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APLF (C2orf13) Is a Novel Human Protein Involved in the Cellular Response to Chromosomal DNA Strand Breaks

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Aprataxin and polynucleotide kinase (PNK) are DNA end processing factors that are recruited into the DNA single- and double-strand break repair machinery through phosphorylation-specific interactions with XRCC1 and XRCC4, respectively. These interactions are mediated through a divergent class of forhead-associated (FHA) domain that binds to peptide sequences in XRCC1 and XRCC4 that are phosphorylated by casein kinase 2 (CK2). Here, we identify the product of the uncharacterized open reading frame C2orf13 as a novel member of this FHA domain family of proteins and we denote this protein APLF (apra- taxin- and PNK-like factor). We show that APLF interacts with XRCC1 in vivo and in vitro in a manner that is stimulated by CK2. Yeast two-hybrid analyses suggest that APLF also associates with the double-strand break repair proteins XRCC4 and XRCC5 (Ku86). We also show that endogenous and yellow fluorescent protein-tagged APLF accumulates at sites of H2O2, or UVA laser-induced chromosomal DNA damage and that this is achieved through at least two mechanisms: one that requires the FHA domain-mediated interaction with XRCC1 and a second that is independent of XRCC1 but requires a novel type of zinc finger motif located at the C terminus of APLF. Finally, we demonstrate that APLF is phosphorylated in a DNA damage- and ATM-dependent manner and that the depletion of APLF from noncycling human SH-SY5Y neuroblastoma cells reduces rates of chromosomal DNA strand break repair following ionizing radiation. These data identify APLF as a novel component of the cellular response to DNA strand breaks in human cells.

DNA single- and double-strand breaks are induced through a variety of ways, including the direct attack of deoxyribose by reactive oxygen species. DNA strand breaks can pose a considerable threat if not rapidly repaired or responded to appropriately, as indicated by the increased genetic instability, cancer frequency, or neurodegenerative pathology observed in diseases in which such processes are absent or attenuated. While the overall mechanisms by which DNA single- and double-strand breaks are repaired are very different, the repair of DNA single- and double-strand breaks is polynucleotide kinase (PNK) (10, 33). PNK associates with the DNA single-strand break repair (SSBR) and double-strand break repair (DSBR) protein complexes through direct interaction with casin kinase 2 (CK2)-phosphorylated XRCC1 and XRCC4, respectively (16, 21). These interactions are mediated through a divergent forhead-associated (FHA) domain in PNK that can specifically target CK2-phosphorylated peptides. Intriguingly, the protein aprataxin, which is mutated in the neurodegenerative disease ataxia-oculomotor apraxia type 1, possesses a similar FHA domain and binds the same CK2-phosphorylated regions of XRCC1 and XRCC4 (6, 11, 12–14, 22, 25). Aprataxin is also an end processing enzyme, repairing abortive 5′ AMP intermediates of DNA ligase activity (1). In the current study, we identify a third member of the aprataxin- and PNK-like FHA domain family which we denote APLF (apra- taxin- and PNK-like factor). We demonstrate that APLF is a novel component of the cellular response to chromosomal DNA single- and double-strand breaks.

