ZBTB2, a Novel Master Regulator of the p53 Pathway*[s]

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We found that ZBTB2, a POK family transcription factor, is a potent repressor of the ARF-HDM2-p53-p21 pathway important in cell cycle regulation. ZBTB2 repressed transcription of the *ARF, p53,* and *p21* genes, but activated the *HDM2* gene. In particular, ZBTB2 repressed transcription of the *p21* gene by acting on the two distal p53 binding elements and the proximal Sp1 binding GC-box 5/6 elements. ZBTB2 directly interacted with Sp1 via its POZ domain and zinc fingers, which was important in the repression of transcription activation by Sp1. ZBTB2 and Sp1 competed with each other in binding to the GC-box 5/6 elements and the two p53 binding elements. ZBTB2 directly interacted with p53 via its zinc fingers, inhibiting p53 binding and repressing transcription activation by p53. The POZ domain, required for transcription repression, interacted with corepressors such as BCoR, NCoR, and SMRT. The interactions deacetylated histones Ac-H3 and -H4 at the proximal promoter. Although ectopic ZBTB2 stimulated cell proliferation, knockdown of ZBTB2 expression decreased cell proliferation and DNA synthesis. Overall, our data suggest that ZBTB2 is a potential proto-oncogenic master control gene of the p53 pathway and, in particular, is a potent transcription repressor of the cell cycle arrest gene *p21* by inhibiting p53 and Sp1.

The POZ domain is an evolutionarily conserved protein-protein interaction motif found in many cellular regulatory proteins (1, 2). POZ domain genes, first identified in *Drosophila* and poxvirus, have since been found in organisms ranging from yeast to humans (3, 4). As many as 184 known human proteins, 96 *Drosophila* proteins, and 137 *Caenorhabditis elegans* proteins are estimated to contain the POZ domain.

POZ domain proteins are involved in many critical cellular processes such as apoptosis (5), development (6, 7), ion channel activity (4), oncogenesis (8–10), and transcription (10–16). In particular, some of the POZ domain Krüppel-like zinc finger (POK)[3] proteins are the major determinants of development, differentiation, and oncogenesis. PLZF-null mice display severe defects in limb development and germ stem cell maintenance (7, 17). T helper-inducing POZ/Krüppel-like factor (Th-POK/cKrox) has been recently reported as a master regulator of T-cell lineage commitment (18). BCL-6, PLZF, and HIC1 have been implicated in non-Hodgkin lymphoma, acute promyelocytic leukemia, and spontaneous malignant tumors, respectively (8, 9, 19). Recently, FBI-1 (also called Pokemon) has been shown to act as a proto-oncogene by repressing transcription of the *ARF* gene, causing down-regulation of p53 and promoting oncogenic cellular transformation (10).

The most striking property of some POZ domain transcription factors is their ability to repress transcription via their POZ domains (10–16, 20), although a few POZ domain transcription factors activate transcription (21, 22). This characteristic probably underlies many biological processes controlled by these factors. The ability of the domain to interact with key regulatory proteins such as corepressor proteins and other transcription factors appears to be important for repression. In particular, the POZ domains of human BCL-6, FBI-1, HIC-1, and PLZF interact with BCoR, histone deacetylase, mSin3A, and SMRT/N-CoR (12–16, 20, 23).

The cyclin-dependent kinase inhibitor p21 is a major player in cell cycle arrest in mammalian cells and the downstream cell cycle regulator of the ARF-HDM2-p53-p21 pathway (Refs. 24 and 25 and references therein). The *p21* gene, mainly regulated at the transcriptional level, is a transcriptional target of tumor suppressor p53 and plays a crucial role in mediating growth arrest when cells are exposed to DNA-damaging agents (Refs. 24–26 and references therein). Overexpression of p21 results in G_1-, G_2-, or S-phase arrest upon exposure to DNA-damaging agents (27–29). Whereas induction of p21 predominantly leads to cell cycle arrest, repression of p21 may have a variety of

