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Structure of the *uvrB* gene of *Escherichia coli*. Homology with other DNA repair enzymes and characterization of the uvrB5 mutation

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ABSTRACT

1. The complete nucleotide sequence of the Escherichia coli uvrB gene has been determined. The coding region of the uvrB gene consists of 2019 nucleotides which direct the synthesis of a 673 aminoacid long polypeptide with a calculated molecular weight of 76.614 daltons.
2. Comparison of the UvrB protein sequence to other known DNA repair enzymes revealed that 2 domains of the UvrB protein (domain I = 6 amino acids, domain II = 14 amino acids) are also present in the protein sequence of the uvrC gene. We show that the structural homologies between UvrB and UvrC are as well reflected by the cross-reactivity of anti-uvrB and anti-uvrC antibodies with UvrC and UvrB protein respectively. In the N-terminal part of UvrB, domain III (17 amino acids) shows a strong homology with one part of the AlkA gene product. Adjacent to domain III, an ATP binding site consensus sequence is found in domain IV.
3. The uvrB5 mutant gene from strain AB1885 has been cloned on plasmid pBL01. We show that the uvrB5 mutation is due to a point deletion of a CG basepair and results in the synthesis of an 18 kD protein composed of the 113 N-terminal amino acids of the wild type uvrB gene and a 43 amino acid long tail coded in the -1 frame.

INTRODUCTION

In Escherichia coli excision repair of damaged DNA is mediated by the UvrA, B and C gene products. The three proteins, which function in concert, recognize a large number of different DNA lesions, affecting both purine and pyrimidine nucleotides (for a review see 1). Such a broad action spectrum suggests that the UvrABC excinuclease recognizes a deformation or irregularity in the DNA helix rather than the DNA adduct itself (2). Consistent with such a concept is the observation that ABC excinuclease hydrolyses the 8th phosphodiesterbond 5' and the 4th or 5th phosphodiesterbond 3' to the modified base (3-5), which suggests that the enzyme might approach the DNA helix from the side opposite to the DNA lesion (2). The individual functions of the different components of the UVR excision nuclease are only beginning to be understood. UvrA is an

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ATPase (6) and binds to single-stranded and UV irradiated duplex DNA with a higher affinity than to unirradiated duplex DNA. The UvrB protein stimulates the ATPase activity of UvrA by a factor of 2.5 in the presence of UV-irradiated double-stranded DNA (2). Only a slight stimulation is observed in the presence of unirradiated duplex DNA whereas in the absence of DNA no stimulation is registered. These experiments have been interpreted to indicate that the enzyme complex is assembled on damaged DNA and does not exist as such free in solution (2). Indeed the UvrB component enhances the ability of the UvrA protein to bind to UV-irradiated duplex DNA. This enhanced binding is ATP dependent (7). After ATP hydrolysis a stable UvrAB-irradiated DNA complex resistant to chelators and high salt is formed (7). It has been suggested that the AB complex is first formed at a non-specific site in UV-irradiated DNA and is than translocated to the damaged site. This translocation would need ATP hydrolysis (8). Once the AB-damaged site complex has been preformed the only addition of the UvrC component results in DNA incision with no need of extra energy. After the incision event the excinuclease-DNA complex persists (9) and both the UvrD protein (DNA helicase II) and the PolA gene product (DNA polymerase I) are necessary to release the 12-13 basepair-long oligonucleotide harboring the DNA adduct, and promote turn-over of the ABC excinuclease (9,10). The simultaneous requirement of all three excinuclease components to promote DNA incision _in vitro_ (11) suggested that the expression of UvrA, B and C might be coordinately regulated. Indeed it has been shown that both UvrA and UvrB are subjected to SOS regulation (12,13). The kinetics of UvrC transcription were different and more difficult to interprete (14).

The structural organization of the regulatory region of the _uvrB_ gene has been described in detail (15,16). The recA-lexA regulated expression of the _uvrB_ gene has been studied both _in vitro_ (16) and _in vivo_ (17). In addition it has been proposed that uvrB expression might be coupled to DNA replication (18).