MATERIALS AND METHODS

DNA constructs and recombinant proteins. To create pGBKT7-APLF: the human APLF open reading frame (ORF) was amplified from the C2orf13 IMAGE clone 6042653 (MRC GeneService) by PCR using the primers 5′-AAAA CCAAGCGCAATGCCGGGCTTCGAGCTG-3′ (the NciI site and the APLF start codon are underlined) and 5′-TTGAATTCGGCAGATATGACTACTA CAGAA-3′ (the EcoRi site and the APLF start codon are underlined, and the His, and Myc tags are italicized) and 5′-AAAAGAATTCGGATTCCTATTT TCTTTTCATAAACC-3′ (the EcoRi site and the APLF start codon are underlined, and the His, and Myc tags are italicized) and 5′-AAAAGAATTCGGGCTTCGAGCTG-3′ (the NciI site and the APLF start codon are underlined, and the His, and Myc tags are italicized) and 5′-AAAAGAATTCGGGCTTCGAGCTG-3′ (the NciI site and the APLF start codon are underlined, and the His, and Myc tags are italicized). Subcloning into the NcoI/EcoRI sites of pGBKT7 (Clontech). To create pcd2E-His-Mye- APLF, the APLF ORF was amplified from IMAGE clone 6042653 by PCR using the primers 5′-AAAAGAATTCGGCAGATATGACTACTA CAGAA-3′ (the EcoRi site and the APLF start codon are underlined) and 5′-TTGAATTCGGCAGATATGACTACTA CAGAA-3′ (the EcoRi site and the APLF start codon are underlined, and the His, and Myc tags are italicized). To create pET16b-APLF, a fragment encoding APLF was removed from pGBK7-APLF and subcloned into pET16b (Novagen) by using NdeI and BamHI. To create pET16b-APLF, a fragment encoding APLF was removed from pGBK7-APLF and subcloned into pET16b (Novagen) by using NdeI and BamHI. To create pET16b-APLF, a fragment encoding APLF was removed from pGBK7-APLF and subcloned into pET16b (Novagen) by using NdeI and BamHI. To create pET16b-APLF, it was linearized with AvrII and the 5′ overhangs filled in with Klenow polymerase prior to religation. pET16b-APLF encodes a polypeptide of 168 amino acids, of which 168...
encode the amino-terminal region of APLF. To create pET16b-APLF 360-511, pET16b-APLF was cut with Sphl and the resulting 3' overhang filled in with Klenow fragment. A 0.5 kb fragment encoding the C-terminal region of APLF was then released with BamHI and subcloned into the blunt-ended NdeII/BamHI sites of pET16b. To create pYEFP-C1-APLF, the APLF ORF was amplified from IMAGE clone 6042653 by PCR using the primers 5'-AAAGAATTCCATGTCGCGGGGCTTCGAGCTG-3' and 5'-AGCTTGCACCCGGCTTGTCTTGGAGTC-3' (the EcoRI site and the stop codon are underlined) and 5'-AAAGAATTCCAGATCTTCTATGCCGGAGATCCGCCTC-3' (the EcoRI site and the APLF start codon are underlined) and subcloned into the EcoRI site of pYEFP-C1 (Clontech). To create pYEFP-C1-APLF \textsuperscript{3794} ILES ET AL. MOL. CELL. BIOL. and pYEFP-C1-APLF \textsuperscript{360-511}, the APLF ORF in pYEFP-C1-APLF was mutated by site-directed mutagenesis using a QuikChange mutagenesis kit and the appropriate primers (Stratagene). To create pYEFP-nls-APLF, pYEFP-nls-APLF \textsuperscript{3794} ILES ET AL. MOL. CELL. BIOL. and pYEFP-nls-APLF \textsuperscript{360-511}, the simian virus 40 (SV40) large T-antigen nuclear localization signal was engineered into the relevant fusion protein between the APLF sequence and the N-terminal yellow fluorescent protein (YFP) tag by subcloning a made oligonucleotides 5'-TCCAGGCCCTAAGAAAAACGGCAAATGTCG-3' and 5'-AGGTCGCCACCCTCAGGCTTCGGCTCTCGCC-3' (the EcoRI site and the XRC1 start codon are underlined) and 5'-TTCTTCGCCTGGCAGCTGACCCCATACAG3- (the Sall site and the stop codon are underlined) and subcloned into the EcoRI/Sall sites of pRFP-C1 encoding monomeric red fluorescent protein (mRFP) (9). To create pRFP-C1-XRC1-C, the XRC1 ORF was subcloned from pCI-neo-Myc-XRC1-C (kindly provided by Flavio Meggio and Lorenzo Pinna). The remainder were blocked in binding buffer (20 mM HEPES, 50 mM NaCl, 1 mM DTT) and bound to His6-APLF and XbaI. All recombinant histidine-tagged proteins expressed in Escherichia coli were purified in BL21(DE3) and purified by metal chelate affinity chromatography using nickel-nitrotriacetic acid agarose (Qiagen).

Protein slot blots and far-Western blotting. Recombinant XRC1-C1-His (10 μg) expressed and purified from bacteria (see above) was phosphorylated with CK2 in 90-μl reaction mixtures (at 30°C for 30 min) containing 10 mM MgCl2, 1 mM ATP, 13.3 mM HEPES, pH 7.5, 0.1 mM DTT, and 0.67 mM 

with goat anti-rabbit horseradish peroxidase-conjugated secondary antibody at a dilution of 1 in 5,000 in 1% NFDY-HYB100 at room temperature for 30 min. Following further washes (three 10-min washes) with 1% NFDY-HYB100, antibody complexes were detected by enhanced chemiluminescence (ECL Plus; Amersham Biosciences) and autoradiography.

Anti-APLF (SK5959) and anti-XRC1 (SK3188) polyclonal antibodies were raised by Eurogentec against recombinant human APLF and XRC1-C1 from E. coli and insect cells, respectively, and were affinity purified against the appropriate recombinant proteins from E. coli.

