The biological and structural characterization of *Mycobacterium tuberculosis* UvrA provides novel insights into its mechanism of action

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ABSTRACT

*Mycobacterium tuberculosis* is an extremely well adapted intracellular human pathogen that is exposed to multiple DNA damaging chemical assaults originating from the host defence mechanisms. As a consequence, this bacterium is thought to possess highly efficient DNA repair machineries, the nucleotide excision repair (NER) system amongst these. Although NER is of central importance to DNA repair in *M. tuberculosis*, our understanding of the processes in this species is limited. The conserved UvrABC endonuclease represents the multi-enzymatic core in bacterial NER, where the UvrA ATPase provides the DNA lesion-sensing function. The herein reported genetic analysis demonstrates that *M. tuberculosis* UvrA is important for the repair of nitrosative and oxidative DNA damage. Moreover, our biochemical and structural characterization of recombinant *M. tuberculosis* UvrA contributes new insights into its mechanism of action. In particular, the structural investigation reveals an unprecedented conformation of the UvrB-binding domain that we propose to be of functional relevance. Taken together, our data suggest UvrA as a potential target for the development of novel anti-tubercular agents and provide a biochemical framework for the identification of small-molecule inhibitors interfering with the NER activity in *M. tuberculosis*.

INTRODUCTION

During its life, *Mycobacterium tuberculosis* is exposed to numerous genotoxic insults originating from both antimicrobial host defence mechanisms and the environment (1). Since persistence within the infected macrophage and reactivation of the bacillus from the dormant state are key features of infection, the maintenance of genome integrity is considered a vital aspect in the biology of *M. tuberculosis* (2,3).

One of the major molecular machines that control chromosome stability in living species is represented by the nucleotide excision repair (NER) system (4–7) that is capable of repairing a wide variety of DNA lesions (reviewed in ref. 5). In Eubacteria and some Archaea, the first steps in NER are carried out by UvrA, UvrB and UvrC proteins, often referred to as the UvrABC endonuclease. This multi-enzymatic complex recognizes the damage and excises a short lesion-containing DNA oligonucleotide, in a multi-step process in which the three proteins act in concert. Briefly, an UvrA•B heteromeric complex scans the DNA searching for damaged sites. The identity of the UvrA•B oligomeric state and of the searching complex have long been the subject of debate and controversy; however, two independent studies using fluorescence resonance energy

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The authors wish it to be known that, in their opinion, the first two authors should be regarded as joint First Authors.

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We report here an integrated analysis of *M. tuberculosis* UvrA. Our data indicate a key functional role for UvrA in protection against reactive oxygen and nitrogen species-triggered DNA damage. Moreover, we show that the DNA binding activity of *M. tuberculosis* UvrA towards various DNA structures mimicking intermediates of DNA repair, is correlated to the amount of single-stranded regions within the DNA substrate and provide evidence that the low intrinsic ATPase activity of *M. tuberculosis* UvrA is markedly stimulated by DNA. Finally, the crystal structure determination of *M. tuberculosis* UvrA in its ligand-free form reveals a remarkable repositioning of the UvrB binding domain and could therefore represent a further insight in the very initial steps of UvrABC complex assembling at the site of DNA lesion.

**MATERIALS AND METHODS**

**Functional characterization of *M. tuberculosis* uvrA mutant strain**

**Bacterial strains, media and culture conditions.** Standard procedures were adopted for cloning and propagation of plasmids in *Escherichia coli*. The *M. tuberculosis* wild-type strain used was 1424, a derivative of *M. tuberculosis* H37Rv carrying a non-restrictive *rpsL* mutation conferring streptomycin resistance (23). The *M. tuberculosis* uvrB mutant strain MHD9 (11,12) was kindly provided by H. Darwin and C. Nathan. Cultures of *M. tuberculosis* were grown in OADC enriched Middlebrook 7H9 medium or modified Dubos (Difco) supplemented with albumin and 0.2% glycerol at 37°C in a rolling incubator at 2 rpm. When appropriate, antibiotics were added at the following concentrations: kanamycin 50 µg/ml; streptomycin 100 µg/ml; gentamicin 5 µg/ml. All procedures with *M. tuberculosis* were carried out under Containment level 3 conditions.

