Different types of interaction between PCNA and PIP boxes contribute to distinct cellular functions of Y-family DNA polymerases

Yuji Masuda^{1,2,†}, Rie Kanao^{1,†}, Kentaro Kaji¹, Haruo Ohmori^{3,4}, Fumio Hanaoka⁴ and Chikahide Masutani^{1,*}

¹Department of Genome Dynamics, Research Institute of Environmental Medicine, Nagoya University, Furo-cho, Chikusa-ku, Nagoya 464-8601, Japan, ²Department of Toxicogenomics, Nagoya University Graduate School of Medicine, 65 Tsurumai-cho, Showa-ku, Nagoya 466-8550, Japan, ³Department of Gene Information, Institute for Virus Research, Kyoto University, Sakyo-ku, Kyoto 606-8517, Japan and ⁴Department of Life Science, Graduate School of Science, Gakushuin University, 1-5-1 Mejiro, Toshima-ku, Tokyo 171-8588, Japan

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ABSTRACT

Translesion DNA synthesis (TLS) by the Y-family DNA polymerases Poln, Poli and Polk, mediated via interaction with proliferating cell nuclear antigen (PCNA), is a crucial pathway that protects human cells against DNA damage. We report that Poln has three PCNA-interacting protein (PIP) boxes (PIP1, 2, 3) that contribute differentially to two distinct functions, stimulation of DNA synthesis and promotion of PCNA ubiguitination. The latter function is strongly associated with formation of nuclear Poly foci, which co-localize with PCNA. We also show that Polk has two functionally distinct PIP boxes, like Pol_{η} , whereas Pol_{ι} has a single PIP box involved in stimulation of DNA synthesis. All three polymerases were additionally stimulated by mono-ubiguitinated PCNA in vitro. The three PIP boxes and a ubiquitinbinding zinc-finger of Poln exert redundant and additive effects in vivo via distinct molecular mechanisms. These findings provide an integrated picture of the orchestration of TLS polymerases.

INTRODUCTION

Translesion DNA synthesis (TLS), a DNA damage tolerance mechanism, is a crucial biological function that protects cells from various genotoxic agents. Particularly in humans, DNA polymerase η (Pol η), a Y-family DNA polymerases (1), plays an important role in preventing cell death and mutagenesis after ultraviolet (UV) light irradiation, and malfunction of Pol η causes the inherited genetic disorder, xeroderma pigmentosum variant (XP-V) (2–4).

Interactions between proliferating cell nuclear antigen (PCNA) and the three Y-family human DNA polymerases (Poln, Polt and Polk) are critically involved in regulation of TLS. Poly and Polk are known to contain two PCNAinteracting protein (PIP) boxes (PIP1 and PIP2) in their central and C-terminal regions, respectively, whereas Polu is known to contain only one functional PIP box (PIP1, in the central region) (5-12). In DNA-damaged cells, PCNA is mono-ubiquitinated at residue K164 by the RAD6-RAD18 complex (13–15), and poly-ubiquitinated by additional factors including UBC13, MMS2, and RAD5/HLTF or SH-PRH (13,16–19). Each of the three Y-family DNA polymerases described above has one or two copies of the ubiquitin-binding domain (UBD), called UBZ (ubiquitinbinding zinc-finger) in Poly and Polk and UBM (ubiquitinbinding motif) in Polt (6). These findings support the notion that mono-ubiquitination of PCNA plays a key role in switching from replicative DNA polymerase stalled at a site of DNA damage to a DNA polymerase (such as Poly, ι or κ) capable of carrying out TLS (14-15,20-21). However, this idea is still controversial (5), and more recent publications report that Poly and Polk are able to carry out TLS independently of PCNA ubiquitination in some circumstances (22-24).

The intracellular functions of the various motifs of Pol η are monitored in two ways: formation of nuclear foci containing Pol η co-localized with PCNA and complementation of UV sensitivity of XP-V cells. Mutations in PIP2 strongly impair the localization of Pol η , indicating that PIP2 plays a crucial role in the accumulation of this protein in replication foci (23,25–27). However, *ubz* mutants also failed to accumulate in replication foci (6,26), and accumulation is barely detectable in a human cell line expressing the PCNA^{K164R} mutant instead of endogenous PCNA (28)

*To whom correspondence should be addressed. Tel: +81 52 789 3871; Fax: +81 52 789 3890; Email: masutani@riem.nagoya-u.ac.jp †These authors contributed equally to the paper as first authors.

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and in a PCNA^{K164R} knock-in murine cell line (23), demonstrating that the PIP2–PCNA interaction itself is not sufficient for foci formation. Recently, Durando and colleagues reported an additional function of PIP2 of Pol η , namely, that Pol η promotes mono-ubiquitination of PCNA in a PIP2-dependent manner (29). It remains unclear how the two PIP2-mediated activities, co-localization of Pol η with PCNA and promotion of PCNA mono-ubiquitination, are linked at the molecular level.

The *pip2* and *ubz* mutants of Pol η exhibit pronounced defects in foci formation, but retain the capacity to complement UV sensitivity of XP-V cells; however, the levels of complementation activity vary amongst studies by different groups (5–6,25–26,30), including one report that showed no role for PIP2 in survival after UV irradiation (27). Even a *pip2 ubz* double mutant (25,26) and a mutant in which PIP2 and UBZ were deleted (30) still exhibited significant levels of complementation activity. By contrast, the *pip1 pip2* double mutant and a mutant lacking the entire PIP1, UBZ and PIP2 domains were severely defective in complementation (5,30).

The biochemical activities of the motifs of human Pol η have been studied *in vitro*. In primer extension assays, both PIP1 and PIP2 contributed to some extent to the stimulation of DNA synthesis in the presence of PCNA (5,8,30). Using a reconstitution system to investigate switching between Pol δ and Pol η at DNA lesions, we demonstrated that the weak enhancement of the recruitment of Pol η to the 3'-end of primer DNA by the UBZ domain depended on mono-ubiquitination of PCNA (21). These biochemical properties of mutant proteins defective for PIP1, PIP2 or UBZ are well correlated with their abilities to complement UV sensitivity of XP-V cells, but not with their abilities to promote accumulation into the replication foci.

Here, we describe the molecular functions of Poln's PIP1, PIP2 and UBZ domains, together with the newly found PIP3, in UV tolerance, and present findings that resolve the controversies raised in previous reports. Our key finding is that Poly has two functionally distinct types of PIP box, one that stimulates DNA synthesis, and another that promotes PCNA mono-ubiquitination and accumulation into replication foci. Both PIP functions, together with the UBZ domain, are redundantly required for survival after UV irradiation. Additionally, we show that Polk has two PIP boxes with different functions, whereas Polt has only one PIP box involved in stimulation of DNA synthesis. Taking the results of previous reports together with the in vivo and in *vitro* data obtained in this study, we propose a model for the cellular functions of the various motifs of $Polm/\iota/\kappa$ in orchestrating TLS.

MATERIALS AND METHODS

Proteins

Expression plasmids were constructed as follows. Human *POLH*, *POLI* (encoding 740 amino-acid residues) (11) and *POLK* were cloned into pET20b(+) (Novagen) to obtain untagged proteins, and into pET15b (Novagen) to obtain N-terminally histidine-tagged proteins. Plasmids for expression of Pol_n, Pol_n^{ubz} and His-Pol_n in *E. coli* were described

previously (21,31). A truncated gene encoding Poly ΔC (32) was cloned into pET21a(+) (Novagen). A gene encoding UBCH5c^{S22R} was cloned into pET15b. Mutations were created by PCR, and nucleotide sequences were verified after cloning.

E1, RAD6-(His-RAD18)₂, RAD6-(RAD18^{Δ C2})₂, ubiquitin, RPA, PCNA, RFC, His-Pol η , Pol η and their mutants were purified as described previously (21,31,33–35). Column chromatography was carried out at 4°C on an FPLC system (GE Healthcare Life Science) using columns from GE Healthcare unless otherwise indicated. Protein concentrations were determined by the Bio-Rad protein assay using BSA (Bio-Rad) as the standard.

Pol $\eta\Delta C$ was purified in the same way as Pol η (21), except that HiTrap Phenyl HP was used instead of an Econopack methyl column (Bio-Rad).