A final understanding of the molecular mechanism of action of the different Uvr components in excision repair or in other cellular processes will depend on the analysis of the specific aminoacid to aminoacid and aminoacid to nucleotide contacts between the different Uvr proteins and DNA. Such studies will depend on the knowledge of the primary sequence of the different proteins. Furthermore the molecular characterization of mutations in the different gene products will be of great value to pinpoint

active sites in the different components of the Uvr excinuclease. The sequence of the uvrC gene and the deduced aminoacid composition of the corresponding protein have been published (19). Here we report the complete nucleotide sequence of the wild type uvrB gene and the characterization of the mutation responsible for the uvrB5 phenotype in strain AB1885.

MATERIALS AND METHODS

Bacterial strains used were: HP3435 (30), AB1885 (33) and JM101 (23). Recombinant DNA techniques were essentially as described by Maniatis et al. (42). Restriction endonucleases, alkaline phosphatase and T4 DNA ligase were purchased from Boehringer. Large fragment of DNA polymerase I (freeze dried lyphozyme) was from BRL. Deletions were created with Bal31 starting from the unique BglII site in uvrB. DNA sequences were determined by the dideoxy chain termination method (22) using the M13 mp8, 9 or 10 phage system. (α-^{35}S)dATP or (α-^{32}P)dCTP were purchased from Amersham, Inc. *In vitro* coupled transcription-translation kits were from Amersham Inc. and used according to the manufacturers instructions with the only exception that RNasin was included at a concentration of 1 unit/μl. Antibodies were prepared in rabbits by several intravenous injections of highly purified Uvr proteins (43). Immuno-dotblot analysis was based on the method described by Hawkes et al. (41).

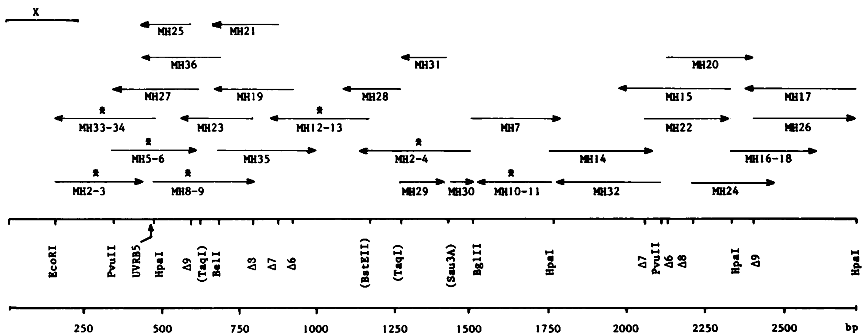

Figure 1. Strategy used in the sequencing of the uvrB gene. The different M13 recombinant clones (MH2-MH36) and the part of the DNA sequence determined from each of these clones is indicated. * Clones from w.t. and mutant sequenced in parallel. UvrB5 indicates the position of the mutation in UvrB5. Restriction sites in brackets: not all sites are represented. Δ 6, 7, 8, 9 indicate the deletion end points of Bal31 generated clones.

