Front. Biol. 2013, 8(4): 363–368
DOI 10.1007/s11515-013-1259-x

MINI-REVIEW

# How two helicases work together within the TFIIH complex, a perspective from structural studies of XPB and XPD helicases

Li FAN (✉)

*Department of Biochemistry, University of California at Riverside, Riverside, CA 92521, USA*



**Abstract** **Xeroderma pigmentosum group B (XPB) and D (XPD) are two DNA helicases inside the transcription factor TFIIH complex required for both transcription and DNA repair. The importance of these helicases is underscored by the fact that mutations of XPB and XPD cause diseases with extremely high sensitivity to UV-light and high risk of cancer, premature aging, etc. This mini-review focuses on recent developments in both structural and functional characterization of these XP helicases to illustrate their distinguished biological roles within the architectural restriction of the TFIIH complex. In particular, molecular mechanisms of DNA unwinding by these helicases for promoter opening during transcription initiation and bubble-creation around the lesion during DNA repair are described based on the integration of the crystal structures of XPB and XPD helicases into the architecture of the TFIIH complex.**

**Keywords** XPB, XPD, TFIIH, helicase, DNA repair, nucleotide excision repair, transcription

## Introduction

Transcription factor TFIIH involved in both transcription and DNA repair is a 10-subunit complex including two helicases (XPB and XPD), a cdk-activation kinase CAK (cyclin H, cdk7 and Mat1) and five non-enzymatic proteins (Compe and Egly, 2012). The 3D model of human TFIIH developed by electron microscopy (EM) analysis shows that the core of TFIIH consists of five subunits (XPB, p62, p52, p44 and p34) and forms a ring-like structure with a hole large enough to hold a double-stranded (ds) DNA helix (Schultz et al., 2000). The CAK subcomplex is anchored by XPD to the core as a bulge. The smallest subunit TTDA (or p8) is also attached to the core. TFIIH is required for basal transcription initiation at RNA polymerase I and II promoters as well as for nucleotide excision repair (NER), a major DNA repair pathway to remove bulky DNA lesions produced by ultraviolet (UV) light and chemical modifications (for recent reviews to see Gillet and Schärer, 2006; Hanawalt and Spivak, 2008; Naegeli and Sugasawa, 2011). The importance of TFIIH in NER is highlighted by mutations in three subunits (XPB, XPD and TTDA) causing diseases of photosensitivity such as Xeroderma pigmentosum (XP), Cockayne syndrome (CS) and trichothiodystrophy (TTD). NER includes two subpathways, the global genome DNA repair (GG-NER) and transcription coupled DNA repair (TCR). The two subpathways mainly differ in the initial DNA damage recognition. GG-NER is initiated by the interactions of XPC-HR23B and the DNA lesion while TCR is initiated by a stalled RNAPII caused by a lesion at the template strand during transcription elongation. The two subpathways merge into a common mechanism by the recruitment of the TFIIH complex. After TFIIH is recruited to the damage site, it opens a bubble around the lesion through the actions of XPB and XPD helicases. This local DNA opening is enhanced by the presence of XPA and RPA proteins. Next, endonucleases XPF-ERCC1 and XPG make a dual incision in the damaged DNA strand about 22 bases at 5′-side and 5 bases at 3′-side away from the lesion, respectively. The incised DNA fragment is then removed, and the gap is finally filled by DNA polymerase and ligase.

Purified XPB and XPD helicases show opposite polarities in unwinding DNA duplex as XPB is a 3′ to 5′ helicase and XPD is a 5′ to 3′ helicase, respectively. In spite of over two decades of research, it is still not clear why TFIIH carries two helicases of opposite polarities, and how XPB and XPD work inside the TFIIH complex to fulfill their biological functions, due to the lack of structure information about XP helicases