Two yeast two-hybrid analyses. Saccharomyces cerevisiae Y190 cells were transformed with the indicated pACT and PGBIK7 constructs and transformants selected on minimal medium plates (glucose plus yeast nitrogen base without amino acids) additionally containing adenine and histidine. Pooled populations of transformants were streaked onto two minimal medium plates with adenine and histidine and one minimal medium plate with adenine and 50 mM 3-amino-1,2,4-triazole. The activation of the His3 reporter gene was induced by comparative growth on minimal medium plates containing adenine and 3-amino-1,2,4-triazole and minimal medium plates containing adenine and histidine after 4 to 6 days at 30°C. The activation of the β-galactosidase (β-Gal) reporter gene was determined by qualitative X-Gal (5-bromo-4-choro-3-indoly-β-n-galactopyranoside) assays on colony filter lifts from minimal medium plates containing adenine and histidine. Quantitative β-Gal assays were conducted essentially as described by Clontech (Yeast Protocols Handbook). Equivalent expression levels of DNA binding domain or activation domain fusion proteins were confirmed by Western blotting both for cell cultures employed for filter lift β-Gal assays and for quantitative β-Gal assays. Cell extracts were prepared in cracking buffer (6 M urea, 5% [w/vol] SDS, 40 mM Tris-HCl [pH 6.8], 0.1 mM EDTA, 0.4 mg/ml bovine serum albumin, 1% glycerol, 20 μg/ml leupeptin, 1% protease inhibitor cocktail [Sigma]) and fractionated by SDS-PAGE, and Myc-tagged APLF (expressed from pGBK7) was detected by immunoblotting with anti-Myc monoclonal antibody (MAB) (9B11; Cell Signaling Technology) and DNA binding domain fusion proteins by immunoblotting with polyclonal anti-GAL4 activation domain antibody (Upstate Biotechnology). Washed membranes were then incubated with the appropriate horseradish peroxidase-conjugated secondary antibody (Dako) and bound antibodies visualized using enhanced chemiluminescence (Amersham Biosciences).

Immunoprecipitations. For immunoprecipitation experiments, ~3 × 10\(^6\) HeLa cells were transiently transfected with pCD2 vector or pCD2-His-Myc-APLF by using GeneJuice transfection reagent (Novagen) and pooled populations of transfected cells were selected in medium containing G418 (0.8 mg/ml) for 5 days. Alternatively, ~3 × 10\(^7\) A549 cells were stably transfected with pCD2 and either empty pSUPER or pSUPER encoding the APLF RNA interference (RNAi) sequence GAAGAAATCTCAGCAGAATA (pSUPER-APLF) by selection with 0.8 mg/ml G418 for 4 weeks. Transfected cells were lysed in 3 ml lysis buffer (20 mM Tris-HCl, pH 7.5, 10 mM EDTA, 100 mM NaCl, 1% Triton X-100, 0.5 mM sodium orthovanadate, 50 mM sodium fluoride, 10 mM β-glycerophosphate, and 1% protease inhibitor cocktail [Sigma]) on ice for 5 min followed by 2 min on 4°C. Cell lysates were then released with 1 h at 4°C with 60 μl of 40 μl protein G-Sepharose beads (Sigma). HeLa cell extract (1.5 ml) was incubated with 1 μl of either anti-Myc MAb (9B11) or anti-Flag MAb (M2; Sigma) and A549 cell extract (1 ml) with either 100 μl anti-XRC1 polyclonal antibody (SK3188) or 0.01 μl rabbit immunoglobulin G (IgG; Dako) overnight at 4°C with gentle agitation. The beads were then washed three times with lysis buffer (300 μl each wash) and bound proteins eluted by heating with 55 μl of 2× SDS-PAGE sample buffer at 90°C for 5 min. Clarified protein samples were fractionated by SDS-PAGE, transferred to nitrocellulose, and immunoblotted with anti-Myc MAb (9B11) or anti-XRC1 (SK3188) or anti-APLF (SK3595) polyclonal antibody.

Direct and indirect immunofluorescence experiments. For direct immunofluorescence experiments, XRC1-C1 mutant EM1 (80, 31) or XRC1-C4 mutant XR-1 (20, 28) CHO cells seeded onto coverslips were transfected with the indicated enhanced YFP or mRFP fusion protein constructs by using GeneJuice transfection reagent (Novagen). After 24 h, cells were washed with phosphate-buffered saline (PBS) and mock treated or treated with 10 mM hydrogen peroxide in PBS for 10 min at room temperature, washed with PBS, and then incubated in drug-free media at 37°C for 20 to 120 min. The coverslips were then washed in PBS and fixed (3 min in 4% paraformaldehyde in PBS). Fixed cells were then permeabilized in 0.2% Triton X-100 for 2 min, washed with PBS, and stained with 0.000025% DAPI (4',6'-diamidino-2-phenylindole) for 5 min. Coverslips were mounted in Vectashield (Vector Labs) and analyzed with a Zeiss Axioplan 2 fluorescence microscope. Photographs were taken at a magnification of ×100.
and YFP-APLF-transfected cells scored for subcellular localization of YFP-APLF.

