Review

The CUL4A ubiquitin ligase is a potential therapeutic target in skin cancer and other malignancies

Jeffrey Hannah¹ and Peng-Bo Zhou^{1,2}

Abstract

Cullin 4A (CUL4A) is an E3 ubiquitin ligase that directly affects DNA repair and cell cycle progression by targeting substrates including damage-specific DNA-binding protein 2 (DDB2), xeroderma pigmentosum complementation group C (XPC), chromatin licensing and DNA replication factor 1 (Cdt1), and p21. Recent work from our laboratory has shown that *Cul4a*-deficient mice have greatly reduced rates of ultraviolet-induced skin carcinomas. On a cellular level, *Cul4a*-deficient cells have great capacity for DNA repair and demonstrate a slow rate of proliferation due primarily to increased expression of DDB2 and p21, respectively. This suggests that CUL4A promotes tumorigenesis (as well as accumulation of skin damage and subsequent premature aging) by limiting DNA repair activity and expediting S phase entry. In addition, CUL4A has been found to be up-regulated via gene amplification or overexpression in breast cancers, hepatocellular carcinomas, squamous cell carcinomas, adrenocortical carcinomas, childhood medulloblastomas, and malignant pleural mesotheliomas. Because of its oncogenic activity in skin cancer and up-regulation in other malignancies, CUL4A has arisen as a potential candidate for targeted therapeutic approaches. In this review, we outline the established functions of CUL4A and discuss the E3 ligase's emergence as a potential driver of tumorigenesis.

Key words Ubiquitination, cullins, DNA damage, cell cycle regulation, skin cancer, therapeutic targets

For most cellular proteins, stability and degradation are regulated by the ubiquitin-proteosome system in which proteins are posttranslationally modified with polyubiquitin chains and recruited to the 26S proteasome for proteolytic degradation. Although ubiquitin molecules are activated by E1 enzymes and physically conjugated to substrate proteins by E2 enzymes, E3 ubiquitin ligases are responsible for conferring substrate specificity and facilitating the interaction between substrates and E2 enzymes. The members of the largest family of E3 ligases in eukaryotes are cullin-RING ubiquitin ligases (CRLs), which share a modular configuration: RING box 1 (Rbx1) and E2 recruitment at the C-terminus of the cullin

doi: 10.5732/cjc.012.10279

scaffold, and one or multiple substrate-recruiting proteins at the N-terminus^[1,2]. For instance, the N-terminus of cullin 4A (CUL4A) directly binds the adaptor protein damage-specific DNA-binding protein 1 (DDB1), which then recruits a number of possible substrate receptors known as DDB1-CUL4-associated factors (DCAFs) to assemble the cullin-RING ligase 4A (CRL4A) complex (Figure 1)^[3]. These DCAFs directly bind to target proteins, enabling CRL4A to regulate their stability and activity and influence a wide variety of key processes of the cell-often, in a multi-tiered manner^[4-6]. For example, when cells experience ultraviolet (UV) irradiation and DNA damage, CRL4A becomes activated and targets multiple regulators of the cell cycle and DNA replication pathways as well as DNA repair proteins. It is noteworthy that CUL4A has a highly similar family member known as CUL4B that is also able to bind DDB1 adaptor and exhibits functional redundancy with CUL4A^[7-12], as well as distinct activities^[13,14]. However, within the CUL4 subfamily, CUL4A is thought to be the major regulator of the processes and substrates described in this review.

Although DDB1 is now known to primarily function as a substrate adaptor to recruit DCAFs and, by extension, substrates to CUL4A and the ubiquitin-conjugating machinery, it was first identified as a

Authors' Affiliations: ¹Department of Pathology and Laboratory Medicine, Weill Cornell Medical College and Weill Cornell Graduate School of Medical Sciences, New York, NY 10065, USA; ²Department of Pathology and Laboratory Medicine, Weill Cornell Medical College, New York, NY 10065, USA.