Received November 14, 2012; accepted February 15, 2013
Correspondence: Li FAN
E-mail: li.fan@ucr.edu

and the TFIIH complex besides the EM structures of yeast and human TFIIH (Chang and Kornberg, 2000; Schultz et al., 2000). In recent years, several crystal structures of archaeal XPB and XPD helicase have been determined (Fan et al., 2006; Fan et al., 2008; Liu et al., 2008; Wolski et al., 2008). These structures have facilitated functional studies on the XP helicases as well. This mini-review focuses on these recent progresses in order to illustrate the molecular mechanisms for XPB and XPD to fulfill their distinguished roles in the cell. However, this mini-review will not intend to give a comprehensive review or update on these studies, which have recently been covered by several excellent review articles (Egly and Coin, 2011; Fuss and Tainer, 2011; Kuper and Kisker, 2013). Instead, the author will focus on applying these results to develop molecular mechanisms of DNA unwinding by XPB and XPD helicases during transcription initiation and DNA repair by integrating the crystal structures of XPB and XPD helicases into the architecture of the TFIIH complex derived from electron microscopic results. This mini-review explains for the first time at the molecular level why a 28-bp DNA bubble is created asymmetrically to the lesion by the TFIIH complex, and proposes that the TFIIH complex is recruited differently to the damaged DNA in TCR than in GG-NER.

## Structure of XPB indicates an unconventional helicase

Crystal structures of *Archaeoglobus fulgidus* XPB (AfXPB) homolog have been determined in the forms of the full-length, an N-terminal half and a C-terminal half (pdb codes 2FWR, 2FZ4 and 2FZL; Fan et al., 2006) but high resolution structures are not available for any eukaryotic XPB helicases at the present time [the crystal structure of the C-terminal half of human XPB was published (Hilario et al., 2013) when this mini-review is in press]. As expected, AfXPB contains two helicase domains HD1 and HD2 (Fig. 1A), where the seven conserved helicase motifs locate. From these AfXPB structures, two new functional motifs were identified (Fan et al., 2006): the RED motif in HD1 near helicase motif III consists of three charged residues Arg, Glu and Asp, and the thumb-like motif (ThM) is an insertion in HD2 with the fold similar to the thumb domain of T7 DNA polymerase. The functional importance of these motifs were further confirmed by mutations of these two motifs [E473A or Δ(516-526)] in human XPB. These mutations prevent human XPB to localize at damaged DNA *in vivo* (Oksenych et al., 2009). In addition, AfXPB contains a potential damage recognition domain (DRD) attached to HD1 at the N terminus. This domain is not like any accessory domains observed in other helicases, but resembles the fold of a mismatch DNA binding domain in MutS and is proposed to bind to bent DNA caused by a bulky DNA damage, the typical damage substrate of NER (Fan et al., 2006). Although it remains to see if DRD directly interacts with damaged DNA, DRD is important for the activity of the helicase-nuclease machinery consisting of archaeal XPB helicase and BAX1, an archaeal nuclease which cuts NER substrate DNA in the same way as the eukaryotic nuclease XPG (Rouillon and White, 2010; Roth et al., 2012).

The most distinguished feature of the full length AfXPB crystal structure is the orientation of the two helicase domains HD1 and HD2 (Fig. 1A), which is strikingly different from other helicases whose two helicase domains form an inter-domain groove for ATP binding and hydrolysis (Singleton et al., 2007). In the full length AfXPB structure, however, the HD1 and HD2 are oriented in such a way that HD2 need to rotate ~170 degrees about the flexible inter-domain hinge in order to form a groove for ATP binding and hydrolysis like any conventional helicases (Fig. 1A and 1B). This unique orientation of helicase domains HD1 and HD2 in AfXPB provides the structural basis for XPB to function as an unconventional helicase to fulfill its biologic functions (Kim et al., 2000), whose mechanism will be illustrated later in this review.