For indirect immunofluorescence experiments, A549 cells were seeded onto gridded coverslips (MatTek) in 10-cm dishes at ~1 × 10⁶ cells/cm² and, after 2 days, preincubated for 10 min with 10 µg/ml Hoechst dye 33258 at 37°C. Selected cells were then irradiated with a 355-nm UVA laser focused through a 40x/1.2-W objective using a Zeiss Axiovert equipped with LSM 520 Meta. UVa (10.47 Μ) was introduced to an area of approximately 15 µm by 2 µm (approximately 0.35 µm²/μm²). After exposure, coverslips were incubated at 37°C for the times indicated and washed in ice-cold PBS, and cells were fixed in ice-cold methanol-acetone (1:1) for 5 min and then permeabilized for 5 min in PBS-0.1% Tween. Coverslips were incubated in PBS-5% FDM for 30 min for blocking and then overnight at 4°C in PBS-1% FDM containing anti-XRCC1 MAb (clone 33-2-5) and anti-APLF polyclonal antibody (both at 1/200 dilutions). Coverslips were then incubated with secondary labeling with Alexa Fluor 488 anti-rabbit antibodies (1/200 in PBS-1% milk; Invitrogen) for 1 h at room temperature. DNA was stained with 0.1 µg/ml DAPI (Sigma). Tracks were then visualized using a Nikon Eclipse 50i microscope fitted with a ×100 oil immersion objective.

**RESULTS**

Database analyses identified a third protein that contains a FHA domain with sequence similarity to the FHA domains present in PNK and aprataxin, A549 cells stably transfected with pCD2E vector (2 µg) and either pMAX-GFP vector (4 µg; Amaxa), pSUPER vector harboring the APLF RNAi sequence GAAGAATTCGTCAAGAGATA (4 µg), or 160 pg of the XRCC1 small interfering RNA (siRNA) duplex GCCUGAAGAUUGCUGA UAUA (sense strand; QIAGEN) by using Nuclease and Nuclease kit V (Amaya). Twenty-four hours after nucleofection, cells were placed into a 5% CO₂ incubation medium containing 0.25 mg/ml G418 and 10 µM all-trans retinoic acid to induce neuronal differentiation. After 5 days of selection, the medium was replaced with medium containing 10 µM retinoic acid only. For alkaline comet assay, 5 × 10⁶ SH-SYSY cells were harvested 6 days after transfection and irradiated (20 Gy of gamma rays) before being returned to 37°C for 7.5, 15, or 30 min. At each time point, 1 × 10⁶ treated cells were removed and DNA damage was measured by single-cell agarose gel electrophoresis, essentially as described previously (5). For γ-H2AX assays, A549 cells stably transfected with pCD2E and either empty pSUPER or pSUPER encoding the APLF RNAi sequence GAAGAATTCGTCAAGAGATA, or SH-SYSY cells 6 days after transient transfection with green fluorescent protein, pSUPER-APLF, or XRCC1 siRNA as described above, were grown on glass coverslips and exposed to 1 to 3 Gy of γ-radiation before being returned to 37°C. At the times indicated, coverslips were washed in PBS, fixed for 5 min in 4% paraformaldehyde in PBS, permeabilized (0.2% Triton X-100 for 2 min), blocked (5% NFDM for 30 min), and incubated with anti-γ-H2AX MAB (clone JBW301, 1/800 in 1% NFDM in PBS; Upstate). Cells were then washed (three times for 5 min each) in PBS containing 0.1% Tween 20 and 0.02% SDS and incubated for 1 h with Alexa Fluor 488 goat anti-mouse IgG secondary antibody (1/200 dilution in 1% milk-PBS). The cells were then washed (five times for 5 min each) as described above, mounted in Vectashield (Vector Labs), and scored for γ-H2AX foci by using a Nikon Eclipse 50i microscope.

