (Supplementary Figure S5). For example, 1, 5, 10, 25 and 50 μM DnaI hydrolyse 0.7, 2.9, 3.9, 8.8 and 14.4 μM ATP, respectively. This may be because as the DnaI concentration is increased not all DnaI molecules have bound ATP or at high DnaI concentrations there may be some kind of regulatory inhibitory effect by DnaI–DnaI interactions or even there may be an ATP-induced oligomer being formed with some DnaI molecules in the oligomer no longer capable of hydrolysing ATP.

A cryptic DNA-binding site is located on the Cd domain

The ssDNA-induced stimulation of Cd ATPase activity implies that this domain binds ssDNA. By comparison, the lack of stimulation of the full-length DnaI in the presence of ssDNA implies that either it does not bind ssDNA or ssDNA binding does not confer the conformational changes required for ATPase stimulation. To distinguish between these two possibilities, the DNA-binding ability of DnaI with single-strand and fork-DNA substrates using gel shift assays was examined (Figure 6A). Under our experimental conditions in the range 0.25–28 μM DnaI-binding to a single-strand 50mer oligonucleotide was undetectable whereas weak binding to fork-substrates was detected (Figure 6A). Binding to ssDNA could only be detected at concentrations higher than 0.9 mM DnaI (data not shown). DnaI exhibited weak binding to 3'- and 5'-tailed DNA substrates (data not shown). The presence of ADPNP or ATP had no effect on DNA binding. Thus, the lack of stimulation of DnaI ATPase activity is a reflection of its inability to bind ssDNA. Instead it exhibits a preference for ss-dsDNA junctions but binding is still weak.

Similar analysis of Cd revealed that it binds to ssDNA and to fork-substrates (Figure 6B), confirming that the observed
stimulation of its ATPase activity is the result of its interaction with ssDNA. The presence of ADPNP or ATP resulted in a marginal decrease of DNA binding. Therefore in the full-length protein, the Nd domain ‘masks’ the DNA-binding site on the Cd domain. This cryptic DNA-binding site has been revealed upon Cd detachment from Nd.

The DnaI–stearoDnaB complex binds ssDNA in the presence of ADPNP

Although DnaI binds to stearoDnaB, the stability of the complex is not affected by ADPNP in the absence of DNA (11). In the presence of 1 mM ADPNP stearoDnaB binds better to ssDNA, as shown before (33), whilst in the presence of 8 μM DnaI and increasing concentrations of stearoDnaB (0.25–28 μM) a super-shifted band was detected representing binding of the DnaI–stearoDnaB complex to DNA (Figure 7A). DnaI does not bind to ssDNA as shown in Figure 6A. In the absence of ADPNP no super-shifted complex was observed (compare left and right segments in Figure 7B). In the presence of 1 mM ATP the super-shifted band disappeared (Figure 7C). More efficient loading was observed at higher DnaI:stearoDnaB molar ratios, 32:1, 16:1, 8:1 (Figure 7A, lanes 1–3 right segment) compared to lower molar ratios 4:1, 2:1, 1:1 (lanes 4–6), indicating that under these experimental conditions excess of DnaI is required to ensure formation of a stable loading complex. These data indicate that binding of the DnaI–stearoDnaB complex to ssDNA is stimulated by ATP-binding and ATP hydrolysis facilitates the dissociation of the complex leaving the helicase on the DNA.

DnaI is required for efficient loading of stearoDnaB onto ssDNA

An assay for DnaI-mediated loading of stearoDnaB onto ssDNA using SPR (BIAcore) was devised in a similar manner to that described for the interaction between the C-domain of E. coli DnaG and E. coli DnaB (31). A 3'-biotinylated (dT)35 was first loaded onto a streptavidin chip, exposing the 5' end. Then either stearoDnaB alone or a mixture of stearoDnaB and DnaI were injected, in the presence of Mg-ATP. No interaction of 175 nM stearoDnaB or 1.75 μM DnaI, alone with DNA was observed (Figure 8A; red and light blue). Binding was detected when the two proteins were combined, and the response depended on the concentration of DnaI. Therefore, formation of a complex of DnaI with stearoDnaB is necessary for helicase loading onto ssDNA. The response consistently decreased by 40% over 2 min to a stable value regardless of [DnaI]. The simplest explanation for this behaviour is that the stearoDnaB–DnaI complex first loads, and then one of the components dissociates. We proceeded to discover which component dissociates from the ternary complex.