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[s] The on-line version of this article (available at http://www.jbc.org) contains supplemental Figs. S1–S6.
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[3] The abbreviations used are: POK, POZ domain Krüppel-like zinc finger; *ARF*, alternative reading frame gene; BCL-6, B-cell lymphoma-6; BCoR, BCL-6 interacting corepressor; BTB, bric-a-brac tramtrack broad complex; POZ, poxvirus and zinc finger; ChIP, chromatin immunoprecipitation; CV-1, African green monkey kidney cell; EMSA, electromobility shift assay; FACS, fluorescence-activated cell sorter; FBI-1, factor that binds to the inducer of short transcripts of human immunodeficiency virus-1; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; GST, glutathione *S*-transferase; HDM2, human analogue of mouse double minute oncogene; *LacZ*, β-galactosidase gene; Luc, luciferase; NCoR, nuclear receptor corepressor; PLZF, promyelocytic leukemia zinc finger protein; Rb, retinoblastoma; SMRT, silencing mediator for retinoid and thyroid receptors; Sp1, specificity protein 1; RT, reverse transcription; siRNA, small interfering RNA; MTT, 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide.

outcomes depending on the cellular context (Ref. 26 and references therein, and Ref. 27). Aside from p53, a variety of other factors, including Smads, AP2, STAT, BRCA1, E2F-1/E2F-3, and C/EBPα and -β, activate the transcription of *p21*. In addition to its role in responding to DNA damage, p21 has also been implicated in terminal differentiation, replicative senescence, and protection from p53-dependent and -independent apoptosis (Ref. 26 and references therein).

Sp1 family transcription factors that bind at the proximal promoter (bp −120 to −50) of the *p21* gene represent another group of major regulators that affect *p21* gene expression (Ref. 26 and references therein). Sp1 is one of the best characterized transcription factors that bind to GC-rich DNA sequences in numerous cellular and viral genes (Refs. 30 and 31 and references therein). The six Sp1 binding GC-boxes of the *p21* gene proximal promoter have been shown to be important; mutation of the sites not only significantly affects transcription but also disrupts synergistic transcription activation by Sp1, p53, and other signals that regulate *p21* gene transcription (26, 32). Among the six GC-boxes, GC-box 3 mediates p21 induction by various agents such as transforming growth factor-β, butyrate, histone deacetylase inhibitor trichostatin A, lovastatin, and Ca^{2+}. In contrast, GC-boxes 1 and 2 mediate transcriptional activation by phorbol esters and okadaic acid, tumor suppressor protein BRCA1, and gut-enriched Krüppel-like factor (GKLF, KLF4). To date, no specific role has been attributed to the most proximal and overlapping GC-boxes 5 and 6 (Ref. 26 and references therein). Together, these observations suggest that the specificity of utilizing different proximal GC-boxes under different *p21* gene regulation conditions is important.

In this article, we investigated whether a novel POK family protein, ZBTB2, could regulate any components of the ARF-HDM2-p53-p21 pathway, and examined the mechanisms and physiological consequences of ZBTB2 action. ZBTB2 repressed transcription of the *ARF*, *p53*, and *p21* genes, and potently activated the *HDM2* gene, which overall down-regulates the p53 pathway significantly. ZBTB2 increased cell proliferation significantly. Our data suggest that ZBTB2 may be a master regulator of the p53 pathway and may play a critical role in important biological processes controlled by *p21* and other genes of the p53 pathway.

EXPERIMENTAL PROCEDURES

Plasmids, Antibodies, and Reagents—The p21-Luc plasmid was kindly provided by Dr. Yoshihiro Sowa of the Kyoto Perpetural University of Medicine (Kyoto, Japan). The various pGL2-p21-Luc, pGL2-p53-Luc, pGL2-ARF-Luc, pGL2-HDM2-Luc, pcDNA3.1-p53, pcDNA3.1-Sp1, pG5-5x(GC-box)-Luc, pPac-Sp1, expression vectors of corepressors, and VP16 corepressors we used have been reported elsewhere (20, 22). The pcDNA3.1-ZBTB2 and pcDNA3.1-ZBTB2ΔPOZ plasmids were prepared by cloning cDNA fragments into pcDNA3.1 (Invitrogen). The GAL4-POZZBTB2 plasmid was prepared by cloning cDNA fragment encoding the POZ domain (amino acids 24–117) into pBIND (Promega). To prepare recombinant GST-POZZBTB2 and GST-ZFZBTB2 proteins, cDNA fragments encoding the POZ domain (amino acids 24–117) and zinc fingers (amino acids 254–468) were cloned into pGEX4T3

(Amersham Biosciences). The pPac-PL-ZBTB2 plasmid was prepared by cloning the cDNA fragments into pPac-PL. All plasmid constructs were verified by sequencing.