A histidine-tagged Polk (His-Polk) and its mutants were purified as follows. BL21 (DE3) harbouring each of the expression plasmids and pMS-tRNA1 (36) was grown in 2 l of Terrific broth (37) supplemented with ampicillin (250 μ g/ml) and kanamycin (30 μ g/ml) at 15°C. His-Polk was induced with 0.2 mM isopropyl β -D-thiogalactopyranoside (IPTG) for 8 h, and then purified by sequential chromatography on Ni²⁺-charged HiTrap chelating HP, POROS 50 HE (Applied Biosystems), Econopack CHT-II (BIO-RAD) and Superdex 200 columns. The peak fraction containing His-Polk was frozen in liquid nitrogen and stored at -80° C.

Polu and Polu^{pip1} were purified as follows. BL21 (DE3) harbouring each of the expression plasmids was grown in 5 l of LB supplemented with ampicillin (250 μ g/ml) at 15°C. Polu was induced with 0.2 mM IPTG for 5 h, and then purified by sequential chromatography on HiTrap Capto MMC, Ni²⁺-charged HiTrap chelating HP, HiTrap SP HP, HiTrap Q HP and Superdex 200 columns. Note that Polu itself (without the His-tag) has weak affinity for the Ni²⁺-charged HiTrap chelating column. For Polu^{pip1}, the gel-filtration chromatography step was omitted. The peak fraction containing Polu was frozen in liquid nitrogen and stored at -80° C.

A histidine-tagged Polt (His-Polt) was purified as follows. BL21 (DE3) harbouring the expression plasmid was grown in 3 l of LB supplemented with ampicillin (250 μ g/ml) at 15°C. Polt was induced with 0.2 mM IPTG for 8 h, and then purified by sequential chromatography on Ni²⁺-charged Hi-Trap chelating HP, HiTrap SP HP, HiTrap Q HP and Superdex 200 columns. The peak fraction containing His-Polt was frozen in liquid nitrogen and stored at -80° C.

His-UBCH5c^{S22R} was purified as follows. BL21 (DE3) harbouring the expression plasmid was grown in 2 l of LB supplemented with ampicillin (250 μ g/ml) at 15°C. His-UBCH5c^{S22R} was induced with 0.2 mM IPTG for 16 h, and then purified by sequential chromatography on Ni²⁺charged HiTrap chelating HP and HiTrap SP HP columns. The peak fraction containing His-UBCH5c^{S22R} was frozen in liquid nitrogen and stored at -80° C.

PCNA-ubiquitination assays

PCNA-ubiquitination assays were performed as described (21). Briefly, the reaction mixture (25 μl) contained 20 mM HEPES-NaOH (pH 7.5), 50 mM NaCl, 0.2 mg/ml BSA, 1 mM DTT, 10 mM MgCl₂, 1 mM ATP, poly(dA)-oligo(dT)

(GE Healthcare) (100 ng), PCNA (1.0 pmol trimer), E1 (0.85 pmol), RAD6A-(His-RAD18)₂ (0.54 pmol trimer), Ub (174 pmol) and DNA polymerases (2.5 pmol unless indicated otherwise). Reaction mixtures were prepared on ice, and then incubated at 30°C for 30 min unless indicated otherwise. The reactions were terminated with sample buffer for SDS-PAGE. Products were analysed by western blotting with anti-PCNA antibody (Santa Cruz Biotechnology, sc-7907). Signals were detected with a Chemi-Lumi One L kit (Nacalai Tesque, 07880–70) using ImageQuantTM LAS 4000 Mini Biomolecular Imager (GE Healthcare), and analysed using ImageQuantTM TL software (GE Healthcare).

DNA polymerase assays

DNA polymerase assays were performed as described (35). Briefly, the reaction mixture (25 µl) contained 20 mM HEPES-NaOH (pH 7.5), 50 mM NaCl, 0.2 mg/ml BSA, 1 mM DTT, 10 mM MgCl₂, 1 mM ATP, 0.1 mM of each deoxynucleotide (dGTP, dATP, dCTP and dTTP), 33 fmol of singly primed M13 mp18 ssDNA (the 5'end ³²P-labelled 36-mer primer, CAGGGTTTTCCCAGT-CACGACGTTGTAAAACGACGG, is complementary to nt 6330-6295), RPA (9.1 pmol), RFC (260 fmol), PCNA (500 fmol trimer) and DNA polymerases (25 fmol for Poly and Polk, 100 fmol for Pol, unless indicated otherwise). The proteins were combined on ice and incubated at 30°C for 10 min. The reactions were terminated with 2 μ l of 300 mM EDTA, and the mixtures were immediately chilled on ice. After precipitation with ethanol, products were resolved on 10% polyacrylamide gels containing 7 M urea, and visualized using Typhoon FLA 9000 (GE Healthcare).

Preparation of mono-ubiquitinated PCNA (mUb-PCNA)

PCNA was mono-ubiquitinated *in vitro* as described previously (38), with minor modifications (28). Briefly, a reaction mixture (800 μ l) containing 50 mM Tris-base, 8 mM HEPES-NaOH (pH 7.5), 44 mM NaCl, 1 mM DTT, 10 mM MgCl₂, 3 mM ATP, PCNA (13 nmol as trimer), E1 (110 pmol), His-UBCH5c^{S22R} (19 nmol) and ubiquitin (36 nmol) were incubated at 37°C for 15 min. Then, 19 nmol of ubiquitin was additionally introduced into the reaction mixture. After an additional 105 min incubation, mUb-PCNA was immediately purified by gel filtration on a Superdex 200 column. The peak fraction containing mUb-PCNA was frozen in liquid nitrogen and stored at -80° C.

PCNA pull-down assays

Four microlitres of MagneticHisTM Ni Particles (Promega V8560) were re-suspended in 10 μ l of a binding buffer containing 20 mM HEPES-NaOH (pH 7.5), 50 mM NaCl, 10 mM imidazole, 0.2 mg/ml BSA and 1 mM DTT, and then incubated at 4°C for 5 min with 10 pmol of each of the polymerases. After washing the beads twice with 50 μ l of the binding buffer, 2.5 pmol of PCNA or mUb-PCNA was introduced and incubated at 4°C for 5 min in 25 μ l of binding buffer. After the beads were washed twice with 50 μ l of binding buffer, proteins that bound to the beads were analysed by western blotting with anti-PCNA antibody as described above.

Cell lines and cultures

SV-40 immortalized XP-V fibroblasts (XP2SASV3) and a SV-40 immortalized normal human fibroblasts (WI38VA13) were maintained in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum (FBS), 0.584 g/L L-glutamine, 0.07 g/L penicillin and 0.15 g/L streptomycin. To obtain stably expressing cells, either wild-type or mutant Poln expression constructs were transfected into XP-V cells using the Neon® transfection system (Invitrogen), followed by 0.2 mg/ml G418 selection. For construction of expression plasmids in human cells, the indicated genes were cloned into pIRESneo2 (Clontech) to create N-terminally FLAG-tagged proteins or pAcGFP1-Hyg-C1 (Clontech) to create GFP fusion proteins, as described previously (28).

Preparation of cellular fractions and western blotting

XP2SASV3 cells were transfected with expression constructs encoding either wild-type or mutant FLAG-Poly using the Neon® transfection system (Invitrogen) and incubated for 24 h. Three hours after 15 J/m² UVC irradiation, cells were harvested and lysed in 1% SDS in PBS to obtain whole cell lysates (WCL). In the case of fractionation, cells were suspended in lysis buffer [20 mM Tris-HCl (pH 7.5), 150 mM KCl, 25% glycerol, 0.5% NP-40, 1.5 mM $MgCl_2$, 1× Complete Protease Inhibitor Cocktail (Roche), $1 \times$ Phosphatase Inhibitor Cocktail Set II (Calbiochem)], and a portion was withdrawn as WCL. Next, soluble materials (soluble fractions) were separated by centrifugation. The precipitants were resuspended in micrococcal nuclease buffer [20 mM Tris-HCl (pH 7.5), 100 mM KCl, 300 mM sucrose, 0.1% Triton X-100, 2 mM MgCl₂, 1 mM CaCl₂, $1 \times$ EDTA-free Complete protease inhibitor cocktail (Roche)] and incubated with 2.5 U of micrococcal nuclease (Roche) at room temperature for 10 min. After centrifugation, soluble materials were collected as chromatin fractions, and precipitates (insoluble fractions) were resuspended in 1% SDS in PBS and solubilized by sonication. Cellular fractions were analysed by western blotting with anti-PCNA (Santa Cruz Biotechnology, sc-7907 or sc-56), anti-Poly (39), anti-Lamin B (Santa Cruz Biotechnology, sc-6216), anti-FLAG (M2 SIGMA, F1804) or anti-GFP (MBL, M048-3) antibodies.