RESULTS AND DISCUSSION

A. Nucleotide sequence of the uvrB gene

The construction of recombinant plasmids carrying the Escherichia coli uvrB gene, including its transcriptional and translational regulatory elements has been reported previously (15). Plasmid pNP12, derived from pACYC177 (20) harbours a 4.8 kb long PstI-BamHI insert originating from the colony bank plasmid pLC25-23 (21) which carries the complete wild type uvrB gene. The promoter as well as the start of the uvrB coding sequence have been localized upstream of a unique EcoRI site (15). The DNA sequence around the EcoRI site (nucleotides 1-219 in fig. 2) has been published previously (van den Berg et al., 1981). In order to determine the complete sequence of the uvrB gene we started sequencing at the unique EcoRI site in pNP12 and proceeded towards the BamHI site. Sequences were determined by the dideoxy chain termination method (22) using the M13 phage system (23). Clones for sequencing were generated by introducing either selected restriction fragments from the EcoRI-BamHI region of pNP12 or fragments generated by Bal31 digestion into mp8, mp9 and mp10 phages. A complete overview of the sequencing strategy is presented in fig. 1. Most of the sequence was determined in both strands with the only exception of 280 nucleotides between position 1000 and 1280 which were sequenced only from the (-) strand but in three different clones (fig. 1). Examination of the complete nucleotide sequence (fig. 2) reveals only one long open reading frame initiating at an ATG codon at position 133-135. This initiation codon has previously been assessed as being the start of the uvrB gene coding region (15). The open reading frame is terminated at an TAA stop codon at position 2152-2154, leaving an open reading frame of 673 amino acids. From these results a molecular weight of 76.614 daltons can be predicted for the UvrB gene product which is in good agreement with the values of 80 K (15) and 84 K (24) determined previously from SDS-PAGE. Fig. 3 shows that the uvrB coding frame can be correctly predicted from theoretical considerations by using the "positional base preference" method of Staden (25). The method relies on the observation that the four bases are unevenly used at different positions in codons namely a preference of G, and to a

Figure 2. Nucleotide sequence of the uvrB gene. Promoters and LexA binding site (15) are indicated. Palindromic sequences downstream of the structural gene are represented by arrows. Domains I-IV (see text) are boxed. C471 deleted in UvrB5, initiation and termination codons of UvrB and UvrB5 are indicated.

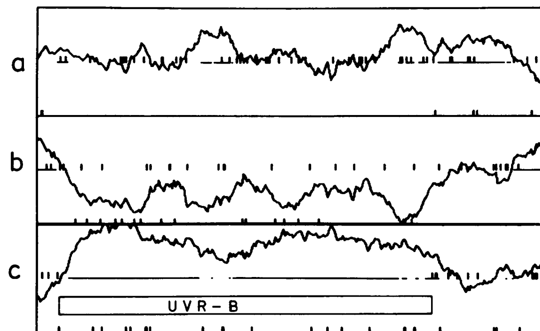

Figure 3. Prediction of the uvrB coding sequence using the "positional base preference" method (Staden, 1984). 3 different frames are indicated (a,b,c). The coding part of the uvrB gene is indicated in the coding frame (c).

lesser extent A, in position 1 and A rather than G in position 2. The slight uncertitude of the plot around codons 250-300 is probably due to a concentration of hydrophobic amino acids in this region (more T's in second position) (25). Downstream of the termination codon a region of extensive dyad symmetry covering more than 100 nucleotides is encountered (fig 2.). Parts of this region fit with the consensus established for repetitive extragenic sequences (REP sequences) (Fig. 4). These structures have been found in non-coding regions at many other locations on the E.coli chromosome (26-28). Their function is not yet known but it has been suggested that they might play a role in mRNA stability (27). The data presented here show that uvrB has two REP sequences.

B. Cloning and characterization of the mutant uvrB5 gene

Chromosomal DNA from strain AB1885 (uvrB5) (29) was digested with PstI and BamHI and ligated to pACYC177 (20) digested with the same enzymes. The ligation mixture was used to transform strain HP3435 (ΔuvrB) (30) to Km^R. Resistant clones were plated on nitrocellulose filters at a density of 12.000 colonies per 13 cm filter, lysed and hybridized to ^{32}P-nicktranslated PstI-BamHI fragment from plasmid pNP12, harboring the wild type uvrB gene. Positive colonies were isolated and found to contain a recombinant plasmid, pBL01, undistinguishable from pNP12 by restriction analysis. However, pBL01 did not confer UV resistance to strain HP3435 (ΔuvrB) as pBL01 harbors the uvrB5 mutant gene. The mutation in pBL01 responsible for the uvrB5 phenotype was localized in the 1360 nucleotide long EcoRI-BglII fragment (fig. 1) representing the N-terminal part of the