**DNA damage-induced modification of APLF.** Subconfluent 1BR3, FD105 (AO1), or A7B1I (A-T) primary fibroblasts were harvested, either exposed to gamma rays (3 Gy) or treated with 10 mM H₂O₂ on ice for 20 min, and then incubated at 37°C for 20 min (H₂O₂) or 30 min (gamma rays) in drug-free media. Cells were then harvested and lysed in SDS-PAGE sample buffer, and aliquots of cell extracts were fractionated by SDS-PAGE (7.5% gels) and immunoblotted with anti-APLF polyclonal antibody (SK395).
FIG. 1. Conserved FHA and tandem ZnF domains in APLF. (A) Alignment of the FHA domains of APLF, aprataxin (APTX), and PNK. Identical residues are in red, highly conserved residues in blue, and similar residues in green. Putative phosphate-binding residues are boxed in red, and the basic residues that are believed to confer specificity for binding CK2-phosphorylated motifs are underlined. (B) APLF protein homologues. BLAST analyses identify multiple homologues of APLF in mouse (Mus musculus), chicken (Gallus gallus), mosquito (Anopheles gambiae), and purple sea urchin (Strongylometos purpuratus). Identical residues are in red, highly conserved residues in blue, and blocks of similar residues in green. Dotted boxes denote the amino-terminal FHA domain and the putative tandem ZnFs at the C terminus. (C) BLAST analyses with the C-terminal putative tandem ZnF motif of APLF identifies 18 additional polypeptides that possess this motif in single copy, many of which are likely DNA repair- and DNA damage-associated proteins. Identical residues are boxed in yellow (note that these are the putative metal coordinating residues), highly conserved residues boxed in green, and blocks of similar residues boxed in blue. Black circles denote the C terminus of the polypeptide.
panels), neither protein bound to control slots blotted with CK2 reaction products lacking XRCC1-His (Fig. 3C, bottom left panel). In contrast to His-APLF and His-APLF1-166, a C-terminal fragment of His-APLF (His-APLF360-511) containing the putative C2H2 ZnFs failed to interact with CK2-phosphorylated XRCC1-His (Fig. 3C, right panel). Similar results were observed by far-Western blotting, in which the CK2-phosphorylated XRCC1-His protein probe detected His-APLF and His-APLF1-166, but not His-APLF360-511, proteins present on renatured Western blots (Fig. 3D). We conclude from these experiments that the FHA domain in APLF interacts with CK2-phosphorylated XRCC1.

To further examine whether APLF is a component of the DNA damage response, we compared the subcellular localization patterns of endogenous XRCC1 and APLF in human A549 cells following UVA laser irradiation. As expected, XRCC1 rapidly accumulated (within 3 min) at sites of UVA damage (Fig. 4A). More significantly, APLF colocalized and accumulated with XRCC1 at these sites, confirming that APLF is a component of the response to UVA-induced cellular damage. To examine the relationship between XRCC1 and APLF in more detail, we compared the subcellular localization patterns of YFP- and RFP-tagged human APLF and XRCC1 before and after treatment with H2O2 in transiently transfected XRCC1 mutant CHO cells (EM9 cells). Whereas RFP-XRCC1 was largely or entirely nuclear in all transfected EM9 cells,
YFP-APLF was largely nuclear or pancellular in ~60% of cells in the presence of RFP-XRCC1 and largely cytosolic or pancellular in ~90% of cells in the absence of RFP-XRCC1 (Fig. 4B and C, left panel). The fraction of cells with largely nuclear YFP-APLF transiently increased after H$_2$O$_2$ treatment in an RFP-XRCC1-dependent manner (Fig. 4C, middle and right panels). The presence of a large proportion of cells with largely nuclear YFP-APLF was also dependent on a functional FHA domain, because the YFP-APLFR27A protein harboring a mutated FHA domain was largely cytoplasmic or pancellular in most cells both before and after H$_2$O$_2$ treatment, even in the presence of RFP-XRCC1 (Fig. 4C). We conclude that RFP-XRCC1 promoted the nuclear import or retention of YFP-APLF in these experiments in a manner that was stimulated by oxidative DNA damage and which required the APLF FHA domain.

In the majority (~83%) of cotransfected cells, YFP-APLF and RFP-XRCC1 colocalized in subnuclear foci after H$_2$O$_2$ treatment (Fig. 4D and 5A, left panel). In contrast, far fewer focus-positive cells (~15%) were observed in EM9 cells transfected with either YFP-APLF alone or a combination of YFP-APLFR27A and RFP-XRCC1 (Fig. 5A). These data suggest that RFP-XRCC1 stimulates the accumulation of YFP-APLF at oxidative DNA strand breaks but that it is not essential for this process. To examine whether this effect of RFP-XRCC1 reflected its impact on the nuclear localization of YFP-APLF, we created YFP-nls-APLFR27A, a derivative of YFP-APLFR27A in which we engineered an SV40 nuclear localization signal.
As expected, YFP-nls-APLFR27A was largely or entirely nuclear and, moreover, accumulated extensively at oxidative DNA strand breaks (Fig. 5A, right panel). These data suggest that XRCC1 facilitates the accumulation of APLF at oxidative SSBs by promoting the nuclear import of APLF, in part at least.