Analysis of co-localization of Poly with PCNA

XP2SASV3 cells were transfected with expression constructs encoding either wild-type or mutant FLAG-Polq using the Neon® transfection system (Invitrogen). Fortyeight hours after transfection, cells were irradiated with 15 J/m² UVC and incubated for 3 h. Triton-soluble materials were removed by incubation with extraction buffer (0.5% Triton X-100, PBS, 0.4 μ g/ml antipain, 0.4 μ g/ml aprotinin, 0.2 μ g/ml leupeptin, 0.16 μ g/ml pepstatin, 0.1 mM EGTA and 0.5 mM phenylmethylsulfonyl fluoride), and then the cells were fixed with 3.5% formaldehyde in PBS and permeabilized with 0.1% Triton X-100 and 3.5% formaldehyde in PBS. After sequential treatments with 70% EtOH, 100% EtOH, and acetone on ice, cells were incubated with anti-POLH (Santa Cruz Biotechnology, sc-5592) and anti-PCNA (Santa Cruz Biotechnology, sc-56) antibodies. Alexa Fluor 488- and 594-conjugated secondary antibodies (Invitrogen) were used to visualize the immune-conjugated proteins. Nuclei were visualized by staining with 2 µg/ml Hoechst 33342. Images were collected using an LSM710 confocal microscope (Zeiss).

RESULTS

Promotion of PCNA mono-ubiquitination by Poly is dependent on PIP2 and PIP3, but independent of PIP1

The three human Y-family DNA polymerases (Poly, u and κ) share a basic architecture. Each protein contains a catalytic domain in the N-terminal half and various motifs/domains involved in interactions with other proteins in the C-terminal half (see Figures 1A and 4A, D). Human Poly contains multiple PIP boxes and a single copy of UBZ, which are believed to be involved in the interaction with mUb-PCNA in DNA-damaged cells. Recently, Durando and co-workers reported that depletion of endogenous Poly decreases the levels of damage-induced mUb-PCNA, and ectopically expressed Poly promotes mono-ubiquitination of PCNA in cells in a manner that depends on PIP2 at the C-terminus (29). However, those authors did not examine the contribution of another PIP box, PIP1, which is located in an internal region (5) (Figure 1A). To determine whether PIP1 plays any role in the promotion of PCNA mono-ubiquitination, we introduced the *pip1* or *pip2* mutation into FLAG-tagged Poly (Figure 1A), expressed the mutant proteins in XP-V cells, and analysed the levels of mUb-PCNA in cells by western blotting. As shown in Figure 1B, the result indicated that the *pip1* mutant and the wild type promoted mono-ubiquitination of PCNA to similar extents. Importantly, PCNA ubiquitination was observed in the presence or absence of UV irradiation, although it was more extensive when the cells were UV-irradiated. By contrast, the *pip2* mutant lost most of the ability to promote mono-ubiquitination. Because the pip1 pip2 double mutant still exhibited weak activity, similar to that of the single pip2 mutant, the residual activity could be attributable to additional PIP box(es). To identify another PIP box in Poln, we employed yeast two-hybrid assays and found one additional PIP box (hereafter, referred to as PIP3), which overlaps with a REV1-interacting region (RIR) (11,40) (Figure 1A; Supplementary Figure S1). Although short peptides carrying the PIP2 sequence interact with PCNA strongly enough for detailed physicochemical and structural analyses (10), the PCNA-binding activity of short peptides carrying the PIP1 sequence has never been detected, even using very sensitive yeast two-hybrid assay (11). Similarly, the PCNA-binding activity of PIP3 is not detected using short fragments; however, the activity of PIP3 appears stronger than that of PIP1, because the *pip3* mutation caused a much more drastic reduction in the positive signal in the yeast two-hybrid assay than the *pip1* mutation (Supplementary Figure S1). Subsequently, we made a series of *pip3* mutants

and expressed them in XP-V cells. As expected, the residual activities of the *pip2* single and *pip1 pip2* double mutants were diminished further by the additional introduction of the *pip3* mutation. The levels of mUb-PCNA in *pip3* pip2 double and pip1 pip3 pip2 triple mutants were similar to that in the vector control. On the other hand, the levels of mUb-PCNA in *pip3* single and *pip1 pip3* double mutants exhibited marginal differences from those in the wild type only in UV-unirradiated samples. Because all of these mutants were similarly detected in the chromatin fraction, the defects in the mutants were not attributed to alteration in sub-cellular localization (Figure 1B, bottom panel). These results indicate that PIP2 and PIP3 play a major and minor role, respectively, whereas PIP1 has no or little role, in promoting mono-ubiquitination of PCNA in cells, suggesting that two functional types of PIP boxes play distinct roles in the regulation of Poly.

Additionally, we showed that the *ubz* mutants severely reduced the ability to promote PCNA mono-ubiquitination (Supplementary Figure S2). However, these mutants had a significantly reduced ability to accumulate in chromatin (26) (Supplementary Figure S2), indicating that the mutations have additional effects, as postulated previously (5). Because the defect in promoting PCNA mono-ubiquitination could be also attributed to additional effects, such as alteration of sub-cellular localization, it remains unclear whether UBZ has the potential to promote ubiquitination of PCNA *in vivo*.

Reconstitution of Poly-dependent mono-ubiquitination of PCNA *in vitro*

To study the molecular mechanisms underlying the promotion of PCNA mono-ubiquitination, we sought to develop in vitro experimental conditions for recapitulating the in vivo situation using purified enzymes (Supplementary Figure S3A) (21,34). Because Poln interacts with both RAD18 and PCNA (8,15,41), we first checked the possibility that such protein-protein interactions could themselves promote PCNA ubiquitination. However, we observed no ubiquitination of PCNA under such conditions (Figure 2A, lane 1). When poly(dA)-oligo(dT) was added into the reaction mixture, PCNA ubiquitination occurred and it was dependent on Poly (lanes 2 and 3) as well as on E1, RAD6- $(His-RAD18)_2$ and ubiquitin (lanes 4–6). No modification was observed with the PCNA^{K164R} mutant, confirming that ubiquitination of PCNA takes place at Lys164 (lane 7). Note that PCNA is spontaneously loaded from the ends of poly(dA)-oligo(dT) without RFC in these experiments (21). Additionally, we found that the specific interaction between RAD18 and Poly was not required for promotion of PCNA mono-ubiquitination in the in vitro reactions, because a mutant of RAD18 lacking the C-terminal region required for its interaction with $Pol_{\gamma}(15,34)$ could promote PCNA ubiquitination as efficiently as full-length RAD18 (Supplementary Figure S4A). These results suggested that a certain mode of Poly-PCNA interaction on DNA is required for the promotion of PCNA ubiquitination, inspiring us to further investigate the mechanism.



Figure 1. Pol η promotion of PCNA ubiquitination depends on PIP3 and PIP2, but not on PIP1. (A) Schematic structure of human Pol η . Parts of PIP and UBZ sequences are shown. Amino-acid residues indicated by asterisks were replaced with alanines in the mutants. (B) Western blot analysis of FLAG-Pol η -expressing cells. XP-V cells were transfected with the indicated plasmids for expression of FLAG-Pol η (wt) or the indicated *pip* mutants, incubated for 24 h, irradiated with UV (15 J/m²) and further incubated for 3 h. Whole-cell lysates (WCL) or chromatin fractions were subjected to western blotting with anti-PCNA, anti-Pol η and anti-Lamin B (loading control) antibodies.