**Isolation of a *M. tuberculosis* uvrA mutant strain and gene complementation analysis.** Allelic replacement techniques (24) were used to generate an *M. tuberculosis* knockout mutant for *uvrA* (*Rv1638*). A 5.9 kb NotI fragment containing the *uvrA* gene was isolated from BAC *Rv401* (25) and cloned into pBluescript KS(-) (Stratagene) previously digested with NotI to result in pBluescript-*uvrA*. For functional inactivation of *uvrA* the plasmid was digested with EcoNI and Stul (deleting 1340 bp) and a 1.2 kb fragment containing the kanamycin resistance cassette from plasmid pUC4K (GE Healthcare) was inserted into the plasmid to result in plasmid puvrA::aph. From this plasmid a 5.9 kb NotI fragment containing the inactivated *uvrA* gene (lacking base pairs 924–2263 of the 2919 bp *uvrA* ORF) was subcloned into plasmid pBluescript-*rpsL* (M.s.) previously digested with NotI resulting in plasmid puvrA::aph-rpsL. pBluescript-rpsL (M.s.) is a derivative of pBluescript carrying a 0.9 kb fragment with the *rpsL* gene of *M. smegmatis*. To isolate a mutant strain, the targeting construct was transformed into the streptomycin-resistant *M. tuberculosis* strain 1424, plating on medium containing kanamycin to select for chromosomal integration of the knockout plasmid. Following the identification of transformants...
that had undergone a homologous single crossover by Southern blot analyses, counter selection on streptomycin in the presence of kanamycin was used to obtain colonies arising from a double crossover event. Southern analyses were performed to identify mutant strains using a 628 bp 3′-probe (Ncol/NotI) with BamHI-digested DNA (Supplementary Figure S1).

For complementation, a 3694 bp fragment of DNA including the entire coding sequence of *uvrA* and 383 bp of the upstream region was cloned into the HindIII site of the integrating plasmid pKP203, resulting in pHJ08. This vector is equivalent to pKP186 (26) but has a fragment conferring gentamycin resistance in place of the kanamycin resistance gene (K.G. Papavinasasundaram, personal communication). As these plasmids lack the integrase gene, pHJ08 was co-transformed into the *uvrA* mutant strain with pBS-Int (27), which is a suicide plasmid that supplies the integrase function but is subsequently lost from the cells.

**Susceptibility to DNA damaging agents.** To assess the susceptibilities of the strains to UV irradiation, cultures were grown rolling to late exponential phase (*A*600 = 0.8–1.0) and or sodium nitrite pH 5.5 (2 mM), cultures were grown including the entire coding sequence of *uvrA* and 383 bp of the upstream region was cloned into the HindIII site of the integrating plasmid pKP203, resulting in pHJ08. This vector is equivalent to pKP186 (26) but has a fragment conferring gentamycin resistance in place of the kanamycin resistance gene (K.G. Papavinasasundaram, personal communication). As these plasmids lack the integrase gene, pHJ08 was co-transformed into the *uvrA* mutant strain with pBS-Int (27), which is a suicide plasmid that supplies the integrase function but is subsequently lost from the cells.

For in vitro survival experiments following exposure to mitomycin C (0.2 mg/ml), t-butyl hydroperoxide (0.1 mM) or sodium nitrite pH 5.5 (2 mM), cultures were grown rolling to late exponential phase (*A*600 = 0.8–1.0) and survival was determined as described (12) with the following modifications. Acidified medium (pH 5.5) was used for the nitrite stress and its pH control only; for the other stresses standard medium was used (pH 7.2). Triplicate 190 μl samples of diluted cell suspensions were incubated with 10 μl stress agent (or medium as control) for 6 days, except for mitomycin C where incubation was for 24 h. Serial dilutions were prepared and plated in triplicate for CFU determination.

In each case, three independent biological replicates were performed. Survival was calculated by the ratio of CFU of the treated cultures compared to the CFU of the untreated controls.