In contrast to RFP-XRCC1, RFP-XRCC4 did not form measurable subnuclear foci after H2O2 and had little or no effect on the subcellular localization of YFP-APLF when expressed in XRCC4 mutant XR-1 CHO cells (data not shown).

However, we did note that large numbers (~40%) of XR-1 cells possessed YFP-APLF or YFP-APLFR27A foci after H2O2 treatment (data not shown). This most likely reflects the XRCC1-independent recruitment/accumulation of recombinant APLF at DNA strand breaks that was observed, albeit to a lesser extent, in EM9 cells. We considered the possibility that the XRCC1-independent recruitment/accumulation of APLF at sites of oxidative DNA damage might be mediated via the putative C2H2 ZnF motifs. To examine this possibility, we expressed derivatives of APLF in which the two putative zinc coordinating cysteine residues in the first (YFP-APLFzf1) or second (YFP-APLFzf2) ZnF were mutated to alanine. Neither of the ZnF mutations reduced XRCC1-dependent nuclear import/retention of YFP-APLF in untreated EM9 cells, although the ZFM1 mutation did reduce the XRCC1-dependent increase in nuclear YFP-APLF observed after H2O2 treatment (Fig. 5B, right panel). The ZFM1 mutation also reduced the formation of YFP-APLF nuclear foci in the presence of XRCC1, by ~30% (Fig. 5C, left panel). More significantly, however, the XRCC1-independent accumulation of YFP-APLF in nuclear foci was reduced by the ZFM2 mutation and ablated by the ZNF1 mutation (Fig. 5C, right panel). These data confirm that the tandem ZnF motif is required for XRCC1-independent recruitment/accumulation of APLF at sites of oxidative DNA strand breakage.

To examine whether the tandem ZnF promoted XRCC1-independent accumulation of YFP-APLF at sites of oxidative DNA damage through an impact on nuclear localization, we employed derivatives of YFP-APLF and YFP-APLFZnF1 that harbored an SV40 NLS, denoted YFP-nls-APLF and YFP-nls-APLFZnF1, respectively. While both YFP-nls-APLF and YFP-nls-APLFZnF1 were able to assemble into subnuclear foci in the presence of XRCC1, only YFP-nls-APLF did so in the absence of RFP-XRCC1 (Fig. 5D, left and middle panels). Thus, the addition of an NLS did not circumvent the requirement for the tandem ZnF, suggesting that the ZnF fulfills a function other than increasing the nuclear import/retention of YFP-APLF. Interestingly, we noted in these experiments that RFP-XRCC1 stimulated the assembly of YFP-nls-APLF nuclear foci, despite the presence of an NLS, and did so in a manner that was dependent on an intact FHA domain (Fig. 5D, middle and right panels). This suggests that the impact of the XRCC1-APLF interaction extends beyond its ability to promote APLF nuclear import/retention. In summary, we conclude from these experiments that the accumulation of YFP-APLF at oxidative DNA strand breaks is promoted by at least three mechanisms: two that are dependent on FHA domain-mediated interaction with XRCC1, including one that involves increased nuclear import/retention of APLF, and one that is...
independent of XRCC1 but dependent on the tandem ZnF motif.

To further examine the involvement of APLF in the re-
sponse to DNA damage, we compared its electrophoretic mo-
bitilities before and after treatment with gamma rays or H2O2.
Notably, the mobility of endogenous APLF during SDS-PAGE
decreased after treatment with either H2O2 or ionizing radia-
tion (IR) in wild-type cells and in aprataxin-defective AOA1
primary fibroblasts (Fig. 6A). However, this shift in electro-
phoretic mobility was not detected in ataxia telangiectasia fi-
broblasts lacking the DSB-responsive protein kinase ATM.

These data support the idea that APLF is involved in the
cellular response to DSBs. To examine whether APLF is re-
quired for chromosomal DNA single- and double-strand break
repair, we mock depleted or depleted APLF or XRCC1 from
differentiated/noncycling SH-SY5Y neuroblastoma cells by
transient siRNA transfection (Fig. 6B, left panel). Whereas the

type of siRNA did not affect the level of DNA strand breaks
induced by IR, as measured by alkaline comet assays, the rate
at which DNA strand breaks declined was significantly delayed
in both XRCC1- and APLF-depleted cells (Fig. 6C). It is likely
that the delay observed here reflects a defect in SSBR, because
95% of the total breaks induced by IR are SSBs (4). To
examine the rate of DSBR, we quantified the level of
\( \gamma\)-H2AX, an established marker of DSBs (26, 27), in gamma ray-treated
SH-SY5Y neuroblastoma cells that were depleted of APLF as
described above or in A549 cells that were stably depleted of
APLF (Fig. 5B, right panels). We consistently observed in
these experiments that \( \gamma\)-H2AX foci declined at significantly
reduced rates in both APLF-depleted neuroblastoma cells and
A549 cells following 1 to 3 Gy of IR (Fig. 6D). In contrast,
repair rates were normal in XRCC1-depleted SH-SY5Y cells,
consistent with the absence of a measurable DSBR defect in
these cells (Fig. 6D, right panel).
DISCUSSION