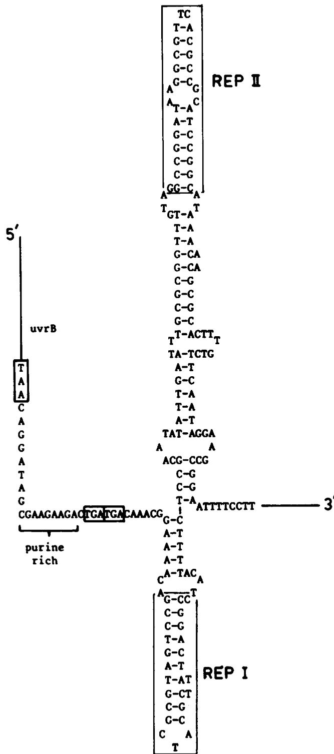

Figure 4. Palindromic sequences downstream of the uvrB coding region: the uvrB TAA stop codon, as well as two downstream TGA stop codons in the same frame, are boxed. The highly conserved REP sequences are boxed.

uvrB gene, by showing that the mutant phenotype could be transfered from pBL01 to pNP12 by exchanging the EcoRI-BglII fragment between the two plasmids. Hence the EcoRI-BglII fragment from pBL01 was sequenced completely in parallel with the corresponding fragment from the wild type uvrB gene. The only difference between the wild type and mutant fragment resides in the absence of a C residue at position 471 in fig. 2 in the case of the uvrB5 mutant gene (fig. 5). This result indicates that the uvrB5 phenotype is due to a point deletion of a C residue 338 nucleotides dowstream of the uvrB initiation codon. The localization of the uvrB5 mutation in this part of the uvrB coding sequence is further substantiated by the following experiment: pBL10 is derived from pBR329 (31) and harbors a 428 nucleotide long TaqI fragment derived from the wild type uvrB gene (position 203-631 in fig. 2) cloned in the Tc^R gene. pBL-10 was found to be able to rescue the uvrB5 mutation by double crossing-over with a frequency of $2x10^{-5}$ whereas when the vector pBR329 was used alone no rescue was found with a frequency higher than 10^{-9}. The experiment indicates

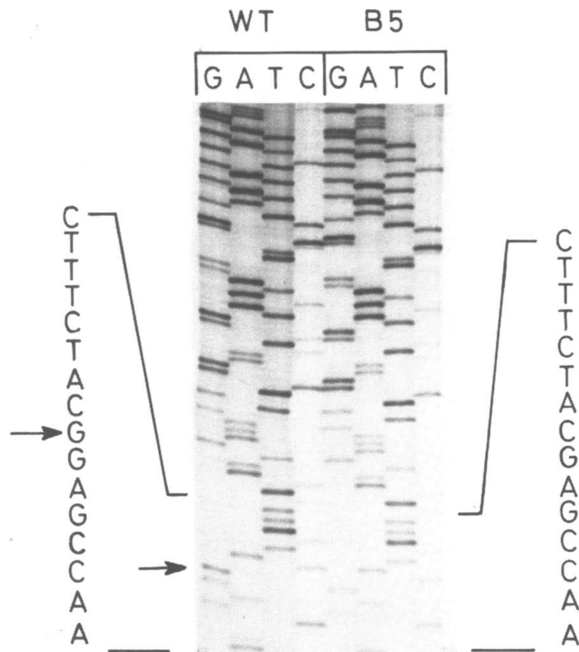

Figure 5. Direct comparison of the DNA sequence of the w.t and uvrB5 gene in the region of the uvrB5 mutation.

that the chromosomal mutation in strain AB1885 is situated in the uvrB coding sequence between position 203 and 631, that it is the only mutation in uvrB responsible for the uvrB5 phenotype and that the possibility that the mutation at position 471 in pBL01 has arisen during the cloning procedure is very unlikely.