Figure 2. In vitro reconstitution of Polη–dependent PCNA ubiquitination. (A) Mono-ubiquitination reactions of PCNA were reconstituted with the indicated factors. Reaction products were analysed by western blotting with an anti-PCNA antibody. KR indicates the PCNA^{K164R} mutant. (B) Titration of Polη and its *pip* mutants. Indicated mutants were subjected to the ubiquitination assays as shown in (A). (C) Relative amounts of ubiquitinated PCNA were measured from gel images of more than three independent experiments, and the average values are plotted in the graph. Error bars show SD.

Effects of *pip* and *ubz* mutations on the promotion of *in vitro* PCNA ubiquitination

Given that Pol η promotes PCNA ubiquitination *in vitro* through direct interaction with PCNA on DNA, we next asked whether one or all of the PIP boxes are required for promotion of ubiquitination. To address this question, the *pip* mutants of Pol η used for the *in vivo* experiments described above (Figure 1; Supplementary Figure S3A) were

examined for the ability to promote ubiquitination *in vitro*. The results demonstrated that *in vitro* promotion of ubiquitination is dependent on PIP3 and PIP2, but independent of PIP1 (Figure 2B, C), in good agreement with the *in vivo* observations (Figure 1B). Together, these results support the interpretation that the *in vivo* accumulation of mUb-PCNA is a consequence of directly promoting *de novo* ubiquitination by Pol_{\phi}.

In addition, we demonstrated that the *ubz* mutant promoted mono-ubiquitination as efficiently as the wild type (Supplementary Figure S4B), indicating that the UBZ function is dispensable for promotion of ubiquitination in our *in vitro* system.

Different roles of the three PIP boxes of Pol $\!\eta$ in stimulation of DNA synthesis

Next, to study how PCNA stimulates the polymerase activity of Poln, we employed the primer extension assay using M13 mp18 ssDNA as a template in the presence of RPA and RFC. As shown in Figure 3A, we clearly detected stimulation of Poln polymerase activity by PCNA. When the *pip* mutants were examined, the stimulation was slightly reduced in each of the single *pip* mutants relative to the wild type (Figure 3B), indicating that all of the PIP boxes contribute to stimulation to some extent. The activities of the *pip1 pip2* and *pip3 pip2* were further reduced. Surprisingly, the activity of the *pip1 pip3* double mutant was inhibited by addition of PCNA, despite the fact that it still contains a PIP2 domain (Figure 3B). Similar inhibition was also observed with the *pip1 pip3 pip2* triple mutant (Figure 3B). Based on these results, we conclude that PCNA binding to PIP1 or PIP3, both located in the adjacent region of the Poly catalytic domain, is critical for the stimulation of DNA polymerase activity, and that even if PCNA binds to PIP2 at the C-terminus, PCNA does not stimulate Poly polymerase activity in vitro unless PIP1 or PIP3 is present. These results suggest that the function of PIP2 in stimulation of DNA synthesis is largely PIP1- and PIP3-dependent.

Functional roles of PIP boxes of Polu and Polk

The findings described above regarding the PIP boxes of Poly prompted us to investigate the PIP boxes of two other Y-family DNA polymerases, Polk and Polt. Polk has a PIP box at the C-terminus, which is required for formation of nuclear foci in cells with DNA damage (42), and has the potential to promote mono-ubiquitination of PCNA in vivo when Pol κ is ectopically expressed (29). More recently, another PIP box was found adjacent to the catalytic domain (Figure 4A; Supplementary Figure S5); therefore, the internal PIP box was named PIP1, and the C-terminal one was renamed PIP2, following the example of Poly (Figure 4A) (11). Unlike the internal PIP1 and PIP3 boxes in Poly, the PCNA-binding activity of the internal PIP1 box in Polk was detected in short fragments by the yeast twohybrid assay, implying that the activity is equivalent to that of the C-terminal PIP2 in Polk (Supplementary Figure S5). When the wild-type Polk protein was introduced into the in vitro PCNA ubiquitination reaction, a large amount of ubiquitinated PCNA was observed (the leftmost panel in Figure 4B), as in the case of Poly. To study the roles of the respective PIP boxes, we examined the pip1, pip2 and double mutants (Figure 4A; Supplementary Figure S3B). As shown in Figure 4B, the *pip1* and *pip2* mutants exhibited reduced levels of PCNA ubiquitination: the *pip2* mutant retained a relatively higher level, whereas the double mutant lost the activity. These results indicate that each of the two PIP boxes functions independently and have similar

affinity for PCNA, and that both are required to promote the maximum level of ubiquitination (Figure 4B). Next, we examined effects of PCNA on DNA polymerase activity of the wild-type and mutant Polk proteins. As shown in Figure 4C, the *pip2* mutant was stimulated as efficiently as the wild type by PCNA, but *pip1* and the double mutants failed to be stimulated by PCNA, indicating that the internal PIP1 box is responsible for stimulation by PCNA but the C-terminal PIP2 is not. Therefore, we conclude that the multiple PIP boxes of Polk serve different functions: PIP1 stimulates DNA synthesis by PCNA, and PIP1 and PIP2 promote PCNA ubiquitination.

Next, we examined Polt (Figure 4D; Supplementary Figure S3C). In contrast to Pol η and Pol κ , Polt did not promote PCNA ubiquitination *in vitro* (Figure 4E). On the other hand, PCNA stimulated DNA synthesis of Polt *in vitro* in a PIP1-dependent manner (Figure 4F), in line with previous reports that Polt has only one functional PIP box (for stimulation of DNA synthesis) immediately adjacent to the catalytic domain (7,10,12).

Subsequently, we examined the levels of mUb-PCNA in cells with ectopic expression of Polk or Poli, with or without UV irradiation (Figure 5). When GFP-Polk was expressed in Poly-deficient (XP-V) or proficient cells, promotion of PCNA mono-ubiquitination was observed in both types of cells (Figure 5A, B). The promoting effect of ectopic expression of Polk is weaker than that of Poln reported previously (29,43). The difference in the extent to which PCNA monoubiquitination was promoted by these enzymes could be attributed to differences in the expression system and/or cell types used in these experiments. Indeed, a difference is evident between the two types of cells used in our study (Figure 5A, B), indicating that it may not be appropriate to compare and draw conclusions from differences in mUb-PCNA levels between different cell lines. By contrast to Poly and Polk, ectopic expression of FLAG-Poli in both cells did not increase the levels of mUb-PCNA (Figure 5C, D). These results are consistent with the in vitro properties described above (Figure 4B, E), implying that Pol κ , but not Pol ι , can promote de novo mono-ubiquitination of PCNA in vivo.

Interactions of Poly, L and K with mUb-PCNA

PCNA is mono-ubiquitinated in DNA-damaged cells. Consequently, Y-family DNA polymerases with UBD(s), as well as PIP box(es), could interact with modified PCNA in preference to unmodified PCNA. To test this in vitro, we compared the stimulatory effects of mUb-PCNA and unmodified PCNA on DNA synthesis in vitro, using a primer extension assay (Figure 6; Supplementary Figure S3D). As shown in Figure 6A, mUb-PCNA stimulated DNA synthesis by Poln more effectively than unmodified PCNA under our assay conditions. As expected, no additional stimulation was observed with the *ubz* mutant of Pol_{η} (Figure 6B). DNA synthesis by either the pip1 pip2 or pip3 pip2 double mutants was stimulated by mUb-PCNA, although it was only marginally stimulated by unmodified PCNA (Figure 6C, D). The activity of the *pip1 pip3* double mutant was slightly higher in the presence of mUb-PCNA than in the absence of PCNA (Figure 6E). The pip1 pip3 pip2 triple mutant exhibited a negative effect by the addition of mUb-



Figure 3. DNA polymerase assays of Pol η in a reconstituted system *in vitro*. (A) DNA replication reactions using singly primed M13 mp18 ssDNA were reconstituted with the indicated factors. The reaction products were resolved in 10% polyacrylamide gels containing 7 M urea, and visualized using a PhosphorImager. (B) Analysis of *pip* mutants of Pol η . Indicated mutants were subjected to replication assays shown in (A) in the presence or absence of PCNA.



Figure 4. Analysis of Pol κ , Pol ι and their *pip* mutants *in vitro*. (A, D) Schematic structures of human Pol κ (A) and Pol ι (D), as shown in Figure 1A. (B, E) PCNA ubiquitination assays of His-Pol κ (B) and Pol ι (E), as shown in Figure 2. (C, F) DNA polymerase assays of His-Pol κ (C) and Pol ι (F), as shown in Figure 3.