**Recombinant MtUvrA expression, purification and biochemical characterization**

**Subcloning.** In order to obtain the pMTHisUvrA expression construct, the *uvrA* ORF of *Mycobacterium tuberculosis* H37Rv (Tuberculist entry: Rv1638) was amplified by PCR using 20 ng of MTCY06H11.01 bacmid DNA (Institut Pasteur, Paris, France) and subcloned into the pET16b vector (Novagen), adopting standard recombinant DNA procedures (28), as detailed in ‘Supplementary Data’. The resulting plasmid drives in *E. coli* the IPTG-inducible synthesis of a N-terminally His-tagged *MtUvrA* (predicted molecular mass of 108 652.1 Da; 993 amino acid residues) (Supplementary Figure S2a).

**DNA substrates.** The sequences of oligonucleotides used in this study are listed in Supplementary Table S1. The oligonucleotides (ODN) were labelled at the 5′-end by [γ-32P]ATP using T4 polynucleotide kinase (New England Biolabs). DNA substrates were prepared and characterized as described previously (29). Briefly, the 32P-labelled ODN was annealed to its complementary strand to generate the specified substrate: single-stranded DNA (ODN1*), bubble duplex (ODN2* annealed to ODN3), flayed duplex (ODN1* annealed to ODN4), 5′-flap (ODN1*, ODN4 annealed to ODN5), 5′-overhang (ODN1* annealed to ODN5), non-damaged duplex DNA (ODN1* annealed to ODN6) and damaged duplex DNA (ODN1* annealed to ODN8*). The asterisk represents the ODN containing the radiolabel at the 5′-end. Details of the procedure adopted for generating each substrate is described in ‘Supplementary Data’.

**Purification of MtUvrA protein.** *Mycobacterium tuberculosis* UvrA was over-expressed in *E. coli* Rosetta2(DE3) pLysS strain harbouring the plasmid pMTHisUvrA and purified through a two-step chromatographic procedure based on Ni-NTA agarose and heparin-agarose columns. Details for protein over-expression and purification are provided as ‘Supplementary Data’.

**Electrophoretic mobility shift assays.** Binding assays (10 μl) contained 50 mM HEPES (pH 7.5), 10 mM MgCl2, 2 mM DTT, 0.25 mM ATPγS, 50 μg/ml BSA, 250 pM of the indicated 32P-labelled DNA and increasing concentrations of *MtUvrA* and were carried out as detailed in ‘Supplementary Data’.

**ATPase assay.** Reaction mixtures (10 μl) contained 50 mM Tris–HCl (pH 7.5), 10 mM MgCl2, 1 mM DTT, 50 μM [γ-32P]ATP, 50 μg/ml BSA, 100 nM DNA substrate as indicated in the figure legends and increasing concentrations of *MtUvrA*. The reactions and were carried out as detailed in Supplementary Data and the amount of [γ-32P]ADP in each spot was determined using UV1 Band software and plotted as the percent ATP hydrolyzed as a function of increasing concentrations of *MtUvrA*.

**Crystallographic study**

**Crystallization.** The protein used in crystallization trials was prepared by optimizing the purification protocol as reported in ‘Supplementary Data’. Optimal crystals were obtained by mixing 1.5 μl of *MtUvrA* protein solution at 5 mg/ml with an equal volume of a reservoir solution containing 1.5 M ammonium sulphate, 0.1 M HEPES pH 7.0 and 1 mM yttrium chloride. The resulting drop was equilibrated against 500 μl of the reservoir solution, at 20°C.

**Structure determination.** Details of the procedure followed for structure determination and refinement are provided as ‘Supplementary Data’. Briefly, diffraction data were collected at 100 K up to 3.4 Å resolution using
Table 1. Data collection and refinement statistics

| MtUvrA |  |
|--------|--|
| Data collection |  |
| Space group | P3_21 |
| Cell dimensions |  |
| a, b, c (Å) | 258.3, 258.3, 204.5 |
| α, β, γ (°) | 90, 90, 120 |
| Resolution (Å) | 93.1–3.4 (3.6–3.4) |
| Observations | 259 797 (37 864) |
| Unique reflections | 106 710 (15 716) |
| Rmerge (%) | 0.091 (0.40) |
| Multiplicity | 2.4 (2.4) |
| Completeness (%) | 98.9 (100.0) |
| Refinement |  |
| No. of protein atoms | 43 673 |
| No. of Zn ions | 14 |
| Rwork (%) | 25.09 |
| Rfree (%) | 33.0 |
| R.m.s. deviation bond lengths (Å) | 0.011 |
| R.m.s. deviation bond angles (°) | 1.56 |
| Mean B value (Å²) | 82 |
| Ramachandran plot analysis |  |
| Most favoured (%) | 82.3 |
| Additionally allowed (%) | 15.6 |
| Generously allowed (%) | 1.4 |
| Disallowed (%) | 0.7 |

*Values in parentheses are for the highest resolution shell.