## Structures of XPD show a unique 4Fe-4S cluster binding domain

No high resolution structural information is currently available for any eukaryotic XPD helicase as well. However, crystal structures of XPD have been determined for archaeal homologs from three different species including *Thermoplasma acidophilum* (2VSF.pdb; Wolski et al., 2008) (TaXPD), *Sulfolobus tokodaii* (2VL7.pdb; Naismith et al., 2008) (StXPD), and *Sulfolobus acidocaldarius* (3CRV.pdb and 3CRW.pdb; Fan et al., 2008) (SaXPD). These archaeal XPD structures contain four domains including two helicase domains HD1 and HD2, an Arch domain and a unique 4FeS domain that contains a 4Fe-4S cluster observed for the first time in any helicase structures (Fig. 1C). The 4Fe-4S cluster is essential for the folding of the 4FeS domain because oxidation of 4Fe-4S cluster in the SaXPD crystals has the majority of the 4FeS domain disordered (Fan et al., 2008) (Fig. 1D). Both the Arch and 4FeS domains are formed by insertions in HD1 domain. These three domains together form a quadrilateral board with a hole at the three-domain junction near the board center. HD2 is attached to the edge between the Arch and HD1 domains. SsDNA is proposed to bind at the groove formed between the Arch and HD2 domains and through the hole, which is big enough for ssDNA to pass through. So bulky adducts like the lesions repaired by NER likely become blocks to stall XPD for transloc -ation along ssDNA during dsDNA unwinding. This is in agreement with early results showing yeast XPD (rad3) helicase stalled by DNA damage (Naegeli et al., 1993). *F. acidarmanus* XPD was recently shown to be stalled by a cyclopyrimidine dimer (CPD) in the translocation strand (Mathieu et al., 2010).