Antibodies against p21, p53, Sp1, GAPDH, Myc tag, FLAG tag, Ac-H3, Ac-H4, and HDAC3 were purchased from Upstate (Charlottesville, VA), Chemicon (Temecula, CA), Calbiochem, and Santa Cruz Biotechnology (Santa Cruz, CA), respectively. Most of the chemical reagents were purchased from Sigma.

Cell Cultures—HEK293A, HeLa, MB352, and CV-1 cells were cultured in Dulbecco's modified Eagle's medium (Invitrogen) supplemented with 10% fetal bovine serum (Invitrogen). Saos-2 cells were cultured in McCoy's 5A medium (Invitrogen) supplemented with 15% fetal bovine serum. *Drosophila* SL2 cells were cultured in Schneider's *Drosophila* medium (Invitrogen) supplemented with 10% fetal bovine serum.

Transcriptional Analysis of ARF, HDM2, p53, and p21 Genes—The pGL2-ARF-Luc, pGL2-HDM2-Luc, pGL2-p53-Luc, and various pGL2-p21-Luc promoter reporter fusion plasmids as well as pcDNA3.1-ZBTB2, pcDNA3.1-ZBTB2ΔPOZ, pcDNA3.1-p53, and pcDNA3.1-Sp1, and pCMV-LacZ in various combinations were transiently transfected into several cell lines such as HEK293A, HeLa, MB352, Saos-2, and CV-1 using Lipofectamine Plus reagent (Invitrogen). After 24–36 h of incubation, cells were harvested and analyzed for luciferase activity. Reporter activity was normalized with cotransfected β-galactosidase activity for transfection efficiency.

RT-PCR of ZBTB2 mRNA Expression in FVB Mice or Cells—Total RNA was isolated from brain, heart, liver, muscle, kidney, spleen, brown adipose tissues, and white adipose tissues or cells using TRIzol reagent (Invitrogen). Synthesis of cDNA was done using 5 μg of total RNA, random hexamer (10 pmol), and Superscript reverse transcriptase II (200 units) in 20 μl using a reverse transcription kit (Invitrogen). The following oligonucleotide PCR primers were used: murine Zbtb2 (forward, 5′-CCAACCATGGACTTATTCTA-3′; reverse, 5′-TTCATC-CTGGATGCCTGTGG-3′), β-actin (forward, 5′-ATGGATG-ACGATATCGCTGC-3′, reverse, 5′-CACACTGTGCCCAT-CTACGA-3′), Human ZBTB2 (forward, 5′-GATCGGATCC-GATTTGGCCAACCATGGA-3′; reverse, 5′-GATCCTCGA-GAGAAAAGGCTCCCTGGCT-3′), p21 (forward, 5′-ATGT-CAGAACCGGCTGGGGATGTCC-3′, reverse, 5′-TTAGGG-CTTCCTCTTGGAGAAGATC-3′), and GAPDH (forward, 5′-ACCACAGTCCATGCCATCAC-3′; reverse, 5′-TCCACCA-CCCTGTTGCTGTA-3′).