The atomic coordinates and structure factors have been deposited with the Protein Data Bank with the accession code 2ygr.

RESULTS AND DISCUSSION

Functional analysis of UvrA in M. tuberculosis

UvrA plays an important role in the recognition of DNA damage for repair by NER (4,5). To confirm the importance of UvrA in the repair of typical NER substrates and to assess its role in surviving more physiologically relevant DNA damage, a strain of M. tuberculosis was constructed in which uvrA was inactivated. The uvrA mutation consisted of a deletion of 1.34 kb within the 2.92 kb coding sequence and insertion of a kanamycin resistance cassette. The genotype was confirmed by Southern analysis (Supplementary Figure S1). The mutant strain was complemented using an integrating plasmid in which uvrA was expressed from its own promoter (see ‘Materials and Methods’ section).

Typical substrates for repair by NER in other bacteria include intra- and interstrand cross-links, such as those generated by UV irradiation (37) and mitomycin C (38,39), respectively. Therefore, survival of the wild-type, uvrA mutant and complemented strains following exposure to these agents was assessed initially, and compared to that previously reported for a uvrB mutant (12). As expected the uvrA mutant was highly sensitive to UV light, at doses which had only minor effects on the wild-type strain (Figure 1a). The extent of susceptibility of the uvrA mutant paralleled that of the uvrB mutant, as would be expected since UvrA and UvrB act together in damage recognition (3,14). Complementation of the uvrA mutant restored survival to levels similar to those of the wild-type, confirming that the increased susceptibility was due to the inactivation of uvrA. Similarly, both the uvrA and uvrB mutants exhibited enhanced susceptibility to mitomycin C compared with the wild-type and uvrA-complemented strains (Figure 1b). These observations confirm the importance of UvrA for NER in M. tuberculosis and show that the protein function is non-redundant, i.e. its loss could not be compensated by another mechanism.

Reactive oxygen and nitrogen intermediates represent more physiologically relevant DNA damaging agents (2). Nitrosative and oxidative stress conditions were modelled by exposure to acidified sodium nitrite and t-butyl hydroperoxide, respectively (Figure 1c and d), which have been shown previously to cause these types of damage (40,41). The survival of the uvrA mutant was reduced compared with the wild-type by exposure to either of these agents. In both cases, the sensitivity of the mutant strain was restored to levels similar to those of the wild-type on complementation. The susceptibility of the uvrA mutant to acidified nitrite resembled that observed previously in M. tuberculosis when uvrB was inactivated (12). However, in contrast to our result, mutation of uvrB was reported to not cause increased sensitivity to oxidative stress. This difference may arise from the use of different assays in the two studies: the disk diffusion assay used in the uvrB study was probably less sensitive than that used in the present work (CFU determination). It is also possible that the effect seen here is a result of alkylation via the formation of an alkoxy radical (42). Taken together, these data confirm that UvrA is important for the repair of nitrosative and to a lesser extent oxidative DNA damage, and is thus likely to play a role in bacterial survival during infection.
The DNA binding activity of purified recombinant \( M.tuberculosis \) UvrA was characterized by means of electrophoretic mobility shift assays. Since the sequential two-step mechanism of nucleotide incision begins with the process of damage recognition by UvrA, we used a variety of DNA substrates (Supplementary Table S1) to explore how the local DNA structure influences the binding of the enzyme that ultimately determines the efficiency of the incision. To this end, we used a bona fide NER substrate (43) (i.e., a damaged duplex DNA molecule containing a site-specific lesion represented by a single internal fluoresceinated-dT adduct) and some common intermediates generated during various DNA metabolic processes, such as DNA replication, repair, recombination and transcription. Typically, the assays were performed with 250 pM of the indicated radio-labelled substrate with increasing concentrations of \( M.tuberculosis \) UvrA in the presence of 0.25 mM ATP and 10 mM MgCl\(_2\). The data from electrophoretic mobility shift assays indicate that \( M.tuberculosis \) UvrA binds to different DNA structures in the following hierarchical manner: single-stranded DNA > duplex DNA containing a site-specific lesion > bubble duplex > flayed 5'-flap > 5'-overhang > non-damaged duplex DNA (Figure 2, panels a–g). Quantification of protein–DNA complexes in the respective autoradiograms suggests robust binding of \( M.tuberculosis \) UvrA to single-stranded and damaged duplex DNA by ~3-fold more efficiently than to the non-damaged duplex DNA (Figure 2, panels h and i). These data are in agreement with the results from \( E.coli \) UvrA, which displays higher affinity for single-stranded DNA (44). It is noteworthy, however, that \( M.tuberculosis \) UvrA has structure-specific DNA binding activity and that the extent of binding correlated with single-stranded DNA within the DNA substrate.