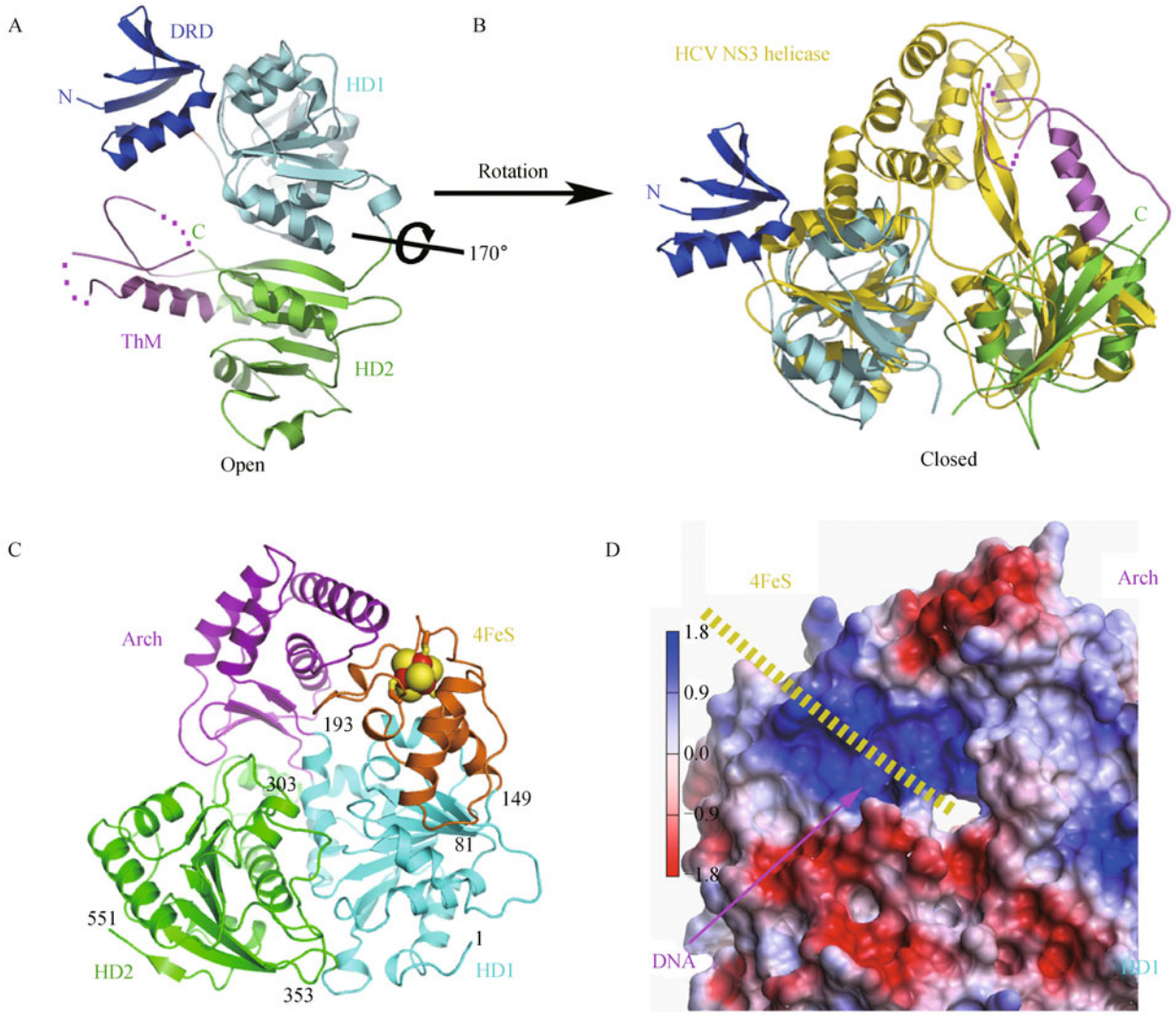


**Figure 1** Structures of archaeal XPB and XPD homologs. (A) Crystal structure of AfXPB. (B) AfXPB in a conventional helicase conformation. HCV helicase NS3 (pdb code 1A1V) is shown in yellow for comparison. (C) Crystal structure of SaXPD. (D) Electrostatic potential surface of SaXPD with proposed ssDNA in dashed line.

## Why XPB is required for transcription initiation but XPD is not

In eukaryotes, both XPB and XPD are components of TFIIH. Most *in vitro* biochemical analyses on XPB or XPD, in particular, all assays on archaeal homologs of XPB and XPD helicases, were carried out in the absence of other components of TFIIH due to the lack of protein homologs. Although these investigations have provided valuable information about the biochemical properties of XPB and XPD, we have to put them in the context of the TFIIH complex in order to fully understand the biologic roles of XPB and XPD inside the cell. So a TFIIH complex model (Fig. 2A) is constructed based on the EM model of human TFIIH (Schultz et al., 2000). The EM model shows that the central hole of TFIIH is about 3.0 nm in diameter, big enough to hold a dsDNA helix (2.0 nm in diameter). EM analysis on the core of human TFIIH indicated a continuum of structures (Schultz et al., 2000) ranging from almost straight filament (27% of 1562 particles), partially ring-shaped structures (39%), and a compact ring structure (34%). In addition, the yeast TFIIH core was isolated without Ssl2 (XPB homolog) and formed a structure similar to a question mark (Chang and Kornberg, 2000) with the ring not completely closed. Together, these data suggest the ring of TFIIH can open and close in solution or in the cell to allow TFIIH to encircle dsDNA. So TFIIH likely encircles the dsDNA helix when it is recruited to the promoter region during transcription initiation or to the damage site for DNA repair (Fig. 2B1 and 2C1). After TFIIH is recruited to the promoter region, ATP binding and hydrolysis is mediated by XPB and results in promoter melting through a so-called “molecular wrench” mechanism

(Kim et al., 2000). When XPB binds to ATP, the HD2 of XPB helicase is required to rotate about 170 degrees around the inter-domain hinge to form a binding groove between HD1 and HD2 (Fan et al., 2006). During this rotational movement, XPB HD2 likely interacts with the dsDNA helix encircled by the TFIIH ring, and brings the dsDNA helix to rotate together with HD2 to the final position (Fig. 2B2-2B3). Because the upstream dsDNA is fixed by the transcription factors (TBP and other factors) and RNA polymerase bound at the promoter, the rotation of dsDNA at the TFIIH binding site will generate torque on the dsDNA helix and "melt" the dsDNA in the middle (Fig. 2B2). Based on the structure of AfXPB and the dimensions of the TFIIH ring, HD2 possibly rotates the dsDNA helix about 60–120 degrees when HD2 itself completes ~170 degrees rotation for ATP binding and hydrolysis, resulting in 2–4 bp (based on ~33 degrees per base pair) of the dsDNA helix to be unwound. Cycles of ATP binding and hydrolysis by XPB will open a transcription bubble at the initiation site for RNA polymerase II to start transcription (Fig. 2B3–B4). In this way, XPB acts like a "molecular wrench" as suggested by early biochemical analysis (Kim et al., 2000). Since XPD is not part of the human TFIIH core to form the ring, XPD is not required for this step during transcription initiation (Fig. 2A and 2B).