Corresponding Author: Peng-Bo Zhou, Department of Pathology and Laboratory Medicine, Weill Cornell Medical College, 1300 York Avenue, New York, NY 10065, USA. Tel: +1-212-746-6415; Fax: +1-212-746-4483; Email: pez2001@med.cornell.edu.

damaged DNA-binding (DDB) protein that exists in a heterodimeric complex with DDB2^[15,16]. DDB2 is the damage recognition subunit that initiates the nucleotide excision repair (NER) pathway. DDB2 is also known as xeroderma pigmentosum (XP) complementation group E (XPE). XP is a condition that is caused by mutations in one of the genes that code for components of the NER pathway (except for the variant form of XP, which is due to loss of a polymerase involved in lesion bypass during DNA replication). As a result, these patients are hypersensitive to UV rays and sunlight and develop frequent squamous cell carcinomas and other skin malignancies. When cells undergo UV irradiation, DDB2 preferentially and directly binds DNA lesions such as 6-4 photoproducts and cyclopyrimidine dimers and recruits other components of the NER machinery to the damaged DNA^[17]. Shortly after this, DDB2 is ubiquitinated and targeted for degradation by CRL4A, which is also active under these conditions^[15,18-20]. In addition to DDB2, another well-characterized NER protein and damaged DNA sensor, XPC, has also been shown to be ubiquitinated by CRL4A^[12,20]. Interestingly, both human DDB2 and XPC are transcriptional targets of the p53 tumor suppressor protein, further demonstrating that CUL4A acts in opposition to the DNA damage response^[18,21].

In addition to DNA repair, CRL4A also regulates the cell cycle by targeting the cyclin-dependent kinase inhibitor p21, which delays S phase entry by inhibiting the Cyclin E/Cdk2 complex, and SET domain-containing protein 7 (Set7) which is a histone H4 Lys20 monomethyltransferase (H4K20me1) that regulates cell cycle progression in G₂/M phase^[10,11,22-26]. CRL4A also targets Cdt1, which is a DNA replication licensing factor that ensures that the origins initiate replication only once per cell cycle^[7-9,27]. Interestingly, for all of these targets, CRL4A uses the DCAF Cdt2, which binds substrates in a proliferating cell nuclear antigen (PCNA)-dependent manner. That is, all of the substrates contain the PCNA-binding motif, known as the PIP box, which is required for recognition by the CRL4A^{Cdt2} ubiquitin ligase. This dependence on PCNA and the observed delays in S phase entry in Cul4a-deficient cells demonstrates that CUL4A, which serves as the basis of the CRL4A complex, is an important regulator of the cell cycle. Upon UV irradiation and subsequent DNA damage, CRL4A becomes activated and targets these regulators of the cell cycle and replication (along with the DNA repair proteins described



above). Therefore, it appears that CUL4A promotes progression of the cell cycle under normal conditions as well as when the cell experiences genotoxic stress. In the latter case, CUL4A arguably antagonizes cellular DNA damage response by degrading crucial NER (e.g., DDB2 and XPC) and checkpoint proteins (e.g., p21), thus reducing repair activity and shortening the time cells have to address genetic insults before replication is initiated^[12,19].

Because CRL4A regulates the cellular threshold of DNA repair and cell cycle checkpoint proteins, we investigated whether CUL4A affects DNA repair capacity and/or the onset of tumorigenesis induced by genotoxic insults^[12]. To do so, we established a germline Cul4a^{-/-} mouse strain and a conditional Cul4a^{iff} K14-CreER^{TAM} mouse strain that expressed tamoxifen-inducible Cre recombinase specifically in the skin. In Cul4a-/- skin and Cul4a-/- mouse embryonic fibroblast (MEF) cells, the half-lives of DDB2, XPC, and p21 were significantly prolonged, leading to increased accumulation of these DNA damage response proteins. As a result, Cul4a- MEF cells exhibited great ability to repair UV-induced DNA lesions. Moreover, those cells displayed stronger DNA damage checkpoint activity: cell cycle arrest in G₁/S phase in Cul4a-deficient MEFs lasted approximately 4-6 h longer than wild-type MEFs following UV damage. We determined that the extended checkpoint arrest seen in Cul4a^{-/-} cells was primarily due to accumulation of p21, as deletion of p21 effectively abrogated the enhancement of G₁/S checkpoint in Cul4a^{-/-} $p21^{-/-}$ MEFs. Notably, CUL4B status did not have any impact on DNA repair capacity or checkpoint activity under these conditions. Finally, we used the Cul4a[#] K14-CreER^{TAM} strain of mice to examine whether CUL4A status affected the onset of skin tumorigenesis in mice that were exposed to UVB irradiation. The results were striking: while all of the control mice developed squamous cell carcinomas between 28 and 48 weeks, Cul4a-deficient mice were essentially resistant to UVB-induced skin cancer under these conditions. With this series of studies, we demonstrated that CUL4A plays an inhibitory role in DNA damage response to UV light via selective degradation of both rate-limiting DNA damage sensors (DDB2 and XPC) of nucleotide excision repair, and a crucial effector (p21) of the G₁/S DNA damage checkpoint. We concluded that CUL4A ablation increases global genomic DNA repair capacity and strengthens G₁/S DNA damage checkpoint, thus allowing the cell more time for repair before the re-