Figure 5. Promotion of mono-ubiquitination of PCNA in cells by Polk but not Polu. **(A, B)** Western blot analysis of Polk-expressing cells. XP-V (A) and normal cells (B) were transfected with a plasmid to express GFP-Polk or GFP-Pol η (as a control). **(C, D)** Western blot analysis of Polk-expressing cells. XP-V (C) and normal cells (D) were transfected with a plasmid to express FLAG-Polu or FLAG-Pol η (as a control). The transfected cells were incubated for 24 h, irradiated with UV (15 J/m²) and further incubated for 3 h. Whole-cell lysates (WCL) were subjected to western blotting with anti-PCNA, anti-Lamin B (loading control) and anti-GFP or anti-FLAG antibodies.

PCNA (Figure 6F). These results suggested that UBZ function requires at least one PIP.

Next, we examined the stimulation of DNA synthesis by Polt and Polk by mUb-PCNA. Additional stimulation, albeit marginal, by mUb-PCNA was reproducibly observed for Polt (Figure 6G) as well as its *pip1* mutant (Figure 6H). Similarly, mUb-PCNA stimulated Polk and its *pip* mutants to a slightly greater extent than unmodified PCNA (Figure 6I, J). The relatively lower contributions of ubiquitin moieties to Polt and Polk activity than to Poln activity could be attributed to the weaker affinity of Polt and Polk for mUb-PCNA than Poln (Supplementary Figure S6).

Cellular functions of the motifs of Poly

After UV irradiation, Poln forms nuclear foci that colocalize with PCNA (6,15,25–27,39,44). To determine the roles of each of Poln's three PIP boxes in foci formation, wild type and *pip* mutants bearing a FLAG-tag, all of which were used in the experiments shown in Figure 1, were transiently expressed in XP-V cells. After UV irradiation, localization of Poln and PCNA was visualized using anti-Poln and anti-PCNA antibodies, respectively. As shown in Figure 7A, Poln foci co-localized with PCNA were observed in all of the samples except for the *pip2* mutant. Because all of the proteins, including the *pip2* mutant, could be detected with similar efficiency by western blotting (Figure 1B) and immunostaining (Supplementary Figure S7), we conclude that PIP2, but not PIP1 or PIP3, plays a crucial role in foci formation along with PCNA.

Next, we examined the abilities of the Poly mutants to complement the UV sensitivity of XP-V cells (Figure 7B). Although the *pip* and *ubz* mutants of Poln have been analvsed previously using such assays, the levels of complementation were inconsistent among studies (5-6,25-27,30). Complementation of the UV sensitivity of XP-V cells differs among clones stably expressing a particular mutant Poln, but is not correlated with the expression levels of $Pol_{\gamma}(26)$. To avoid such complexities due to differences among clones, we used for our survival assays a mixture of the cells that were transfected with pIRESneo2 carrying wild-type or mutant Poly and selected by G418. As shown in Figure 7B, the results indicated that the single and double *pip* mutants could complement the UV sensitivity of XP-V cells as efficiently as the wild type. By contrast, the *pip1 pip3 pip2* triple mutant exhibited clearly reduced complementation activity (Figure 7B).

In contrast to such subtle phenotypes of individual single and double *pip* mutants, the *ubz* single mutant exhibited a severe defect (Supplementary Figure S8) (6,26). However, because the *ubz* mutant accumulated poorly in the chromatin fraction (see Supplementary Figure S2) (26), we hypothesized that this defect could be attributed to secondary effects due to the *ubz* mutation. To investigate this possibility, we made use of a deletion mutant carrying the 1-511 region of Poly (Poly ΔC) (2–3,32) (Figure 1A). Because Poly ΔC lacks the nuclear localization signal (NLS) as well as PIP2 and UBZ, we introduced an artificial NLS at the C-terminus. Because of the lack of PIP2, Poln ΔC was expected to have a lower ability to promote PCNA ubiquitination and fail to form foci in co-localization with PCNA. Those properties were confirmed in vivo and in vitro (Supplementary Figure S9). Nevertheless, $Poln\Delta C$ retained the ability to accumulate in the chromatin fraction (Supplementary Figure S9D), in contrast to the ubz mutants of fulllength Poly (Supplementary Figure S2), supporting the idea that some ubz mutations provoke secondary effects (5,30). More importantly, $Poln\Delta C$ could complement the UV sensitivity of XP-V cells much better than the ubz mutant (Supplementary Figure S8). As shown in Figure 7B, the pip1 and *pip3* derivatives of Poly ΔC exhibited reduced complementation activity, and the *pip1 pip3* derivative of Poly ΔC exhibited a severer defect than the *pip1 pip3 pip2* triple mutant of full-length Poln. The defects were not attributable to alterations in the sub-cellular localization (Supplementary Figure S9D). Together, these results suggest that PIP1, PIP3, PIP2 and UBZ exert additive and redundant effects that protect cells from the lethal effects of UV irradiation.

DISCUSSION

Cellular functions of the respective motifs of Pol η are routinely monitored in two ways: co-localization with PCNA and complementation of UV sensitivity of XP-V cells. In this study, we demonstrated that these two phenotypes are mediated by different PIP boxes and distinct modes of interaction with PCNA. We also showed that the diverse functions of PIP boxes are conserved in Pol κ , but not in Pol ι .



Figure 6. Interactions between Y-family DNA polymerases and mUb-PCNA *in vitro*. (A–J) Analysis of DNA synthesis by Pol_{η} (A–F), Pol_{ν} (G–H) and His-Pol_k (I–J), as shown in Figure 3, in the absence or presence of PCNA (designated as PCNA or +) or mUb-PCNA (designated as uPCNA or u). Concentrations of polymerases increase in the order 0.25, 0.5, and 1 nM (A–F and I) or 1, 2, and 4 nM (G–H), or remain constant at 1 nM (J).

Functions of PIP boxes in ubiquitination of PCNA and foci formation

In this study, we found that $Pol\eta$ promotes monoubiquitination of PCNA in a manner dependent on PIP2 and to a lesser extent on PIP3, but independent of PIP1 *in vivo* (Figure 1B). These findings were perfectly correlated with the *in vitro* observations regarding promotion of PCNA mono-ubiquitination by purified proteins (Figure 2B, C). Together, the data strongly suggest that the intracellular accumulation of mUb-PCNA with ectopically expressed Poln is a consequence of direct promotion of *de novo* ubiquitination. Importantly, we found that DNA is an absolute requirement for Poln-dependent PCNA ubiquitination reactions *in vitro* (Figure 2A). We suggest that



Figure 7. Cellular functions of the motifs of Pol η . (A) Co-localization of Pol η with PCNA. XP-V cells were transiently transfected with plasmids encoding wild-type FLAG-Pol η or the indicated mutants. After UV irradiation, FLAG-Pol η and PCNA were visualized by immunostaining with anti-Pol η and anti-PCNA antibodies, respectively. Nuclei were stained by Hoechst 33342. Scale bars represent 5 μ m. Control experiments confirming expressions of FLAG-Pol η were shown in Supplementary Figure S7. (B) UV sensitivities of XP-V cells stably expressing FLAG-Pol η . Cells were irradiated with the indicated dose of UVC, incubated with 1 mM caffeine for 4 days, and their viabilities were measured. Error bars show SD from three independent experiments. (C) A model for a regulatory network for foci formation and the TLS function of Pol $\eta/\iota/\kappa$. Interactions of Pol η/κ with PCNA, together with RAD6-(RAD18)₂, leads to their accumulation by promoting mono-ubiquitination of PCNA around stalled 3'-OH ends. Interactions of Pol $\eta/\iota/\kappa$ with mUb-PCNA via PIPs and UBDs stimulate DNA synthesis at stalled 3'-OH ends. See text for details.

the mode of interaction between PIP3 or PIP2 and PCNA on DNA for the promotion of PCNA ubiquitination could act in such a way as an appropriate substrate for RAD6-(RAD18)₂ catalysis, which was independent of the interaction between RAD18 and Pol η *in vitro*. The partial involvement of the interaction in the promotion of PCNA ubiquitination *in vivo* (29) could be attributed to an additional function, such as recruitment of Pol η to damage sites (15).