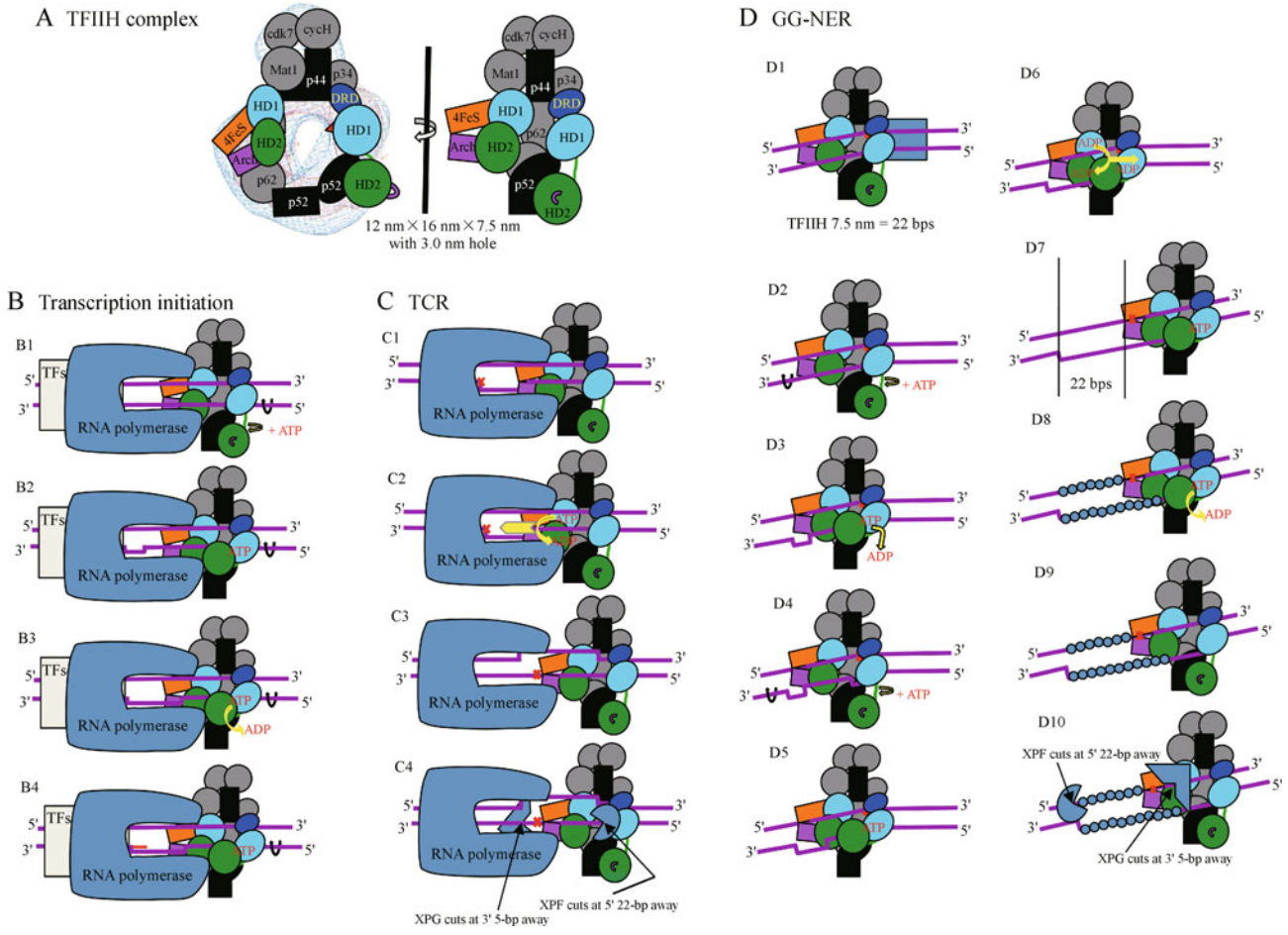


**Figure 2** Schematic mechanisms showing how XPB and XPD function inside TFIIH during transcription initiation and DNA repair. (A) The TFIIH complex. The TFIIH complex contains only nine subunits due to the absence of TTDA subunit in the TFIIH complex used for the EM (shown in the background on the left panel) analysis, showing that the thickness of the TFIIH ring is 7.5 nm, covering about 22-bp long dsDNA when the DNA passes through the hole of the ring. The TFIIH subunits are presented in gray or black objects except for XPB and XPD. XPB is presented in four domains: HD1 in light blue, HD2 in green, DRD in blue and ThM in magenta. XPD is also presented in four domains: HD1 in light blue, HD2 in green, 4FeS domain in Orange, and Arch in magenta. (B) Transcription initiation. Transcriptional factors are indicated by TFs. RNA polymerase II is shown as an U-shaped object. (C). Transcription coupled DNA repair. (D) Global genome DNA repair. DsDNA is presented by two paralleled purple lines showing phosphate backbones with base-paring not shown for simplicity. Damaged bases are shown as red crosses. Damage recognition XPC-HR23B complex is shown as a light blue box. The unwound regions of DNA are presented with widen gaps between the two strands of DNA. RPA proteins are shown as small light blue circles. Endonucleases XPF and XPG are shown as indicated in the diagram. The direction of TFIIH movement is indicated by yellow arrows with ATP hydrolysis by curved arrows.

## XPB functions as the "transmission" and XPD acts as the "driving wheel" for TFIIH to open damaged DNA for an asymmetrical dual incision

Both XPB and XPD are essential for DNA repair although only XPB is required for transcription initiation. In transcription coupled DNA repair, RNA polymerase II stalls at a damage site, leading to the recruitment of TFIIH. TFIIH is likely recruited at the dsDNA-transcriptional bubble junction, downstream to the stalled RNA polymerase (Fig. 2C1). The TFIIH ring encircles the downstream dsDNA of the transcription bubble while the two DNA strands interact with XPB and XPD separately (Fig. 2C1). Because the opposite polarities of the two XP helicases, the template DNA strand containing the damaged base likely interacts with XPD (5′ to 3′) while the other strand interacts with XPB (3′ to 5′). In this way, through ATP binding and hydrolysis, XPD moves along the template strand in a 5′ to 3′ direction and XPB in a 3′ to 5′ direction along the other DNA strand to drive the TFIIH complex upstream, therefore, pushing RNA polymerase II backward or off the DNA (Fig. 2C2). After TFIIH reaches the damage site inside the previous transcription bubble, XPD is blocked by the bulky damaged base and therefore causes the whole TFIIH complex to stall. This will result in the recruitment of XPG and XPF endonucleases. XPG binds to 3′ of the damage site through the interactions with one dsDNA-ssDNA junction and with XPD. It has been shown in vitro that XPG binds