> Figure 1. The cullin-RING ligase 4A (CRL4A) ubiquitin ligase complex. Cullin 4A (CUL4A) serves as the scaffold that uses two adaptors—RING domain-containing Rbx1 and triple WD40 domain-containing damage-specific DNA-binding protein 1 (DDB1)—to recruit the ubiquitincharged E2 ubiquitin-conjugating enzyme and the DDB1-CUL4-associated factors (DCAF) substrate receptor that is loaded with the substrate, respectively. This assembly of individual subunits of the complex places the E2 and the substrate in close proximity, facilitating transfer of the ubiquitin molecule from the enzyme to the substrate protein. The three WD40 β -propeller (BP) domains of DDB1 are designated BPA, BPB, and BPC. S, substrate; Ub, ubiquitin; E2, ubiquitin-conjugating enzyme.

initiation of DNA synthesis and, thereby, conferring resistance to UVinduced skin tumors in mice.

The data from this report strongly implicate CUL4A as an influential factor in UV-induced skin cancer. CUL4A seemingly promotes the accumulation of DNA damage by reducing the threshold levels of DNA repair proteins as well as promoting cell cycle progression. Most interestingly, our work has revealed that human cells are evidently functioning below peak levels of DNA repair capacity (Figure 2). That is, stabilization of the DDB2 and XPC repair proteins as well as the checkpoint protein p21 allowed Cul4a-deficient cells to resolve UV-induced DNA damage more efficiently than their Cul4a-proficient counterparts. As such, targeted inhibition of the CRL4A ubiquitin ligase is expected to provide new avenues for cancer prevention. Moreover, UV rays expedite the skin aging process as a result of increased accumulation of unrepaired DNA lesions, an unfortunate side effect of certain professions or life styles that involve routine, prolonged exposure to sunlight. In principle, targeted inhibition of the CRL4A ubiquitin ligase complex may reduce skin damage and slow down the aging effect caused by chronic exposure to harmful UV rays. Conversely, excess CUL4A is expected to cause premature destruction of rate-limiting

NER and checkpoint factors, resulting in increased accumulation of unrepaired DNA lesions and genomic instability. Evidence from genomic analyses conducted by other groups reveal an up-regulation of CUL4A in breast cancer^[28,29], hepatocellular carcinomas^[30], squamous cell carcinomas^[31], adrenocortical carcinomas^[32], childhood medulloblastomas^[33], and malignant pleural mesotheliomas^[34] as a result of gene amplification or overexpression.

The role of CUL4A in promoting tumorigenesis is anticipated to be the focus of future investigations. Indeed, our work suggests the intriguing possibility that a CRL4A inhibitor could be used to prevent UV-associated pathologies such as skin cancer and premature aging. Furthermore, we believe that targeting *Cul4a* presents low risk to patient health because, in our studies, *Cul4a*-deficient mice did not show any adverse phenotypes (which could potentially be explained by CUL4B compensating for the loss of CUL4A). In summary, CUL4A directly regulates processes that are relevant to tumorigenesis, and is more highly expressed in a number of cancers; loss of CUL4A expression is predicted to have minimal effects in humans. For all these reasons, CUL4A is an enticing potential therapeutic target in treating cancer and premature aging.