From the sequencing data it can be predicted that the UvrB5 protein is composed of the 113 N-terminal amino acids of the wild-type uvrB gene and a 43 aminoacid long tail coded in the -1 frame and terminated at an TGA stop codon at position 602-604 (fig. 2). From these data a molecular weight of 18.047 D can be calculated for the UvrB5 protein. Fig. 6 shows that, in agreement with the theoretical predictions, plasmid pBL01 directs the synthesis of a protein of approximately 17-18 K in an *in vitro* transcription-translation system.

C. Sequence homologies between the UvrB and UvrC proteins

From the action mechanism of the Uvr excinuclease (simultaneous incision of the damaged DNA strand at two different positions, one at each side of

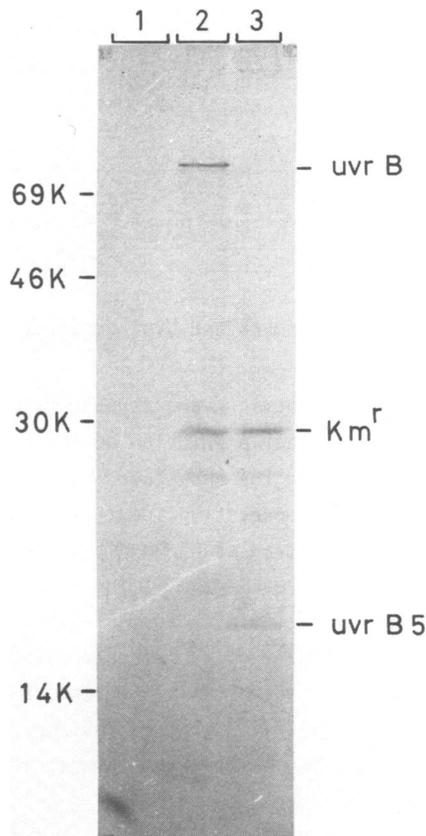

Figure 6. In vitro transcription-translation directed either by pNP12 (lane 2) or pBL01 (lane 3). In lane 1 no plasmid has been added to the system.

the DNA adduct) one might expect to find in the protein sequence of the 3 excinuclease subunits homologous regions which might be localized either on one Uvr protein or on several proteins. In this respect it was interesting to compare the protein sequence of the uvrB gene to the published sequence of the UvrC protein (Sancar et al., 1984). Protein sequences were compared using the computer program "DIAGON" of Staden (32). The results represented here were obtained with the "perfect matching" option. Two regions of significant homology between the UvrB and UvrC proteins have been identified (fig. 7). Domain I contains 6 consecutive identical residues (amino acids 352-357 in UvrB and 326-331 in UvrC) flanked by a tyrosine residue in

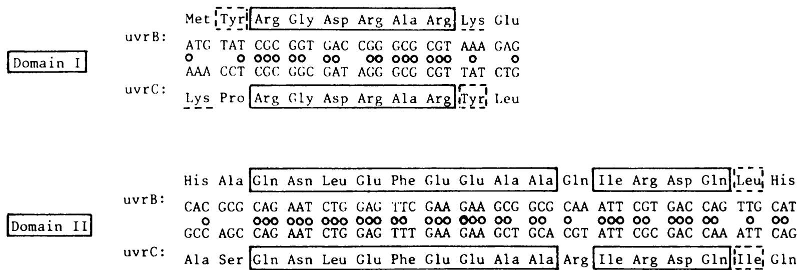

Figure 7. Homologous domains in UvrB and UvrC proteins.

each case. Both regions have a basic character and might be involved in DNA-protein interactions. No clear prediction on the tertiary structure of these regions could be made using the Chou and Fassman predictive rules (33). Domain II contains 14 consecutive identical residues with only one mismatch at position 10 (Arg instead of Gln). This domain is localized in the C-terminal region of the uvrB gene (amino acids 648-661) and in the N-terminal half of the uvrC gene (amino acids 197-210). Using the Chou and Fassman predictive rules both regions can unequivocally be assessed as α-helical. Interestingly, in UvrB this region is part of a large α-helical region formed by the 44 C-terminal residues of UvrB. The homologous region in UvrC constitutes as well the largest α-helix which can be found in the protein sequence (not shown).