Western Blot Analysis—Cells were harvested and lysed in RIPA buffer (50 mM Tris-HCl, pH 8.0, 1% Nonidet P-40, 0.25% sodium deoxycholic acid, 150 mM NaCl, 1 mM EGTA, complete Mini-Protease mixture). Cell extracts (40 μg) were separated using 12% SDS-PAGE gel electrophoresis, transferred onto Immun-Blot™ polyvinylidene difluoride membranes (Bio-Rad), and blocked with 5% skim milk (BD Biosciences). Blotted membranes were incubated with antibodies against FLAG tag (Sigma), GAPDH (Chemicon), p21, p53, Sp1, Myc tag, (Santa Cruz Biotechnology) and then incubated with horseradish peroxidase-conjugated anti-mouse and anti-rabbit secondary antibody (Vector Laboratory). Protein bands were visualized with ECL solution (PerkinElmer Life Sciences).
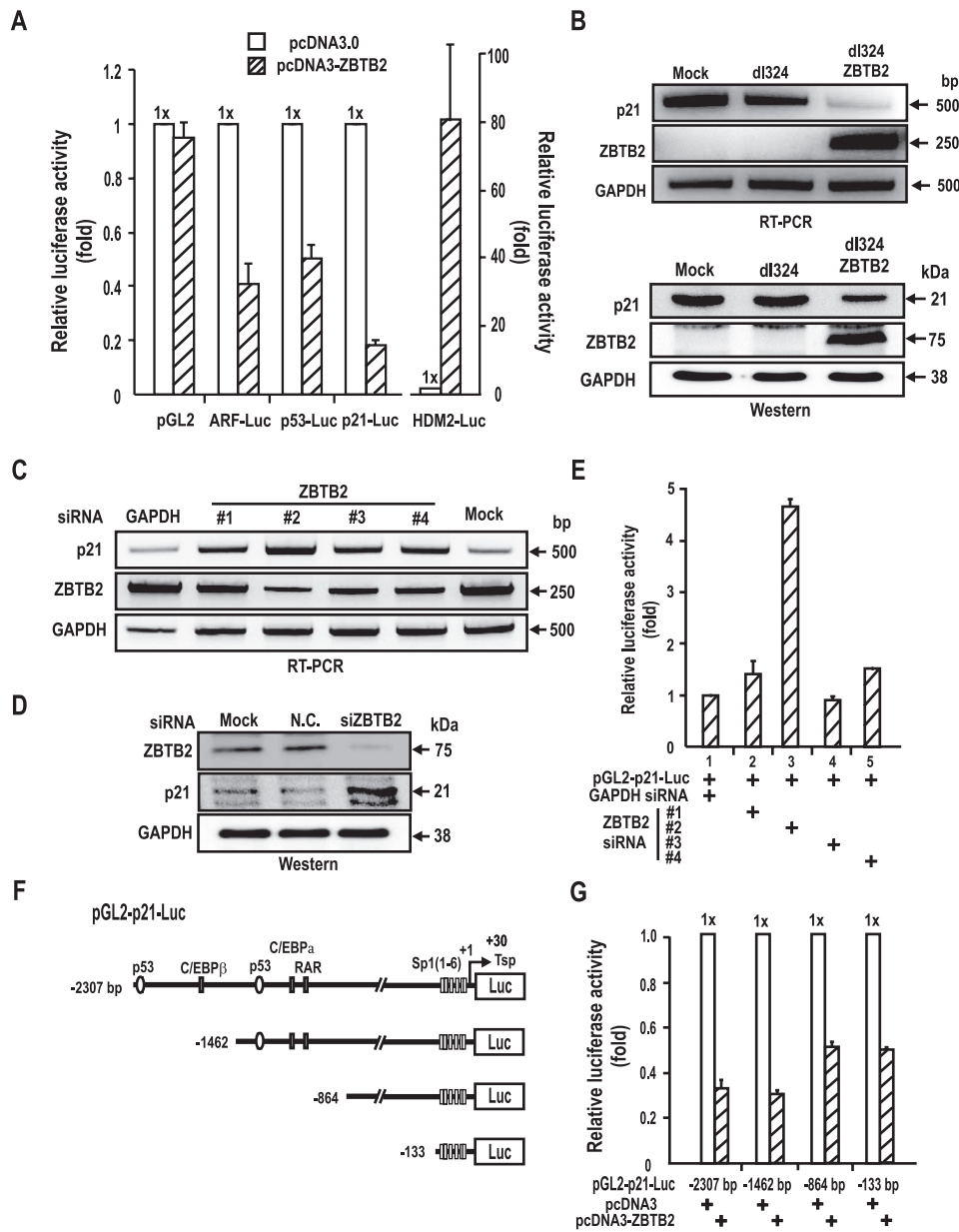
FIGURE 1. **ZBTB2 represses transcription of the *ARF, p53,* and *p21* genes, and activates *HDM2* transcription.** *A,* transcription regulation of the genes of the p53 pathway by ZBTB2. Expression vectors of ZBTB2 and reporter plasmids were transiently co-transfected into HEK293A cells and luciferase activity was measured. *Error bars* represent standard deviations. *B,* RT-PCR and Western blot analysis of HEK293A cells infected either with control adenovirus (*dl324*) or recombinant adenovirus overexpressing ZBTB2 (*dl324-ZBTB2*). *C,* knockdown and RT-PCR analysis of ZBTB2 mRNA of HEK293A cells by four different siRNAs. siRNA-2 resulted in the most efficient knock-down. *D,* Western blot analysis of cell lysates prepared from the HEK293A cells transfected with negative control scrambled siRNA (*N.C.*) or siZBTB2 RNA-2. *E,* transcription assays. Knockdown of ZBTB2 mRNA-derepressed *p21* gene expression. pGL2-p21-Luc (−2.3 kb) reporter plasmid and four different siRNA were transiently co-transfected into HEK293A cells and analyzed for luciferase activity. *F,* structures of various *p21* gene promoter constructs tested. *G,* transcription assays. ZBTB2 expression vector and pGL2-p21-Luc reporter plasmid with a variable upstream sequence were transiently co-transfected into HEK293A cells and analyzed for luciferase activity.