\( M.tuberculosis \) UvrA displays DNA-dependent ATPase activity

The interaction of UvrA with DNA is regulated by ATP binding and its hydrolysis (5). \( Escherichia\, coli \) UvrA was originally characterized as a DNA-independent ATPase (44). However, subsequent studies showed decrease in the \( k_M \) and \( V_{max} \) for ATP hydrolysis with the addition of increasing concentrations of double-stranded DNA (45). Currently, it is thought that ATP binding is not essential for DNA binding, but ATP hydrolysis is...
believed to drive UvrA dimer dissociation and consequently reduces DNA binding (5). Despite this general picture, the mechanistic details of how ATP binding and its hydrolysis regulate the interaction of UvrA with DNA are poorly understood.

We used recombinant MtUvrA to test the effect of single- and double-stranded DNA on its ATPase activity. Notably, we observed that MtUvrA has a low intrinsic ATPase activity that can be stimulated by single- as well double-stranded DNA (Figure 3, panels a–c). Furthermore, stimulation was greater in the presence of double-stranded DNA compared to single-stranded DNA. In particular, we observed a 5-fold increase in ATPase activity in the presence of double-stranded DNA (Figure 3d). We conclude that the ATPase activity of MtUvrA is more efficient in the presence of DNA than in its absence. Similarly, others have shown that the ATPase activity of Bacillus caldotenax UvrA was stimulated ~3-fold in the presence of single-stranded or damaged DNA (43).

MtUvrA overall structure

The structure of a ligand-free form of MtUvrA was solved at 3.4 Å. Four out of the six chains that are present in the MtUvrA asymmetric unit are arranged in two tight homodimers (namely BD and CE) showing the same quaternary structure arrangement described in the crystal structure of UvrA proteins reported so far (16–18), while the remaining A and F subunits are observed as independent monomers (Supplementary Figure S3, left panel).
Since these last subunits form equivalent dimers with crystallographic symmetry-related mates, hexameric assemblies, based on three identical homodimers and reminiscent of asymmetric saddles, are observed in the crystal lattice (Supplementary Figure S3, right panel). In order to investigate the occurrence of hexamers in solution we carried out a biochemical investigation by means of gel-filtration chromatography and atomic force microscopy (AFM). Size-exclusion chromatography revealed the presence of oligomeric assemblies sensibly larger than hexamers (‘Materials and Methods’ section of Supplementary Data and Supplementary Figure S2b). On the other hand, when inspected by AFM in water environment (‘Material and Methods’ and ‘Results’ in Supplementary Data) MtUvrA displayed the typical pattern shown in the Supplementary Figure S4, where globular objects of homogeneous size corresponding to dimers, represented the prevailing morphology. We, therefore, conclude that the oligomeric assembly observed in the crystal is unlikely to have a physiological significance and appears more likely the result of experimental conditions (i.e. crystal lattice constrains and/or high protein concentration).
concentration). Instead, a classic dimeric organization emerges as the functional unit in MtUvrA as described in other species.

Similarly to what has been observed in the structures of UvrAs reported so far (16–18)—independently from their membership to class I or class II, the molecular architecture of each MtUvrA chain (Figure 4a) is organized around a roughly globular catalytic core split in two NBD (NBD-I and NBD-II) that contribute to build up two functional ATP/ADP binding sites by juxtaposition.
and that are connected by a conserved flexible loop (residues 608–625). The comparison of the catalytic core of MtUvrA with the equivalent region of available UvrA structures revealed no significant conformational changes, allowing us to affirm that the bulk body of UvrA is highly structurally conserved in different species. At the same time, our data add an independent confirmation to the emerging concept that the structuring of the ATP/ADP binding sites of each UvrA monomer depends exclusively on the observed intra-chain folding and not on oligomerization events.