Homologies between UvrB and UvrC could not only be revealed by protein sequence comparisons but also by immunological techniques. The results represented in fig. 8 show that antibodies produced against purified UvrB protein crossreact with the UvrC protein and antibodies against UvrC recognize the UvrB protein. No crossreactivity was found between UvrA and UvrB, whereas only a slight reactivity is observed between UvrA and UvrC. None of the three antibodies reacted with BSA (fig. 8) or EF-Tu a major E.coli protein (not shown). These immunological data suggest that common regions in UvrB and UvrC are localized at the protein surface. Such regions might constitute functionally important domains. Site-directed mutagenesis studies are in progress to clarify this point.

E. Sequence homologies between UvrB and other DNA repair enzymes

Comparison between UvrB and AlkA (35) revealed a region of significant homology (fig. 9) localized in the N-terminal part of UvrB (domain III: amino acids 66-84). This 19 residue long domain harbors 2 stretches of amino acids identical in both proteins (6 and 3 residues respectively),

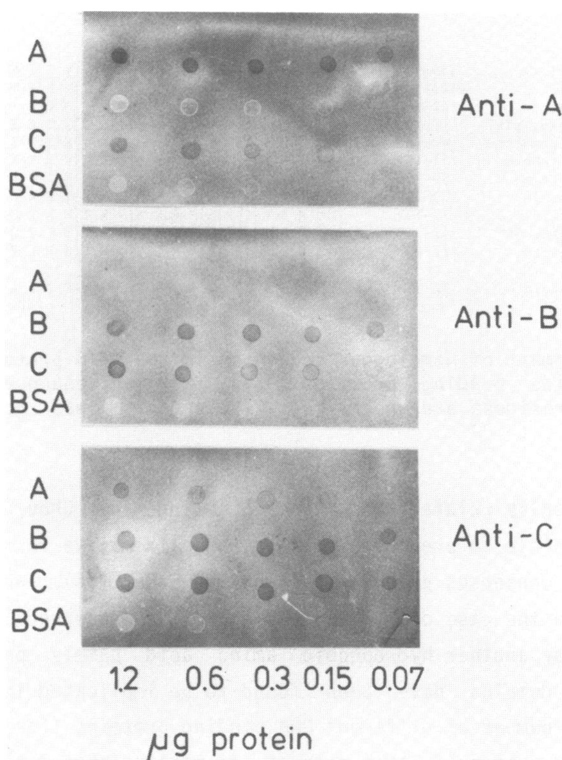

Figure 8. Dot immunobinding assay with anti-UvrA, anti-UvrB and anti-UvrC antibodies. Purified Uvr proteins (43) were spotted onto nitrocellulose membranes at the amounts indicated and assayed with the specifific antibody essentially as described by Hawkes et al., 1982. Bovine serum albumin (BSA) was used as a control.

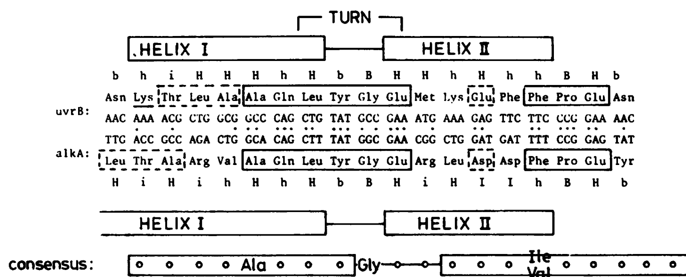

Figure 9. Homology between the UvrB and the AlkA proteins: The Chou and Fassmann helical assessments for each aminoacid are indicated (H: strong helix former; h: helix former; I: weak helix former; i: indifferent; B: strong helix breaker; b: weak helix breaker) (Chou and Fassman, 1978). The consensus proposed for bihelical regions is represented (Pabo and Sauer, 1984).