The contribution of individual Poly PIP boxes to colocalization with PCNA was correlated with the effect on promotion of PCNA ubiquitination. These effects could be largely attributed to PIP2 (Figures 1B, 2B, C and 7A). Polk also promotes mono-ubiquitination of PCNA (Figures 4B and 5A, B) (29) and co-localizes with PCNA (42). Polt failed to promote mono-ubiquitination of PCNA (Figures 4E and 5C, D) and failed to co-localize with PCNA by itself (45,46). These results suggest that a large part of the function of the PIP2 box in foci formation is the promotion of PCNA mono-ubiquitination, which is a prerequisite for co-localization of polη with PCNA in nuclear foci. The following observation supports this idea: first, accumulation is dependent on RAD18 and its catalytic activity (15,29). Second, accumulation of Polη is barely detectable in a human cell line in which the PCNA ^{K164R} mutant is expressed instead of endogenous PCNA (28), or in a PCNA^{K164R} knock-in murine cell line (23). Therefore, we

suggest that one of the functions of PIP2 in foci formation is to promote mono-ubiquitination of PCNA. The resultant mUb-PCNA could stabilize Poly via interaction with UBZ, because mUb-PCNA has a higher affinity for Poly than unmodified PCNA (Supplementary Figure S6). Thus, even though UBZ is dispensable for the promotion of PCNA ubiquitination (at least *in vitro*), UBZ may still contribute to stable foci formation. This idea does not exclude another role for PIP2 in foci formation via direct interaction with PCNA. Indeed, among the three PIPs of Poln, only the PIP2 peptide has been shown to interact directly with PCNA in yeast two-hybrid and structural analyses (10,11). Furthermore, enhancement of the PIP2-PCNA interaction of Polk by manipulations of its PIP2 sequence (10) improves foci formation (29,47). These results suggest that stable interactions with mUb-PCNA via both PIP and UBZ are required for detectable focus formation.

Interestingly, PIP3 and RIR1 share the same FF residues for binding to PCNA and REV1, respectively (40). Therefore, it is unlikely that PIP3 could act as a PIP box and RIR at the same time. However, Pol η has two RIRs, RIR1 and RIR2 (40). So far, we have been unable to detect any defect in the pol η -REV1 interaction in the *rir1* single mutant in cells (39) or in yeast-two hybrid assays (40) (Supplemental Figure S1). We believe that the PIP3-PCNA interaction or *pip3* mutation does not interfere with REV1-related function(s) because of the presence of RIR2.

Functions of PIP and UBD in stimulating DNA synthesis

In this study, we demonstrated that all three PIP boxes of Poly play roles in stimulating DNA synthesis, although the mechanisms are different. We showed that PIP-less Poly has an intrinsic defect in accessing the PCNA-loaded 3'-end; the presence of PIP1 or PIP3, but not PIP2, compensates for this inhibition (Figure 3B). It is likely that both PIP1 and PIP3 stimulate DNA synthesis via direct interaction with PCNA, and that PIP2 facilitates the PIP1-PCNA and PIP3-PCNA interactions. Because PIP1 and PIP3 are proximal to the catalytic domain of Poln, the PCNA-Poln interaction via PIP1 or PIP3 may enable the active site of Poly to effectively bind the 3'-OH end of the primer-terminus, whereas the interaction via PIP2, located distant from the C-terminus, may be less efficient in this respect. This mechanism seems conserved in Polk and Pol, since each PIP1 box located adjacent to the catalytic domain can stimulate DNA synthesis. More recently, during the preparation of this manuscript, another group reported that PIP1 in Polk is responsible for PCNA stimulation of in vitro DNA synthesis (48).

We demonstrated for the first time that mUb-PCNA stimulates DNA synthesis by human Pol η , ι and κ (Figure 6A–H). We showed that the UBZ-function of Pol η is largely PIP1- and PIP3-dependent and slightly PIP2-dependent (Figure 6A–F), suggesting that adequate stimulation by mUb-PCNA requires interaction with at least one PIP box. Alternatively, an increased local concentration of Pol η around the primer end, achieved through PIP–PCNA interactions, indirectly promotes the interaction between UBZ and the ubiquitin moiety. Collectively, these

results suggest that interactions between mUb-PCNA and Poly stimulate DNA synthesis via diverse mechanisms.

Functions of PIP and UBZ in $Pol\eta$ in enhancing survival after UV irradiation

All three PIP boxes and UBZ of Poln serve additive and redundant functions in enhancing survival after UV irradiation (Figure 7B). The survival rate in vivo (Figure 7B) correlated well with the level of stimulation of DNA synthesis by these mutants by PCNA or mUb-PCNA in vitro (Figure 6A–H). However, there were two exceptions. One was the ubz point mutant that exhibited severe defects (Supplementary Figure S8), which might be attributed to a secondary effect related to accumulation on chromatin (Supplementary Figure S2). Indeed, the deletion mutation of UBZ and PIP2 in Poly ΔC restored the sub-cellular localization (Supplementary Figure S9D) and increased the ability to complement the UV sensitivity of XP-V cells relative to the *ubz* point mutant (Supplementary Figure S8). This partial contribution of UBZ is consistent with reports of PCNA ubiquitination-independent TLS in PCNA^{K164R} knock-in murine cells (22,23). The other exception was the pip1 pip3 double mutant. The defect in complementation of UV sensitivity of XP-V cells by the pip1 pip3 mutant was marginal (Figure 7B), although its DNA synthesis was poorly stimulated by mUb-PCNA in vitro (Figure 6E). Because the mutant is proficient in the promotion of PCNA ubiquitination and foci formation (Figures 1B, 2B and 7A), the elevated local concentration of the mutant could compensate for the defect in stimulation, and this could explain the minor defect of the pip1 pip3 mutant in vivo. Overall, the data suggest that the level of stimulation of DNA synthesis by mUb-PCNA could directly affect the efficiency of TLS in vivo.

A model for the cellular functions of PIP and UBD of Pol $\eta/\iota/\kappa$ in the orchestration of TLS

Taking the results of previous reports together with the in vivo and in vitro data obtained in this study, we propose a model for cellular functions of the various motifs of Pol $\eta/\iota/\kappa$ (Figure 7C). We suggest that interactions between Poly/ κ and PCNA constitute a network that regulates promotion of mono-ubiquitination and accumulation of Poln/L/K. PCNA is concentrated on DNA in close proximity to replication forks (21,35,49). In the model, $Pol_{\eta/\kappa}$ are recruited to these locations via interactions with PIP boxes together with RAD18 (15,41,43). The initial PIP-PCNA interactions are too transient and unstable to be detected as foci, but the interaction turns PCNA into an appropriate substrate for RAD6-(RAD18)₂ catalysis, which promotes ubiquitination of PCNA. The resultant mUb-PCNA recruits additional Poly/L/K molecules via interaction with both PIPs and UBDs. Because Poly has a much higher affinity for mUb-PCNA than Polk and Poli (Supplementary Figure S6), it is likely that Pol_{η} is predominantly recruited. In the case of Poly, the interactions are sufficiently stable for detectable foci formation, but in the case of Polk they are relatively weak. By contrast, Poli binds mUb-PCNA too weakly to form stable foci by itself. Increased

local concentrations of Pol η/κ further promote ubiquitination of PCNA. Consequently, Pol η/κ and ubiquitinated PCNA robustly accumulate around the stalled primer ends until accumulation of Pol η/κ is saturated. Any mutation that disrupts the regulatory network should attenuate the response *in vivo* via activities of de-ubiquitination enzymes. This model is compatible with the dynamic mobile properties of Pol η/ι in cells (50).