to RNA polymerase II and a bubbled DNA, but the bound RNA polymerase II blocks bubble incision by XPG (Sarker et al., 2005). This blockage can be removed by a TFIIH-dependent ATP hydrolysis (to push back), allowing bubble incision by XPG (Sarker et al., 2005). On the other hand, XPF binds to the 5′ of the damage site through the interactions with XPB and the dsDNA-ssDNA junction at the other end. Therefore, XPG cuts at the 3′-side 5 bases away from the damaged base and XPF cuts at the 5′-side 22 bases away to make an asymmetrical dual incision (Fig. 2C4).

DNA damage is initially recognized by XPC-HR23B complex during GG-NER. The crystal structure of yeast XPC ortholog Rad4 bound to Rad23 and DNA containing a cyclobutane pyrimidine dimer (CPD) lesion was determined (Min and Pavletich, 2007). Interestingly, Rad4 interacts with DNA exclusively on one side of the CPD lesion: an 11-bp segment of undamged dsDNA at 3′ side from the CPD on the damaged strand and a 4-bp segment containing the CPD. Rad4 inserts a beta-hairpin through the dsDNA helix and causes two bases paired to CPD to flip out of the duplex helix, making a 2-bp bubble and resulting in a bent dsDNA helix at the lesion (Min and Pavletich, 2007). When TFIIH is recruited to this damage site, it encircles the dsDNA at the 5′ side of the CPD (Fig. 2D1). The bent DNA duplex likely interacts directly with XPD even though XPD is not part of the core TFIIH ring. When ATP binds to XPB and causes the HD2 containing C-terminal half to rotate around the inter-domain hinge about 170 degrees, this rotation again will bring the dsDNA duplex to rotate with the HD2 of XPB. Because XPD interacts directly with downstream dsDNA (5-10 bps away based on the dimensions of SaXPD crystal structure), this rotation likely causes the unwinding of 2-4 bps near the XPD-dsDNA interaction site (Fig. 2D2-D3). Cycles of ATP binding and hydrolysis by XPB will lead to the unwinding of 10-bp duplex to allow XPD to form an active helicase-DNA complex (Fig. 2D4-D5). By this way, XPB functions as a "transmission" to engage XPD in the unwinding of dsDNA helix. At the same time, ATP binding and hydrolysis mediated by XPD (and XPB) will then drive XPD (and the whole TFIIH complex) along the damaged strand in 5′ to 3′ direction toward the lesion and XPB along the undamaged strand in a 3′ to 5′ direction away from the lesion (Fig. 2D5-D6). The RED motif of XPB inserts into the 2-bp bubble created at the lesion by XPC-HR23B complex, and likely acts as the wedge to separate the downstream dsDNA helix when XPB translocates along the DNA. Therefore, XPD functions as the "driving wheel" of TFIIH to open the damaged dsDNA. When XPD reaches the lesion, the lesion will block the translocation of XPD and stall the TFIIH complex after it has created a 22-bp bubble at the 5′ side of the lesion (Fig. 2D6). RPA then binds to the ssDNA strands (Fig. 2D9). Finally, endonucleases XPG and XPF-ERCC1 bind to the bubbled DNA and carry out the dual asymmetrical incision (Fig. 2D10).