Figure 2. Proposed inhibitory role of CRL4A ubiquitin ligase in controlling the threshold of DNA repair and DNA damage checkpoint pathways after ultraviolet (UV) irradiation. The DNA damage response in mammals is normally operating below optimal capacity due to targeted ubiquitination and degradation of nucleotide excision repair (NER) sensors (damage-specific DNAbinding protein 2 and xeroderma pigmentosum complementation group C) and G₁/S checkpoint effector (p21) by CRL4A. Cells with high levels of CUL4A expression are further compromised in their NER and checkpoint capacity and, as a result, are expected to accumulate unrepaired DNA lesions, leading to genomic instability and subsequent predisposition to skin cancer and aging. Conversely, inhibition of CUL4A promotes both NER and checkpoint pathways, thereby conferring better protection against UV- or chemical carcinogen-induced tumorigenesis.

Acknowledgment

This work was supported by grants from National Institutes of Health Grant (No. CA098210), the Natural Science Foundation of China (No. 30901754), and the Tianjin City Thousand Person Plan grants. J.H. is supported in part by a Ruth L. Kirschstein National

References

- Petroski MD, Deshaies RJ. Function and regulation of cullin-RING ubiquitin ligases. Nat Rev, 2005,6:9–20.
- [2] Sarikas A, Hartmann T, Pan ZQ. The cullin protein family. Genome Biol, 2011,12:220.
- [3] Lee J, Zhou P. DCAFs, the missing link of the CUL4-DDB1 ubiquitin ligase. Mol Cell, 2007,26:775–780.
- [4] Lee J, Zhou P. Pathogenic role of the CRL4 ubiquitin ligase in human disease. Front Oncol, 2012,2:21.
- [5] Lee J, Zhou P. Cullins and cancer. Genes Cancer, 2010,1:690– 699.
- [6] Jackson S, Xiong Y. CRL4s: the CUL4-RING E3 ubiquitin ligases. Trends Biochem Sci, 2009,34:562–570.
- [7] Higa LA, Mihaylov IS, Banks DP, et al. Radiation-mediated proteolysis of CDT1 by CUL4-ROC1 and CSN complexes constitutes a new checkpoint. Nat Cell Biol, 2003,5:1008–1015.
- [8] Hu J, Xiong Y. An evolutionarily conserved function of proliferating cell nuclear antigen for Cdt1 degradation by the Cul4-Ddb1 ubiquitin ligase in response to DNA damage. J Biol Chem, 2006,281:3753–3756.
- [9] Jin J, Arias EE, Chen J, et al. A family of diverse Cul4-Ddb1– interacting proteins includes Cdt2, which is required for S phase destruction of the replication factor Cdt1. Mol Cell, 2006,23:709– 721.
- [10] Abbas T, Sivaprasad U, Terai K, et al. PCNA-dependent regulation of p21 ubiquitylation and degradation via the CRL4Cdt2 ubiquitin ligase complex. Genes Dev, 2008,22:2496–2506.
- [11] Kim FJ, Beeche AA, Hunter JJ, et al. Characterization of the nuclear export signal of human T-cell lymphotropic virus type 1 Rex reveals that nuclear export is mediated by position-variable hydrophobic interactions. Mol Cell Biol, 1996,16:5147–5155.
- [12] Liu L, Lee S, Zhang J, et al. CUL4A abrogation augments DNA damage response and protection against skin carcinogenesis. Mol Cell, 2009,34:451–460.
- [13] Yin Y, Lin C, Kim ST, et al. The E3 ubiquitin ligase Cullin 4A regulates meiotic progression in mouse spermatogenesis. Dev Biol, 2011,356:51–62.
- [14] Liu L, Yin Y, Li Y, et al. Essential role of the CUL4B ubiquitin ligase in extra-embryonic tissue development during mouse embryogenesis. Cell Res, 2012,22:1258–1269.
- [15] Tang J, Chu G. Xeroderma pigmentosum complementation group E and UV-damaged DNA-binding protein. DNA Repair (Amst), 2002,1:601–616.
- [16] Hannah J, Zhou P. Regulation of DNA damage response pathways by the cullin-RING ubiquitin ligases. DNA Repair (Amst), 2009,8:536–543.

Service Award (NRSA) Institutional Research Training Grant (No. T32 GM008539).

Received: 2012-11-22; revised: 2013-03-16; accepted: 2013-04-18.