Accumulation of Poln in replication foci plays a minor role in survival, as reflected by the observation that accumulation-defective PIP2 mutant could perfectly complement UV sensitivity of XP-V cells (Figure 7B) (27). In addition, $Poln\Delta C$ with a C-terminal deletion encompassing UBZ and PIP2 also exhibited considerable complementation activity (Figure 7B). These results suggest that Polm can perform TLS of UV lesions without accumulating in foci. The minor contribution of foci formation to cellular function is also true in other members of the Y family. Although accumulation of Polu in replication foci is dependent on Poly (45, 46), Pol appears to be functional in TLS of UV lesions in Poln-knockout mice (51). Deficiency in the Polndependent co-localization of REV1 with UV lesions does not affect survival, but does modulate mutagenesis (39). In this scenario, one of physiological functions of the accumulated mUb-PCNA could be to establish an order of recruitment for TLS polymerases, via dynamic interactions between mUb-PCNA and their PIPs and UBDs, depending on their respective affinities around the stalled primer ends (50). This possibility is compatible with the observation that Polk can be induced by specific agents that produce DNA damage cognate for Pol κ (52). Increasing the ratio of Pol κ forces it to predominantly access specific DNA damage. We believe that this model provides an integrated picture of the cellular functions of various motifs of the Y-family DNA polymerases.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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REFERENCES

- Ohmori,H., Friedberg,E.C., Fuchs,R.P., Goodman,M.F., Hanaoka,F., Hinkle,D., Kunkel,T.A., Lawrence,C.W., Livneh,Z., Nohmi,T. *et al.* (2001) The Y-family of DNA polymerases. *Mol. Cell*, 8, 7–8.
- Masutani, C., Araki, M., Yamada, A., Kusumoto, R., Nogimori, T., Maekawa, T., Iwai, S. and Hanaoka, F. (1999) Xeroderma pigmentosum variant (XP-V) correcting protein from HeLa cells has a thymine dimer bypass DNA polymerase activity. *EMBO J.*, 18, 3491–3501.
- Masutani, C., Kusumoto, R., Yamada, A., Dohmae, N., Yokoi, M., Yuasa, M., Araki, M., Iwai, S., Takio, K. and Hanaoka, F. (1999) The *XPV* (xeroderma pigmentosum variant) gene encodes human DNA polymerase η. *Nature*, **399**, 700–704.
- Johnson, R.E., Kondratick, C.M., Prakash, S. and Prakash, L. (1999) hRAD30 mutations in the variant form of xeroderma pigmentosum. Science, 285, 263–265.
- Acharya, N., Yoon, J.H., Gali, H., Unk, I., Haracska, L., Johnson, R.E., Hurwitz, J., Prakash, L. and Prakash, S. (2008) Roles of PCNA-binding and ubiquitin-binding domains in human DNA polymerase η in translesion DNA synthesis. *Proc. Natl. Acad. Sci.* U.S.A., 105, 17724–17729.
- Bienko,M., Green,C.M., Crosetto,N., Rudolf,F., Zapart,G., Coull,B., Kannouche,P., Wider,G., Peter,M., Lehmann,A.R. *et al.* (2005) Ubiquitin-binding domains in Y-family polymerases regulate translesion synthesis. *Science*, **310**, 1821–1824.
- Haracska,L., Acharya,N., Unk,I., Johnson,R.E., Hurwitz,J., Prakash,L. and Prakash,S. (2005) A single domain in human DNA polymerase umediates interaction with PCNA: implications for translesion DNA synthesis. *Mol. Cell. Biol.*, 25, 1183–1190.
- Haracska,L., Johnson,R.E., Unk,I., Phillips,B., Hurwitz,J., Prakash,L. and Prakash,S. (2001) Physical and functional interactions of human DNA polymerase η with PCNA. *Mol. Cell. Biol.*, 21, 7199–7206.
- Haracska,L., Unk,I., Johnson,R.E., Phillips,B.B., Hurwitz,J, Prakash,L. and Prakash,S. (2002) Stimulation of DNA synthesis activity of human DNA polymerase κ by PCNA. *Mol. Cell. Biol.*, 22, 784–791.
- Hishiki,A., Hashimoto,H., Hanafusa,T., Kamei,K., Ohashi,E., Shimizu,T., Ohmori,H. and Sato,M. (2009) Structural basis for novel interactions between human translesion synthesis polymerases and proliferating cell nuclear antigen. J. Biol. Chem., 284, 10552–10560.
- Ohmori, H., Hanafusa, T., Ohashi, E. and Vaziri, C. (2009) Separate roles of structured and unstructured regions of Y-family DNA polymerases. *Adv. Protein Chem. Struct. Biol.*, 78, 99–146.
- Vidal,A.E., Kannouche,P., Podust,V.N., Yang,W., Lehmann,A.R. and Woodgate,R. (2004) Proliferating cell nuclear antigen-dependent coordination of the biological functions of human DNA polymerase u. J. Biol. Chem., 279, 48360–48368.
- Hoege, C., Pfander, B., Moldovan, G.L., Pyrowolakis, G. and Jentsch, S. (2002) RAD6-dependent DNA repair is linked to modification of PCNA by ubiquitin and SUMO. *Nature*, 419, 135–141.
- Kannouche,P.L., Wing,J. and Lehmann,A.R. (2004) Interaction of human DNA polymerase η with monoubiquitinated PCNA: a possible mechanism for the polymerase switch in response to DNA damage. *Mol Cell.*, 14, 491–500.
- Watanabe,K., Tateishi,S., Kawasuji,M., Tsurimoto,T., Inoue,H. and Yamaizumi,M. (2004) Rad18 guides polη to replication stalling sites through physical interaction and PCNA monoubiquitination. *EMBO J.*, 23, 3886–3896.
- Motegi,A., Liaw,H.J., Lee,K.Y., Roest,H.P., Maas,A., Wu,X., Moinova,H., Markowitz,S.D., Ding,H., Hoeijmakers,J.H. *et al.* (2008) Polyubiquitination of proliferating cell nuclear antigen by HLTF and SHPRH prevents genomic instability from stalled replication forks. *Proc. Natl. Acad. Sci. U.S.A.*, **105**, 12411–12416.
- Motegi,A., Sood,R., Moinova,H., Markowitz,S.D., Liu,P.P. and Myung,K. (2006) Human SHPRH suppresses genomic instability through proliferating cell nuclear antigen polyubiquitination. *J. Cell Biol.*, **175**, 703–708.
- Unk,I., Hajdu,I., Fatyol,K., Hurwitz,J., Yoon,J.H., Prakash,L., Prakash,S. and Haracska,L. (2008) Human HLTF functions as a ubiquitin ligase for proliferating cell nuclear antigen polyubiquitination. *Proc. Natl. Acad. Sci. U.S.A.*, **105**, 3768–3773.