## Summary

Significant progresses have been achieved on the structures and functions of XP helicases. Based on these results, a molecular mechanism has been proposed here to illustrate the distinguished roles played by XPB and XPD for the functions of TFIIH in transcription and DNA repair. This proposed mechanism explains for the first time, to my knowledge, why the dual incision by XPF and XPG produces a fragment of ~28-bp DNA asymmetrical to the lesion (having 22 bases at the 5′- side and 5 bases at the 3′-side of the lesion). In addition, the proposed mechanism suggests that TFIIH is recruited to the damage site by two distinguished ways for TCR and GG-NER, which can be tested experimentally. During TCR, the TFIIH complex is recruited by the stalled RNA polymerase through the interactions of XPD with RNA polymerase and likely XPG, CSA and CSB. In this way, the TFIIH complex is recruited at least 22-bp away from the lesion on the 5′-side of the template strand, then it moves toward the lesion driving by the 5′ to 3′ helicase XPD on the template strand (and possibly also by the 3′ to 5′ helicase XPB on the non-template strand). This movement likely pushes back RNA polymerase and away from the stalled transcriptional bubble, allowing the lesion to be exposed. When XPD reaches the lesion, the whole TFIIH complex stalls and the lesion never passes through the ring of TFIIH (Fig. 2C).

However, during GG-NER, TFIIH is recruited directly at the lesion site through the interactions of XPB with the DNA damage (via the Damage Recognition Domain of XPB) and the XPC-HR23B complex (Fig. 2D1). When the TFIIH complex is driven by XPD on the damaged strand in 5′ to 3′ direction and by XPB on the other strand in 3′ to 5′ direction, the lesion passes through the ring of TFIIH (Fig. 2D). This movement will knock off the XPC-HR23B complex from the dsDNA, allowing a bubble to develop around the lesion for the dual incision by XPG and XPF-ERCC1 endonucelases.

## Acknowledgements

I am grateful to John Tainer, in whose laboratory at The Scripps Research Institute I have determined the structures of AfXPB and SaXPD. I would like also to thank the Department of Biochemistry and CNAS (particularly Thomas Baldwin, Richard Debus and Russ Hille) at University of California-Riverside for many supports in establishing my own laboratory. This project has been supported by grants from UCR and the Hellman Fellowship. I apologize to people whose research activities have contributed to our understandings about the topic but are not cited here due to space limitation.

## Compliance with ethics guidelines

Li Fan declares that he has no conclict of interest. This article does not contain any studies with human or animal subjects performed by the any of the authors.