AGGGCGAUCCAUUUU-3′, 5′-PAAUGGAUCGCCCUUCGUC-UUU-3′. The siRNA (200 pmol) were transfected into HEK293A cells using Lipofectamine 2000 (Invitrogen). After transfection, cells were harvested, and total RNA was prepared. RT-PCR analysis of mRNA was performed as described above.

Chromatin Immunoprecipitation (ChIP) Assays—The molecular interaction between ZBTB2 and p53 or Sp1 on the *p21* gene promoter and histone modification at the *p21* proximal promoter in HEK293A, Saos-2, and *Drosophila* SL2 cells were analyzed by following the standard ChIP assay protocol, as described elsewhere (20, 22).

PCR of chromatin immunoprecipitated DNA was carried out using oligonucleotide primer sets designed to amplify the upstream regulatory regions and proximal promoter region of the *p21* gene. p53 RE-1 binding primers (bp, −2307–1947), forward, 5′-TGC-TTGGGCAGCAGGCTGTG-3′, reverse, 5′-GCAACCATGCACTT-GAATGT-3′; p53 RE-2 binding primers (bp, −1462–1128), forward, 5′-TGTCCTCCCACCCC-TACCTGG-3′, reverse, 5′-AGA-AATGAGTGATGTGTC-3′; proximal GC-boxes ChIP primers (bp, −261 to approximately +39), forward, 5′-GGCTCACTTCGTG-GGGAAAT-3′, reverse, 5′-CACA-AGGAACTGACTTCGGC-3′. To analyze histone H3 and H4 modification at the proximal promoter (bp, −133 to +100), forward 5′-GCGCTGGGCAGCCAGGAGCC-3′ and reverse 5′-CGCTCTCTCA-CCTCCTCT-3′ primers were used.

Immunoprecipitation Assays—Cells were washed, pelleted, and resuspended in a lysis buffer supplemented with protease inhibitors (20 mM Tris-HCl, pH 7.5, 150 mM NaCl, 10% glycerol, 1% Triton X-100). Cell lysate was precleared, and the supernatant was incubated overnight with anti-FLAG antibody on a rotating platform at 4 °C, followed by incubation with protein A-Sepharose Fast Flow beads. Beads were collected, washed, and resuspended in equal volumes of 5× SDS loading buffer. Immunoprecipitated proteins were separated with 12% SDS-PAGE. Western blot assay was performed as described above.

Knock-down of ZBTB2 mRNA by siRNA—Four siRNA against ZBTB2 mRNA were designed and purchased from Dharmacon (Lafayette, CO): siZBTB2-1, 5′-GAUCAUCAGU-UGAGACAAGUU-3′, 5′-PCUUGUCUCAACUGAUGAU-CUU-3′; siZBTB2-2, 5′-CAGGUGAAUCGGACAAAUAUU-3′, 5′-PUAUUUGUCCGAUUCACCUGUU-3′; siZBTB2-3, 5′-CGACCCGGUUCGAUUAGAAUU-3′, 5′-PUUCUAA-UCGAACCGGGUCGUU-3′; and siZBTB2-4, 5′-AGACGA-

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Mammalian Two-hybrid Assays—CV-1 cells were co-transfected with pG5-Luc, pGal4-POZZBTB2, pVP16-corepressors, and pCMV-LacZ. After 24 h of transfection with Lipofectamine Plus (Invitrogen), CV-1 cells were harvested and assayed for luciferase activity. Luciferase activity was then normalized with cotransfected β-galactosidase activity.