We describe here a new component of the DNA single- and double-strand break repair machinery. This protein is a previously uncharacterized ORF (C2orf13) that we have denoted APLF based on the presence of an aprataxin- and PNK-like FHA domain at its amino terminus. Consistent with the presence of this domain, APLF interacts with both XRCC1 and XRCC4, the same components of the single- and double-strand break repair machinery that are bound by PNK and aprataxin (11, 12, 14, 16, 22, 33). Moreover, similar to the situation with PNK and aprataxin, the interaction of XRCC1 with full-length APLF in vitro or with a fragment of APLF containing the FHA domain was largely dependent on the phosphorylation of XRCC1 by CK2. Intriguingly, a yeast two-hybrid screen employing APLF as bait recovered not only multiple clones of both XRCC1 and XRCC4 but also multiple clones of XRCC5 (Ku86). Of 109 cDNA clones recovered, 6 encoded XRCC1, 15 encoded XRCC4, and 7 encoded XRCC5 (Ku86) (data not shown). APLF may thus associate with the nonhomologous end-joining machinery through interactions with both XRCC4 and the Ku86 heterodimer.

Direct evidence of a role for APLF in the cellular response to DNA damage emerged from the observations that endogenous APLF accumulates at sites of UVA laser damage in human A549 cells and that recombinant YFP-APLF accumulates in subnuclear foci in H2O2-treated CHO cells. Whereas the UVA laser tracts most likely contain sites with both single- and double-strand breaks (data not shown), the H2O2-induced foci most likely reflect just SSBs. This is because they colocalize and are stimulated by RFP-XRCC1 and because they do...
not significantly colocalize with sites of γ-H2AX (data not shown). In addition, we failed to detect accumulation of the DSBR protein XRCC4 in H2O2-induced subnuclear foci under the same experimental conditions. It is also noteworthy that, in collaborative experiments with Akira Yasui, we observed the accumulation of YFP-APLF at UVA laser-induced damage under conditions where SSBs are selectively induced (19; unpublished observations).

The ability of RFP-XRCC1 to stimulate the accumulation of YFP-APLF in subnuclear foci most likely reflected, at least in part, the impact of recombinant XRCC1 on the nuclear import or retention of YFP-APLF. This is because the addition of an NLS to YFP-APLF circumvented the requirement of RFP-XRCC1 for high levels of YFP-APLF nuclear foci. However, these experiments do not rule out an additional role(s) for XRCC1 during the accumulation of YFP-APLF at sites of DNA damage. This is because the NLS had a much greater impact on the nuclear import/retention of YFP-APLF than did recombinant RFP-XRCC1, perhaps thereby masking additional roles for XRCC1. Indeed, consistent with this notion, the coexpression of RFP-XRCC1 stimulated the appearance of YFP-nls-APLF nuclear foci, albeit to a lesser extent than YFP-APLF foci (fivefold versus twofold), despite the presence of an NLS. The nature of the alternative mechanism by which XRCC1 might promote the accumulation of YFP-APLF at sites of oxidative DNA damage is not known. However, since this mechanism required an intact FHA domain in APLF, one attractive possibility is that it reflects the scaffolding role of XRCC1. A similar explanation has been suggested for the observation that XRCC1 also promotes the accumulation of aprataxin, PNK, and DNA polymerase β at sites of H2O2-induced DNA damage (21; unpublished observations).

H2O2-induced YFP-APLF foci were observed in 15 to 40% of CHO cells in the absence of XRCC1, and a similar fraction of YFP-APLF focus-positive cells was observed when RFP-XRCC1 was coexpressed with YFP-APLF lacking an intact FHA domain. Thus, although greatly stimulated by the coexpression of recombinant XRCC1, the recruitment/accumulation of YFP-APLF at sites of oxidative DNA damage can occur independent of XRCC1. Intriguingly, this XRCC1-independent mode of APLF recruitment/accumulation required the two tandem ZnF motifs, suggesting the notion that these structures represent a novel class of DNA strand break-responsive motifs. The amino acid sequences of the tandem ZnFs in APLF appear to be distinct from those present in other SSBR/DSBR proteins, such as aprataxin and poly(ADP-ribose) polymerase 1, as indicated by the limited number of proteins detected as containing this motif in database searches (Fig. 1C). It is not yet clear what function these putative ZnFs fulfill, but the presence of this structure in a variety of other DNA repair and DNA metabolic proteins suggests that it is an important one. The impact of the ZnFs on the XRCC1-independent recruitment/accumulation of YFP-APLF at sites of oxidative DNA damage was not mediated via increased nuclear import or retention of APLF, because the addition of an NLS did not compensate for the absence of intact ZnFs. We suggest that the ZnF may bind to DNA strand breaks directly, thereby promoting XRCC1-independent recruitment of APLF at sites of chromosomal damage.