In parallel to what revealed by the crystal structure of *Bacillus stearothermophilus* (16) and *T. maritima* (17) UvrA, the NBD-I of MtUvrA appears to be interrupted by an additional ‘dumb-bell’-folded region, distinguishing these proteins from other ABC ATPase superfamily members (15); in class I UvrAs this peculiar region consists of the UvrB binding domain (UvrB-BD, residues 129–255) and of the insertion domain (ID, residues 290–411), which are joined by a stem bearing the Zn modules 1 and 2 (Figure 4a). Finally, the DNA recognizing C-terminal Zn finger (residues 753–779), which buds from the NBD-II and points towards the interior of the monomer, contains a zinc ion that coordinates four strictly conserved cysteine residues with tetrahedral geometry (Figure 4a, inset).

Previous studies suggested that the UvrB-BD could be subjected to major movements in order to deliver bound UvrB protein to the damaged DNA molecule (16,17,21), which is indeed housed at the ventral surface of the UvrA functional dimer upon the displacement of the C-terminal Zn fingers (17). Similarly, the structural comparison of DrUvrA2 protomers in different ligand-bound states showed the ability of the ID to undergo dramatic repositioning during DNA recognition and nucleotide binding (18).

Interestingly, the optimal superposition of the structure of ligand-free MtUvrA to either BstUvrA in complex with ADP (16) or TmUvrA associated with damaged DNA (17) (r.m.s.d. of 1.2 and 3.9 Å for the 582 Cz pairs building up the catalytic domain, respectively) as well as DrUvrA2 (r.m.s.d. ranging from 1.8 to 2.0 Å for 503 Cz pairs, depending on the chain and the model considered) revealed a remarkable structural rearrangement affecting the UvrB-BD and ID domains. In particular, in MtUvrA the UvrB-BD appears to undergo a striking 90° rotation towards the interior of the protein compared to the conformation it assumes in the other two class I UvrA structural models, where it is observed as fully exposed to the bulk solvent (Figure 4b and c, Supplementary Movie 1). Moreover, the ID in MtUvrA adopts the most open conformation with respect to what observed in the structures of BstUvrA•ADP and TmUvrA•DNA as well as DrUvrA2 in which it is located closer to the central axis of the monomer (Figure 4d).

Overall our observation further highlights the conformational flexibility featuring the UvrB-BD and ID in UvrA proteins and strongly supports the view that significant conformational changes, possibly triggered by substrates binding, accompany the dynamics of the functional interplay between UvrA, UvrB and the DNA (19).

**Structural analysis of the MtUvrA functional dimer**

The peculiar conformation adopted by the UvrB-BD in ligand-free MtUvrA profoundly impacts the overall architecture of the functional homodimer, compared to the structure of UvrA in complex either with ADP (16) or modified dsDNA (17) (Figure 5). Indeed, while a number of molecular contacts, involving residues of the dorsal side of opposing subunits, are conserved in UvrA structures reported so far, including DrUvrA2 (Supplementary Figure S5), in the MtUvrA structure additional inter-chain bonds are established between the region Lys160–Asp165 of the UvrB-BD of one subunit and residues adjacent to the C-terminal Zn finger of the opposing monomer in the dimer (Figure 5, inset).

It must be noticed that in both BstUvrA•ADP and TmUvrA•DNA structures the equivalent region of UvrB-BD is disordered (Figures 4 and 5), most probably due to the fact that it is not stabilized by protein–protein contacts as it is in MtUvrA.

Based upon molecular modelling (Figure 6a) the distinctive arrangement displayed by the MtUvrA dimer would not hamper the accessibility of ideal double-stranded DNA to the highly conserved residues Arg725, Lys735, Arg737 and Arg743, whose structural equivalents have been demonstrated to be essential for DNA binding in BstUvrA by site-directed mutagenesis (16). In contrast, when we modelled the modified DNA molecule as observed in TmUvrA•DNA structure (17) in the optimally superimposed MtUvrA dimer, steric hindrance became appreciable on both sides of the fluoresceinated-dT containing lesion at the level of both the UvrB-BD and the C-terminal Zn fingers (Figure 6b and Supplementary Movie).