- [17] Min JH, Pavletich NP. Recognition of DNA damage by the Rad4 nucleotide excision repair protein. Nature, 2007,449:570–575.
- [18] Rapic-Otrin V, McLenigan MP, Bisi DC, et al. Sequential binding of UV DNA damage binding factor and degradation of the p48 subunit as early events after UV irradiation. Nucleic Acids Res, 2002,30:2588–2598.
- [19] Chen X, Zhang J, Lee J, et al. A kinase-independent function of c-Abl in promoting proteolytic destruction of damaged DNA binding proteins. Mol Cell, 2006,22:489–499.
- [20] Sugasawa K, Okuda Y, Saijo M, et al. UV-induced ubiquitylation of XPC protein mediated by UV-DDB-ubiquitin ligase complex. Cell, 2005,121:387–400.
- [21] Adimoolam S, Ford JM. P53 and DNA damage-inducible expression of the xeroderma pigmentosum group C gene. Proc Natl Acad Sci U S A, 2002,99:12985–12990.
- [22] Abbas T, Shibata E, Park J, et al. CRL4(Cdt2) regulates cell proliferation and histone gene expression by targeting PR-Set7/ Set8 for degradation. Mol Cell, 2010,40:9–21.
- [23] Centore RC, Havens CG, Manning AL, et al. CRL4(Cdt2)mediated destruction of the histone methyltransferase Set8 prevents premature chromatin compaction in S phase. Mol Cell, 2010,40:22–33.
- [24] Oda H, Hubner MR, Beck DB, et al. Regulation of the histone H4 monomethylase PR-Set7 by CRL4(Cdt2)-mediated PCNAdependent degradation during DNA damage. Mol Cell, 2010,40:364-376.
- [25] Jorgensen S, Eskildsen M, Fugger K, et al. SET8 is degraded via PCNA-coupled CRL4(CDT2) ubiquitylation in S phase and after UV irradiation. J Cell Biol, 2011,192:43–54.
- [26] Lee J, Zhou P. Setting the clock for histone H4 monomethylation. Mol Cell, 2010,40:345–346.
- [27] Zhong W, Feng H, Santiago FE, et al. Cul-4 ubiquitin ligase maintains genome stability by restraining DNA-replication licensing. Nature, 2003,423:885–889.
- [28] Chen LC, Manjeshwar S, Lu Y, et al. The human homologue for the Caenorhabditis elegans cul-4 gene is amplified and overexpressed in primary breast cancers. Cancer Res, 1998,58:3677–3683.
- [29] Melchor L, Saucedo-Cuevas LP, Munoz-Repeto I, et al. Comprehensive characterization of the DNA amplification at 13q34 in human breast cancer reveals TFDP1 and CUL4A as likely candidate target genes. Breast Cancer Res, 2009,11:R86.
- [30] Yasui K, Arii S, Zhao C, et al. TFDP1, CUL4A, and CDC16 identified as targets for amplification at 13q34 in hepatocellular carcinomas. Hepatology, 2002,35:1476–1484.
- [31] Shinomiya T, Mori T, Ariyama Y, et al. Comparative genomic

hybridization of squamous cell carcinoma of the esophagus: the possible involvement of the DPI gene in the 13q34 amplicon. Genes Chromosomes Cancer, 1999,24:337–344.

[32] Dohna M, Reincke M, Mincheva A, et al. Adrenocortical carcinoma is characterized by a high frequency of chromosomal gains and high-level amplifications. Genes Chromosomes Cancer, 2000,28:145-152.

- [33] Michiels EM, Weiss MM, Hoovers JM, et al. Genetic alterations in childhood medulloblastoma analyzed by comparative genomic hybridization. J Pediatr Hematol Oncol, 2002,24:205–210.
- [34] Hung MS, Mao JH, Xu Z, et al. Cul4a is an oncogene in malignant pleural mesothelioma. J Cell Mol Med, 2011,15:350–358.

Submit your next manuscript to *Chinese Journal of Cancer* and take full advantage of:

- · Open access
- No charge to authors
- Quickly published
- Thorough peer review
- Professionally edited
- No space constraints
- Indexed by PubMed, CA, and Google Scholar

Submit your manuscript at www.cjcsysu.com