In contrast to RFP-XRCC1, RFP-XRCC4 did not promote the redistribution of APLF to nuclei or the accumulation of APLF in H2O2-induced subnuclear foci. This may reflect the nature of the cellular response to DSBs because accumulation in discrete subnuclear foci does not appear to be a general feature of nonhomologous end-joining enzymes such as XRCC4 and Ku following oxidative stress. However, further evidence that APLF is involved in the response to DSBs was suggested by the change in the electrophoretic mobility of this protein induced by IR or H2O2. Significantly, this phenomenon was dependent on the DB sensor protein kinase ATM, suggesting that APLF is phosphorylated in an ATM-dependent manner in response to DSBs, though we cannot rule out that ATM is activated in this context by some other type of lesion or event. It also remains to be determined whether APLF is a substrate for ATM or whether APLF is modified via ATM indirectly.

Alkaline comet and γ-H2AX assays suggested that the depletion of APLF by siRNA retards the rate of DNA single- and double-strand break repair at early times after IR. We observed a DBS defect in both proliferating A549 lung carcinoma cells and noncycling SH-SY5Y neuroblastoma cells, as measured by γ-H2AX staining. However, using alkaline comet assays, we detected a DNA strand break repair defect only in noncycling SH-SY5Y cells (data not shown). Since alkaline comet assays measured primarily SSBs in these experiments, due to the abundance of SSBs relative to DSBS induced by IR (~20:1), we suggest that this reflects a difference in the redundancies of APLF during SSBR in proliferating versus noncycling cells. Differences in polypeptide requirements during SSBR in S-phase versus nonreplicating cells have been reported previously (24, 29). The impact of APLF depletion on DNA strand break repair rates was subtle, though in the case of SSBs, it was no less subtle than in cells depleted of XRCC1, which is the archetypal SSBR protein (7, 32). The relatively small impact on repair rates observed in these experiments could thus be due to the incomplete depletion of XRCC1 and APLF by siRNA. Alternatively, it is possible that APLF is required for the rapid repair of only a subset of DNA strand breaks, such as those with specific types of DNA termini. This is also most likely the case for aprataxin, which removes rare 5′ AMP adducts from DNA strand breaks in vitro but does not have a measurable impact on global rates of DNA strand break repair in vivo (1).

What role might APLF play during DNA strand break repair? Given that APLF most likely binds the same regions of XRCC1 and XRCC4 that are bound by PNK and aprataxin, both of which are end processing enzymes, it is tempting to speculate that APLF fulfills or facilitates a similar activity. This suggests a model in which CK2-phosphorylated XRCC1 or APLF can recruit one of at least three different end processing activities to an SSB or DSB, depending on the nature of the damaged termini. The unusual nature of the tandem ZnFs may be informative in this respect. Combined sequence/structure database analyses assign this motif as a tandem ZnF most closely related to the CCCH tandem ZnFs present in the tristetrapolin family of mRNA binding proteins (3, 17). Interestingly, these tandem ZnFs appear to be required to facilitates the deadenylation of 3′ poly(A) tails of specific mRNAs, most likely through the recruitment of an RNase (18). Although they share some similarities, the APLF tandem ZnFs and...
tristetraprolin family ZnFs are clearly distinct, most notably in the spacing between the zinc coordinating residues and the absence of specific residues critical for mRNA binding. It is thus tempting to speculate that the tandem putative ZnFs in APLF target DNA rather than RNA, thereby facilitating the processing of a specific type of DNA 3′ terminus.

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REFERENCES

AUTHOR’S CORRECTION

APLF (C2orf13) Is a Novel Human Protein Involved in the Cellular Response to Chromosomal DNA Strand Breaks

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Volume 27, no. 10, p. 3793–3803, 2007. Page 3799: In the legend to Fig. 4C, “HeLa” should read “EM9 CHO.” Page 3800: In the legends to Fig. 5B, C, and D, “HeLa” should read “EM9 CHO.” Page 3793: The postal code for Sussex should read as shown above.