**Modelling of the UvrA•UvrB complex in different states**

When we superimposed the UvrB-BD of MtUvrA onto the crystal structure of *B. stearothermophilus* UvrA•UvrB complex, which consists only of the reciprocally interacting domains of the two partners (21), no major structural rearrangements could be observed and the conformation adopted by the UvrB-BD domain in our ligand-free MtUvrA structure appears to be accessible by UvrB (Figure 7a). Therefore, based on such a structural superposition, we constructed a model of the MtUvrA•UvrB complex (Figure 8b, left panel) by using the crystal structure of full-length UvrB from *B. caldotenax* in complex with a 20 bp haipin DNA substrate containing a fluoresceinated-dT adduct (PDB-ID: 2FDc) (46). The resulting MtUvrA•UvrB complex would be compatible with both an UvrA2•UvrB2 (Figure 7b, upper panels) and an UvrA2•UvrB (not shown) stoichiometry. Moreover, the different conformation adopted by the UvrB-BD, respectively, in the structure of ligand-free MtUvrA, BstUvrA•ADP (16) and TmUvrA•DNA (17) (Figure 7b, from top to bottom), appears in all cases competent for the concomitant association to UvrB and DNA, although with different geometry. In fact, while in the MtUvrA2•UvrB2 model the double-strand DNA should be hosted inside an only partially solvent-accessible track, which is built up by the facing ventral surfaces of
both protein components, in the other two models the UvrB-BD repositioning would result in the exposure of the DNA molecule to the bulk solvent. We therefore propose that the described three alternative conformations could represent different structural snapshots along the process of UvrB delivering to the damaged DNA.

On the basis of the available structural information, we are tempted to propose the following model, possibly illustrating the sequence of the first steps in NER (Figure 8). According to this model, the UvrA₂•UvrB₂ structural unit scanning DNA could display the UvrB-BDs in the closed conformation we observe in the structure of the ligand-free MtUvrA. Upon ATP hydrolysis taking place in UvrA the UvrB-BDs would flip out resulting in the conformation observed in BstUvrA•ADP (16); however, this would be insufficient to promote both UvrA₂•UvrB₂ complex disassembling and UvrA₂ dimer dissociation. When a lesion is encountered on DNA, the displacement of the UvrB-BDs could unlock the C-terminal Zn fingers that could move apart one from each other to make room for the DNA molecule;
this phenomenon indeed observed in the \(TmUvrA\)DNA crystal structure (17) weakens the inter-chain contacts stabilizing the UvrA2 dimer, which could subsequently dissociate leaving UvrB bound to the damaged DNA.

**CONCLUSIONS**

NER is an extremely conserved molecular system that governs DNA integrity and stability in all organisms (4); however, the proteins acting in the first events of this pathway substantially differ between bacteria and eukaryotic cells (37) and bioinformatics analyses fail in identifying human orthologues of the UvrABC components. Our results provide experimental evidence that UvrA is required for optimal \(M.\) \textit{tuberculosis} survival to physiological DNA-damaging stress, possibly implicating this gene in the persistence of the bacillus in the host. The herein reported crystal structure of UvrA in its ligand-free form further highlights the remarkable conformational plasticity displayed by UvrA along the series of molecular events that features the protein function. Overall, our genetics, biochemical and structural investigations revealed novel insights into the function of \(MtUvrA\) and provide a significant contribution toward the understanding of the mechanistic aspects of the NER pathway in \(M.\) \textit{tuberculosis}.

**ACCESSION NUMBER**

The atomic coordinates and structure factors have been deposited with the Protein Data Bank with the accession code 2ygr.
occur leaving UvrB stably associated to the DNA. Weakening of UvrA inter-subunit contacts, UvrA dissociation would however, in the presence of distorted damaged DNA that causes a weakening of UvrA inter-subunit contacts, UvrA dissociation would occur leaving UvrB stably associated to the DNA.

**SUPPLEMENTARY DATA**

Supplementary Data are available at NAR Online.

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