Protein	Residues	Sequences
ATPase β, ox	150-171	G G K I G L F G G A G V G K T V F I M E L I
ATPase β	143-164	G G K V G L F G G A G V G K T V N M M E L I
ATPase α	162-183	G Q R E L I I G D R Q T G K T A L A I D A I
AMP kinase, pig	8- 29	S K I I F V V G G P G S G K G T Q C E K I V
Myosin, nematode	162-183	N Q S M L I T G E S G A G K T E N T K K V I
Myosin, rabbit	171-192	N Q S I L I T G E S G A G K T V N T K R V I
RecA protein	59- 80	G R I V E I Y G P E S S G K T T L T L Q V I
DnaB protein	223-244	S D L I I V A A R P S M G K T T F A M N L V
Rho protein	172-192	G Q R G L I V A P P K A G K T M L L Q N I A
TdR kinase, HSF	47- 69	L L R V Y I D G P H G M G K T T T T Q L L V
UvrD protein	22-43	R S N L L V L A G A G S G K T R V L V H R I
UvrB protein	32-53	L A H Q T L L G V T G S G K T F T I A N V I

Figure 10. Alignment of homologous sequences in the UvrB protein and other adenine nucleotide binding proteins (34). Similar sequences are boxed. Conserved basic residues are underlined. The organism was E.coli unless specified.

flanked by chemically related amino acids. Using the Chou and Fassman rules it is possible to predict a helix-turn-helix motive for this region. Helix I fits the consensus proposed by Pabo and Sauer (36), whereas helix II is shorter in the case of UvrB and AlkA and the conserved Ile/Val residue is replaced by another hydrophobic amino acid namely phenylalanine. Such bihelical domains have been found to be implicated in protein-DNA recognition in a number of different DNA binding proteins (for a review see 36). It is interesting, in this respect, to mention that the AlkA enzyme, like the Uvr excinuclease does not recognize one specific DNA adduct, but a large number of different (alkylation-) products, both on purine and pyrimidine nucleotides (37). As with the Uvr excinuclease, it has been reasoned that AlkA recognizes in a first instance a deformation or irregularity in the DNA helix rather than the DNA adduct itself (37). Hence, Uvr excinuclease and AlkA might harbour homologous domains, involved in helix irregularity recognition. That such a domain would be localized on the UvrB excinuclease subunit, is in agreement with experimental findings (see introduction), which show that UvrB targets the excinuclease specifically to damaged DNA. Obviously, such a hypothesis has to be considered with care. However, we believe that the results reported here might provide a valuable tool to study the damage recognition process in both systems.

Comparison of the UvrB and UvrD sequences (34) revealed the presence of an identical pentapeptide, Gly-Ser-Gly-Lys-Thr, localized at position 42-46 in UvrB and 32-36 in UvrD. Interestingly, this pentapeptide, in UvrD, is part of a consensus sequence found in a large number of ATP binding proteins (34,38). The sequence found in UvrB completely fits into this

proposed consensus (fig. 10; domain IV in fig. 2). What might be the reason for such an ATP binding site in UvrB? UvrB is not an ATPase by itself, but stimulates efficiently the UvrA ATPase activity, when the AB complex is assembled on damaged DNA (see Introduction). These results, taken together with the structural data reported here, are in favor of a model where ATP binding site (situated on UvrB) and ATPase site (situated on UvrA) have to be correctly juxtaposed (a situation obtained when the complex is assembled at a damaged site in DNA), in order to be able to efficiently hydrolyse ATP. Physical measurements have indicated that the extent of the deformation induced in DNA by different agents can vary greatly (Pearlman et al., 1985). Nevertheless it has been shown that DNA damaged by these agents is incised by the Uvr excinuclease in a very similar way (see Introduction). We tentatively propose that ATP hydrolysis is needed to bring damaged DNA into a common, incisable, conformation. Interestingly, an ATP binding site consensus has as well been identified in the rad3 gene (40) as well as in several other rad genes (E.C. Friedberg, personal communication), all involved in excision repair in *Saccharomyces cerevisiae*, suggesting that the model proposed here might not only be confined to *Escherichia coli*.

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