GST Fusion Protein Purification, in Vitro Transcription and Translation of Corepressors, p53, or Sp1, and Pull-down Assays—Recombinant GST, GST-POZZBTB2, and GST-ZFZBTB2 fusion proteins were prepared from *Escherichia coli* BL21 (DE3) grown for 5 h at 37 °C in a medium containing 1 mM isopropyl 1-thio-β-D-galactopyranoside. *E. coli* were lysed and purified using glutathione-agarose 4 bead affinity chromatography (Peptron, Taejeon, Korea). The purified proteins were then resolved with 12% SDS-PAGE to quantitate and assess purity. Corepressor, p53, and Sp1 polypeptides were prepared by incubating 1 µg of pcDNA3.0-corepressor, pcDNA3.1-p53, and pcDNA3.1-Sp1 expression plasmid with TNT Quick-coupled Transcription/Translation Extract (Promega) containing 40 µl of TNT Quick Master Mix and 2 µl of [35S]methionine (1175.0 Ci/mol) (PerkinElmer Life Sciences) at 30 °C for 90 min. Polypeptide expression levels were then analyzed by running 1 µl of the total mixture through 12% SDS-PAGE and autoradiography.

For GST fusion protein pull-down assays, GST fusion protein-agarose bead complexes were incubated with 10 µl of *in vitro* translated [35S]methionine-labeled corepressors, p53, and Sp1 polypeptides at 4 °C for 4 h in HEMG buffer. The reaction mixtures were centrifuged, pellets were rinsed, and the bound proteins were separated using 12% SDS-PAGE. Gels were then exposed to x-ray film using an image-intensifying screen (Kodak).

Preparation of Recombinant Adenovirus Overexpressing ZBTB2—ZBTB2 cDNA was cloned into the adenovirus E1 shuttle vector pCA14 (Microbix, Ontario, Canada), to generate pCA14-ZBTB2. The pCA14-ZBTB2 shuttle vector was linearized by XmnI digestion, and

the adenovirus vector vmdl324Bst (from Dr. Verca at the University of Fribourg, Switzerland) containing the Ad5 genome deleted in the E1 and E3 regions was also linearized with BstBI digestion. The linearized pCA14-ZBTB2 and vmdl324Bst
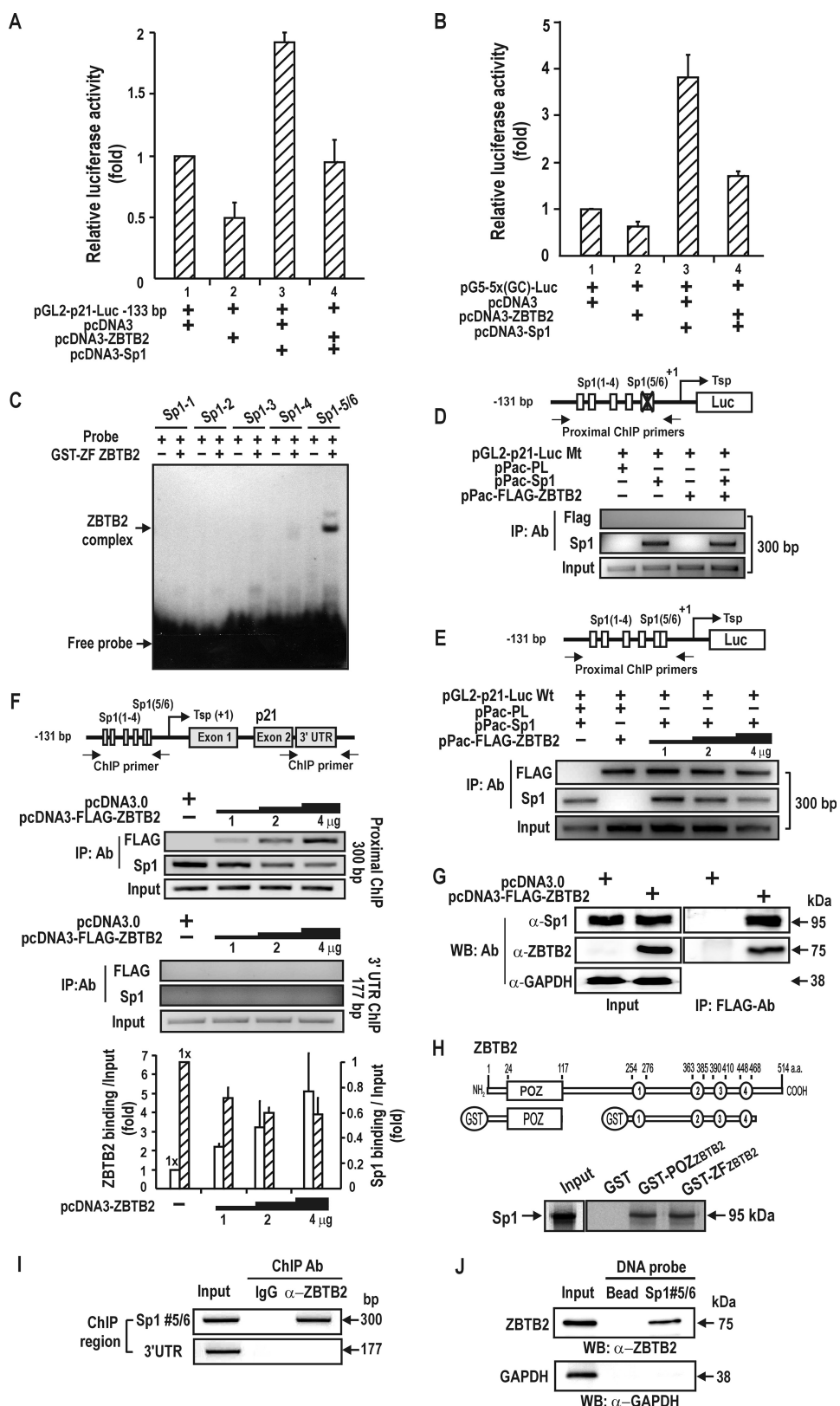
digested with BstBI were co-transformed into *E. coli* BJ518 for homologous recombination. Proper homologous recombinant adenoviral plasmid was digested with PacI and transfected into HEK293 cells to generate the adenovirus expressing ZBTB2 (dl324-ZBTB2). Propagation and titration of the recombinant virus were carried out by standard methods. PCR amplification and DNA sequencing using primers specific to ZBTB2 confirmed the adenovirus genotype.