DnaI dissociates after the helicase is loaded onto ssDNA

The ternary complex was formed by injection of a mixture of stearoDnaB–DnaI (175 nM:1.75 μM). After the fast dissociation phase, the same concentration of DnaI (1.75 μM) alone was injected again and the second binding response indicated re-formation of the ternary complex (Figure 8B; blue). When stearoDnaB was injected instead, very little binding to ssDNA was observed under these conditions, while no binding was apparent on the same flow cell after stearoDnaB was stripped from the ssDNA (data not shown). Therefore, it is the stearoDnaB that remains stably bound to the DNA after dissociation of DnaI and the ternary complex re-forms upon addition of more DnaI.

Stoichiometry of the complex loaded onto ssDNA

The conditions used in this assay permitted visualization of a biphasic dissociation curve with dissociation rates different enough (fast for DnaI, slow for stearoDnaB) to allow extrapolation to zero time of both parts of the response curve to obtain quantitative measures of the amount of stearoDnaB–DnaI loaded and of stearoDnaB remaining after dissociation of DnaI. Determination of the ratio of bound stearoDnaB to
total complex loaded showed that for every ratio of components used to generate the data in Figure 8A, the mass ratio was close to 0.6. This corresponds closely to the ratio of masses of the proteins, indicating strict 1:1 stoichiometry of helicase and DnaI in the loaded complex. The high response compared to the ssDNA that is available on the chip, and the well-established properties of hexameric helicases, suggests that it is the hexameric form of the helicase that is loaded, and therefore the only species in the mixture capable of being productively loaded onto the exposed 5' end of ssDNA was the stearoDnaB6–DnaI6 complex. Complexes with fewer than six molecules of DnaI per helicase hexamer are either not formed in the mixtures because of highly cooperative association of DnaI, or if they are, they are not capable of being loaded at the exposed 5' end of the ssDNA.

The stearoDnaB6–DnaI6 stoichiometry implied by SPR is different than the apparent stearoDnaB6–DnaI6 or 2 stoichiometry implied by gel filtration [(11) and Figure 1]. The latter was deduced based upon the assumption that all of the available stearoDnaB was in complex with DnaI. If this is not true then the peak of the hexameric stearoDnaB will overlap with the peak from the complex and free stearoDnaB will co-elute with the complex, thus giving an apparent impression of less DnaI in the complex. It is indeed difficult to assess the precise stoichiometry of this complex by gel filtration since the resolution power of Superdex S200 is not enough to separate clearly complexes above 200 kDa in size. Also, there appear to be some variability in the stoichiometry of this complex. For example, B.subtilis DnaC and DnaI form mainly a DnaC6–DnaI6 complex, when they are co-expressed and co-purified but other complexes with fewer than six DnaI molecules are also apparent (16). When the two proteins are separated and mixed, again they appear to form complexes with fewer than six DnaI molecules per DnaC hexamer (16). In addition, the effect of DNA on the stoichiometry of the complex has not been assessed and one possibility may be that in the presence of ssDNA the stearoDnaB6–DnaI6 complex is more stable.

Not surprisingly, we have been unable to find conditions where the Nd domain of DnaI is capable of loading stearoDnaB onto ssDNA in these SPR assays. One reason is that it lacks the cryptic DNA-binding region in the Cd domain. Another is that it probably lacks regions in the Cd required for cooperative interactions with the helicase.