- Unk,I., Hajdu,I., Fatyol,K., Szakal,B., Blastyak,A., Bermudez,V., Hurwitz,J., Prakash,L., Prakash,S. and Haracska,L. (2006) Human SHPRH is a ubiquitin ligase for Mms2-Ubc13-dependent polyubiquitylation of proliferating cell nuclear antigen. *Proc. Natl. Acad. Sci. U.S.A.*, 103, 18107–18112.
- Garg,P. and Burgers,P.M. (2005) Ubiquitinated proliferating cell nuclear antigen activates translesion DNA polymerases η and REV1. *Proc. Natl. Acad. Sci. U.S.A.*, **102**, 18361–18366.
- Masuda, Y., Piao, J. and Kamiya, K. (2010) DNA replication-coupled PCNA mono-ubiquitination and polymerase switching in a human *in vitro* system. J. Mol. Biol., 396, 487–500.
- 22. Hendel, A., Krijger, P.H., Diamant, N., Goren, Z., Langerak, P., Kim, J., Reissner, T., Lee, K.Y., Geacintov, N.E., Carell, T. et al. (2011) PCNA ubiquitination is important, but not essential for translesion DNA synthesis in mammalian cells. *Plos Genetics*, 7, e1002262.
- 23. Krijger,P.H., van den Berk,P.C., Wit,N., Langerak,P., Jansen,J.G., Reynaud,C.A., de Wind,N. and Jacobs,H. (2011) PCNA ubiquitination-independent activation of polymerase η during somatic hypermutation and DNA damage tolerance. *DNA Repair* (*Amst.*), **10**, 1051–1059.
- 24. Wit,N., Buoninfante,O.A., van den Berk,P.C., Jansen,J.G., Hogenbirk,M.A., de Wind,N. and Jacobs,H. (2015) Roles of PCNA ubiquitination and TLS polymerases κ and η in the bypass of methyl methanesulfonate-induced DNA damage. *Nucleic Acids Res.*, 43, 282–294.
- Bienko,M., Green,C.M., Sabbioneda,S., Crosetto,N., Matic,I., Hibbert,R.G., Begovic,T., Niimi,A., Mann,M., Lehmann,A.R. *et al.* (2010) Regulation of translesion synthesis DNA polymerase η by monoubiquitination. *Mol. Cell*, **37**, 396–407.
- 26. Despras, Ê., Delrieu, N., Garandeau, C., Ahmed-Seghir, S. and Kannouche, P.L. (2012) Regulation of the specialized DNA polymerase η: revisiting the biological relevance of its PCNA- and ubiquitin-binding motifs. *Environ. Mol. Mutagen.*, **53**, 752–765.
- 27. Gueranger, Q., Stary, A., Aoufouchi, S., Faili, A., Sarasin, A., Reynaud, C.A. and Weill, J.C. (2008) Role of DNA polymerases η, ι and ζ in UV resistance and UV-induced mutagenesis in a human cell line. *DNA Repair (Amst.)*, **7**, 1551–1562.
- Kanao, R., Masuda, Y., Deguchi, S., Yumoto-Sugimoto, M., Hanaoka, F. and Masutani, C. (2015) Relevance of simultaneous mono-ubiquitinations of multiple units of PCNA homo-trimers in DNA damage tolerance. *PLoS One*, **10**, e0118775.
- Durando, M., Tateishi, S. and Vaziri, C. (2013) A non-catalytic role of DNA polymerase η in recruiting Rad18 and promoting PCNA monoubiquitination at stalled replication forks. *Nucleic Acids Res.*, 41, 3079–3093.
- Acharya, N., Yoon, J.H., Hurwitz, J., Prakash, L. and Prakash, S. (2010) DNA polymerase η lacking the ubiquitin-binding domain promotes replicative lesion bypass in humans cells. *Proc. Natl. Acad. Sci.* U.S.A., 107, 10401–10405.
- Masuda, Y. and Kamiya, K. (2006) Role of single-stranded DNA in targeting REV1 to primer termini. J. Biol. Chem., 281, 24314–24321.
- Kusumoto, R., Masutani, C., Shimmyo, S., Iwai, S. and Hanaoka, F. (2004) DNA binding properties of human DNA polymerase η: implications for fidelity and polymerase switching of translesion synthesis. *Genes Cells*, 9, 1139–1150.
- Fukuda,K., Morioka,H., Imajou,S., Ikeda,S., Ohtsuka,E. and Tsurimoto,T. (1995) Structure-function relationship of the eukaryotic DNA replication factor, proliferating cell nuclear antigen. *J. Biol. Chem.*, 270, 22527–22534.
- 34. Masuda, Y., Suzuki, M., Kawai, H., Suzuki, F. and Kamiya, K. (2012) Asymmetric nature of two subunits of RAD18, a RING-type ubiquitin ligase E3, in the human RAD6A-RAD18 ternary complex. *Nucleic Acids Res.*, 40, 1065–1076.
- Masuda,Y., Suzuki,M., Piao,J., Gu,Y., Tsurimoto,T. and Kamiya,K. (2007) Dynamics of human replication factors in the elongation phase of DNA replication. *Nucleic Acids Res.*, 35, 6904–6916.
- Gu, Y., Masuda, Y. and Kamiya, K. (2008) Biochemical analysis of human PIF1 helicase and functions of its N-terminal domain. *Nucleic Acids Res.*, 36, 6295–6308.

- Gomes,X.V., Gary,S.L. and Burgers,P.M. (2000) Overproduction in *Escherichia coli* and characterization of yeast replication factor C lacking the ligase homology domain. *J. Biol. Chem.*, 275, 14541–14549.
- Hibbert, R. G. and Sixma, T.K. (2012) Intrinsic flexibility of ubiquitin on proliferating cell nuclear antigen (PCNA) in translesion synthesis. *J. Biol. Chem.*, 287, 39216–39223.
- Akagi, J., Masutani, C., Kataoka, Y., Kan, T., Ohashi, E., Mori, T., Ohmori, H. and Hanaoka, F. (2009) Interaction with DNA polymerase η is required for nuclear accumulation of REV1 and suppression of spontaneous mutations in human cells. *DNA Repair* (*Amst.*), 8, 585–599.
- Ohashi, E., Hanafusa, T., Kamei, K., Song, I., Tomida, J., Hashimoto, H., Vaziri, C. and Ohmori, H. (2009) Identification of a novel REV1-interacting motif necessary for DNA polymerase κ function. *Genes Cells*, 14, 101–111.
- 41. Yuasa,M.S., Masutani,C., Hirano,A., Cohn,M.A., Yamaizumi,M., Nakatani,Y. and Hanaoka,F. (2006) A human DNA polymerase η complex containing Rad18, Rad6 and Rev1; proteomic analysis and targeting of the complex to the chromatin-bound fraction of cells undergoing replication fork arrest. *Genes Cells*, **11**, 731–744.
- Ogi,T., Kannouche,P. and Lehmann,A.R. (2005) Localisation of human Y-family DNA polymerase κ: relationship to PCNA foci. J. Cell Sci., 118, 129–136.
- 43. Bi,X., Barkley,L.R., Slater,D.M., Tateishi,S., Yamaizumi,M., Ohmori,H. and Vaziri,C. (2006) Rad18 regulates DNA polymerase κ and is required for recovery from S-phase checkpoint-mediated arrest. *Mol. Cell. Biol.*, **26**, 3527–3540.
- 44. Kannouche, P., Broughton, B.C., Volker, M., Hanaoka, F., Mullenders, L.H. and Lehmann, A.R. (2001) Domain structure, localization, and function of DNA polymerase η, defective in xeroderma pigmentosum variant cells. *Genes Dev.*, **15**, 158–172.
- 45. Kannouche, P., Fernandez de Henestrosa, A.R., Coull, B., Vidal, A.E., Gray, C., Zicha, D., Woodgate, R. and Lehmann, A.R. (2003) Localization of DNA polymerases η and ι to the replication machinery is tightly co-ordinated in human cells. *EMBO J.*, 22, 1223–1233.
- 46. McIntyre, J., Vidal, A.E., McLenigan, M.P., Bomar, M.G., Curti, E., McDonald, J.P., Plosky, B.S., Ohashi, E. and Woodgate, R. (2013) Ubiquitin mediates the physical and functional interaction between human DNA polymerases η and ι. *Nucleic Acids Res.*, **41**, 1649–1660.
- Jones, M.J., Colnaghi, L. and Huang, T.T. (2012) Dysregulation of DNA polymerase κ recruitment to replication forks results in genomic instability. *EMBO J.*, **31**, 908–918.
- Yoon,J.H., Acharya,N., Park,J., Basu,D., Prakash,S. and Prakash,L. (2014) Identification of two functional PCNA-binding domains in human DNA polymerase κ. *Genes Cells*, **19**, 594–601.
- 49. Chilkova,O., Stenlund,P., Isoz,I., Stith,C.M., Grabowski,P., Lundstrom,E.B., Burgers,P.M. and Johansson,E. (2007) The eukaryotic leading and lagging strand DNA polymerases are loaded onto primer-ends via separate mechanisms but have comparable processivity in the presence of PCNA. *Nucleic Acids Res.*, 35, 6588–6597.
- Sabbioneda,S., Gourdin,A.M., Green,C.M., Zotter,A., Giglia-Mari,G., Houtsmuller,A., Vermeulen,W. and Lehmann,A.R. (2008) Effect of proliferating cell nuclear antigen ubiquitination and chromatin structure on the dynamic properties of the Y-family DNA polymerases. *Mol. Biol. Cell*, **19**, 5193–5202.
- Ohkumo, T., Kondo, Y., Yokoi, M., Tsukamoto, T., Yamada, A., Sugimoto, T., Kanao, R., Higashi, Y., Kondoh, H., Tatematsu, M. *et al.* (2006) UV-B radiation induces epithelial tumors in mice lacking DNA polymerase η and mesenchymal tumors in mice deficient for DNA polymerase *ι. Mol. Cell. Biol.*, **26**, 7696–7706.
- 52. Ogi, T., Mimura, J., Hikida, M., Fujimoto, H., Fujii-Kuriyama, Y. and Ohmori, H. (2001) Expression of human and mouse genes encoding polκ: testis-specific developmental regulation and AhR-dependent inducible transcription. *Genes Cells*, **6**, 943–953.