## References

Chang W H, Kornberg R D (2000). Electron crystal structure of the transcription factor and DNA repair complex, core TFIIH. Cell, 102 (5): 609–613

Compe E, Egly J M (2012). TFIIH: when transcription met DNA repair. Nat Rev Mol Cell Biol, 13(6): 343–354

Egly J M, Coin F (2011). A history of TFIIH: two decades of molecular biology on a pivotal transcription/repair factor. DNA Repair (Amst), 10(7): 714–721

Fan L, Arvai A S, Cooper P K, Iwai S, Hanaoka F, Tainer J A (2006). Conserved XPB core structure and motifs for DNA unwinding: implications for pathway selection of transcription or excision repair. Mol Cell, 22(1): 27–37

Fan L, Fuss J O, Cheng Q J, Arvai A S, Hammel M, Roberts V A, Cooper P K, Tainer J A (2008). XPD helicase structures and activities: insights into the cancer and aging phenotypes from XPD mutations. Cell, 133(5): 789–800

Fuss J O, Tainer J A (2011). XPB and XPD helicases in TFIIH orchestrate DNA duplex opening and damage verification to coordinate repair with transcription and cell cycle via CAK kinase. DNA Repair (Amst), 10(7): 697–713

Gillet L C J, Schärer O D (2006). Molecular mechanisms of mammalian global genome nucleotide excision repair. Chem Rev, 106(2): 253–276

Hanawalt P C, Spivak G (2008). Transcription-coupled DNA repair: two decades of progress and surprises. Nat Rev Mol Cell Biol, 9(12): 958–970

Hilario E, Li Y, Nobumori Y, Liu X, Fan L (2013). Structure of the C-terminal half of human XPB helicase and the impact of the disease-causing mutation XP11BE. Acta Crystallogr D Biol Crystallogr, 69 (Pt 2): 237–246

Kim T K, Ebright R H, Reinberg D (2000). Mechanism of ATP-dependent promoter melting by transcription factor IIH. Science, 288 (5470): 1418–1422

Kuper J, Kisker C (2013). DNA Helicases in NER, BER, and MMR. Adv Exp Med Biol, 767: 203–224

Liu H, Rudolf J, Johnson K A, McMahon S A, Oke M, Carter L, McRobbie A M, Brown S E, Naismith J H, White M F (2008). Structure of the DNA repair helicase XPD. Cell, 133(5): 801–812

Mathieu N, Kaczmarek N, Naegeli H (2010). Strand- and site-specific DNA lesion demarcation by the xeroderma pigmentosum group D helicase. Proc Natl Acad Sci U S A, 107(41): 17545–17550

Min J H, Pavletich N P (2007). Recognition of DNA damage by the Rad4 nucleotide excision repair protein. Nature, 449(7162): 570–575

Naegeli H, Modrich P, Friedberg E C (1993). The DNA helicase activities of Rad3 protein of *Saccharomyces cerevisiae* and helicase II of *Escherichia coli* are differentially inhibited by covalent and noncovalent DNA modifications. J Biol Chem, 268(14): 10386–10392

Naegeli H, Sugasawa K (2011). The xeroderma pigmentosum pathway: decision tree analysis of DNA quality. DNA Repair (Amst), 10(7): 673–683

Oksenych V, Bernardes de Jesus B, Zhovmer A, Egly J M, Coin F (2009). Molecular insights into the recruitment of TFIIH to sites of DNA damage. EMBO J, 28(19): 2971–2980

Roth H M, Römer J, Grundler V, Van Houten B, Kisker C, Tessmer I (2012). XPB helicase regulates DNA incision by the *Thermoplasma acidophilum* endonuclease Bax1. DNA Repair (Amst), 11(3): 286–293

Rouillon C, White M F (2010). The XBP-Bax1 helicase-nuclease complex unwinds and cleaves DNA: implications for eukaryal and archaeal nucleotide excision repair. J Biol Chem, 285(14): 11013–11022

Sarker A H, Tsutakawa S E, Kostek S, Ng C, Shin D S, Peris M, Campeau E, Tainer J A, Nogales E, Cooper P K (2005). Recognition of RNA polymerase II and transcription bubbles by XPG, CSB, and TFIIH: insights for transcription-coupled repair and Cockayne Syndrome. Mol Cell, 20(2): 187–198

Schultz P, Fribourg S, Poterszman A, Mallouh V, Moras D, Egly J M (2000). Molecular structure of human TFIIH. Cell, 102(5): 599–607

Singleton M R, Dillingham M S, Wigley D B (2007). Structure and mechanism of helicases and nucleic acid translocases. Annu Rev Biochem, 76: 23–50

Wolski S C, Kuper J, Hänzelmann P, Truglio J J, Croteau D L, Van Houten B, Kisker C (2008). Crystal structure of the FeS cluster-containing nucleotide excision repair helicase XPD. PLoS Biol, 6(6): e149