**DISCUSSION**

**DnaI interacts with the helicase via its Nd domain**

DnaI is the putative helicase loader in B.subtilis but the helicase loading mechanism is still unknown. Our data show that DnaC consists of an Nd domain that contains a Zn2+-binding module involved in the interaction with the helicase, and a Cd domain with ATPase and DNA binding activities. However, the weak interaction between Cd and the helicase was also detected only by yeast two hybrid. Quantification of this weak interaction with six different Cd clones revealed that it is variable. Some clones exhibited slightly better signal than others did, albeit they were all just above the negative control levels. The functional significance of this observation is not clear but it could be argued that a secondary patch that interacts weakly with the helicase resides on Cd. One could speculate that cooperativity in binding of multiple DnaI molecules to the helicase hexamer may also involve protein–protein interactions within or between Cd domains. In the analogous E.coli DnaC helicase loader, a single point mutation near the N-terminus also abolished binding to the helicase whilst retaining its ability to bind ATP (34).

**DnaI has a cryptic DNA-binding site on its Cd domain**

We were unable to detect significant binding of DnaI to ssDNA even at high concentrations in the presence or absence of ADPnP, suggesting that the native protein does not bind ssDNA. Weak binding to fork and tail (5' or 3') DNA substrates was detected indicating a slight preference for ds-ssDNA junctions. The weak nature of this interaction makes its biological significance uncertain. Cd exhibited DNA-binding activity. The simplest interpretation of these data is that the Nd domain masks the DNA-binding site for ds-ssDNA junctions. The weak nature of this interaction makes its biological significance uncertain. Cd exhibited DNA-binding activity. The simplest interpretation of these data is that the Nd domain masks the DNA-binding site for ds-ssDNA junctions. The weak nature of this interaction makes its biological significance uncertain. Cd exhibited DNA-binding activity.

The helicase-loader can now deliver the helicase to the DNA but it can do so only when bound to ATP. This is consistent with the inability of the stearoDnaB–DnaI complex to produce a super-shifted complex on ssDNA in the absence of the ATP analogue ADPnP. Having eliminated misfolding problems, the partial insolubility of Cd is likely to indicate that certain hydrophobic patches on its surface are protected by the presence of Nd in the intact protein and exposed in its absence. It is likely that this allosteric control of domain movement in DnaI is an important functional property regulating helicase loading. Taking into account the combined data, we propose a model for the DnaI-mediated helicase loading (Figure 9). By comparison, the Gram-negative E.coli helicase loader DnaC has been reported to exhibit a cryptic ssDNA binding activity only when bound to the
helicase (35) and to interact weakly to ssDNA in the absence of the helicase, with ATP strengthening this interaction (36).

B. subtilis DnaI has weak ATPase activity

Despite the presence of Walker A and B motifs characteristic of ATP-metabolising enzymes (39) no ATPase activity has been demonstrated for DnaI. Our data reveal that DnaI binds ATP in a 1:1 stoichiometry and hydrolyses ATP. ATP appears to be essential for the formation of a DnaC<sub>DnaI</sub> complex when the two proteins are co-expressed and purified from E. coli (16) but in its absence complexes of different stoichiometry DnaB<sub>B</sub>-DnaI<sub>1</sub> or 2 also have been observed with the stearoDnaB protein (homologous to B. subtilis DnaC). Interestingly, the DnaC<sub>C</sub>-DnaI<sub>I</sub> complex cannot be fully reconstituted with purified DnaC and DnaI proteins (16). In the E. coli DnaC helicase loader, ATP has been reported to be essential for the formation of a stable helicase loader-helicase complex and binds only to one of two DnaI protein conformations that exist prior to nucleotide binding (12,13,40,41). ATP-binding induces conformational changes that increase its affinity for the helicase, whilst ADP-binding acts as a negative effector. In a similar manner, ATP-binding may also modulate the DnaI conformation thus increasing its affinity for the helicase in vivo, although no such effect has been detected in vitro. However, the non-hydrolysable analogue ADPNP is able to promote binding of the helicase loader (DnaI) helicase (stearoDnaB) complex to DNA (Figure 7).

The importance of the ATP-binding site for the conformation of DnaI is highlighted by the effect of the K174A mutation. This mutation affected the solubility of the protein but its CD spectrum and behaviour through gel filtration are identical to wtDnaI, indicating no problems with overall folding. In addition, it retains some ATPase activity suggesting that altering residues in the active site can affect subtly the ATP-binding pocket and ATPase activity. The fact that K174A has reduced ATPase activity compared to wtDnaI indicates that this residue is not directly involved in catalysis, but could be participating along with other residues in ATP-binding. In other ATPases, the effect of mutating the equivalent lysine also appears to have variable consequences. For example, in the F<sub>1</sub>F<sub>0</sub>-ATPase β-subunit, the K to N/E mutation causes only a 3- to 5-fold reduction in ATPase activity (42) and an equivalent mutation in UvrA causes only a 2-fold decrease in <i>k<sub>cat</sub></i>, while the K405S mutation in NS-1 of the minute virus of the mouse (MVM) results in a mutant protein with 87% of the ATPase activity of the wild-type protein (44). In the PcrA helicase, the equivalent K37A mutation produces a protein with reduced <i>k<sub>cat</sub></i> but tighter <i>K<sub>m</sub></i> retaining reasonable levels of helicase activity (45). Therefore, it is not clear whether the conserved lysine residue of the Walker A motif is involved in nucleotide binding or hydrolysis or in both activities collectively or alternatively in coupling the ATPase reactions with other activities. In contrast, the equivalent K112R mutation in the putative Walker A GKN motif of E. coli DnaC produced a soluble protein that was defective in ATP hydrolysis (36). The ATP-binding site in E. coli DnaC includes the recognition of many structural elements of the ATP, including the base, ribose, β and γ phosphate groups and these complex interactions may couple ATP-induced conformational changes to allosteric sites elsewhere in the protein (46). E. coli DnaC does not hydrolyse ATP but in the presence of an ATPase-dead DnaB mutant or ssDNA, it turns over ATP at 0.6 min<sup>-1</sup> and 0.9 min<sup>-1</sup>, respectively. Maximal activity of 3.5 min<sup>-1</sup> is observed in the presence of both the mutant DnaB and ssDNA (36). Our data indicate that in B. subtilis, ATP-binding promotes the association of the helicase loader–helicase complex with DNA and the ATPase activity of DnaI is stimulated upon binding to DNA. ATP hydrolysis promotes the dissociation of the complex leaving the helicase bound to the DNA (Figure 9). Therefore, a single helicase-loader (DnaI) is sufficient to load the hexameric helicase onto the DNA and there is no absolute requirement for a dual helicase loader system as has been suggested before (16).

The role of the Zn<sup>2+</sup>-binding module

A comparison with DnaI proteins from other species reveals that the Zn<sup>2+</sup>-binding module is not strictly conserved. Streptococcus, Listeria and Enterococcus proteins have no obvious Zn<sup>2+</sup>-binding residues. Staphylococcus and Oceanobacillus iheyensis proteins have HX<sub>2</sub>HX<sub>2</sub>CX<sub>2</sub>H and CX<sub>2</sub>CX<sub>2</sub>CX<sub>S</sub> sequences, respectively, that could potentially coordinate Zn<sup>2+</sup>. Even in other Bacillus strains, the Zn<sup>2+</sup>-binding motif is not strictly conserved. For example, the Bacillus halodurans protein has the sequence CX<sub>2</sub>CX<sub>2</sub>CX<sub>Q</sub> that could also coordinate Zn<sup>2+</sup>. The C67, C70 and H84 residues are involved in Zn<sup>2+</sup>-coordination but the status of C76 and C101 could not be established unequivocally. A plausible explanation may be that while mutations in the C67, C70
and H84 residues abolish Zn$^{2+}$-binding, mutations in the C76 and C101 residues may cause local structural rearrangements, thus allowing C101 to substitute C76 for Zn$^{2+}$. The biological significance of the apparent structural plasticity of the Zn$^{2+}$-module and its poor conservation will need further investigation.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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