Electromobility Shift Assays (EMSA)—EMSAs were carried out as described previously (20, 22, 33). The probe sequences of Sp1 response elements on the *p21* gene proximal promoter or the sequences of p53 response elements on the *p21* gene distal promoter used in EMSA were as follows (only top strands are shown): GC-box 1, 5′-GATCGGGAGGGCGGTCCCG-3′; GC-box 2, 5′-GATCTCCCGGGCGGCGCG-3′; GC-box 3, 5′-GATCCGAGCGCGGGTCCCGCCTC-3′; GC-box 4, 5′-GAT-CCTTGAGGCGGGCCCG-3′; GC-box 5/6, 5′-GATCGGGCG-GGGCGGTTGTATATCA-3′; p53 RE-1, 5′-GATCCGTTAGA-GGAAGAAGACTGGGCATGTCTG-3′; and p53 RE-2, 5′-GATCCATCAGGAACATGTCCCAACATGTTGAGCTC-3′.

Oligonucleotide Pull-down Assays—HEK293A cells were lysed in HKMG buffer (10 mM HEPES, pH 7.9, 100 mM KCl, 5 mM $MgCl_2$, 10% glycerol, 1 mM dithiothreitol, and 0.5% Nonidet P-40). Cellular extracts were incubated with 1 μg of biotinylated double-stranded oligonucleotides (p53 RE-1, p53 RE-2, and Sp1 GC-box 5/6) for 16 h. The sequences of the oligonucleotides are as follows (only top strands are shown): Sp1 GC-box 5/6, 5′-CCTTGAGGCGGGCCCGGGCGGGGCGGTTG-TATATCAGGGC-3′; p53 RE-1, 5′-GTCAGGAACATGTCC-CAACATGTTGAGCTC-3′; p53 RE-2, 5′-TAGAGGAAGA-AGACTGGGCATGTCTGGGCA-3′. To collect DNA-bound proteins, the mixtures were incubated with streptavidin-agarose beads for 2 h, washed with HKMG buffer, and precipitated by centrifugation. The precipitate was analyzed by Western blot assay as described above.

FACS Analyses—HEK293A cells were transfected with pcDNA3.1-ZBTB2 expression vector or siZBTB2 RNA in the presence or absence of p53 expression vector. Cells were washed, fixed with methanol, and stained with 50 μg/ml of propidium iodide in 100 μg/ml of ribonuclease A for 30 min at 37 °C in the dark. DNA content, cell cycle profiles, and forward scatter were analyzed by FACSCalibur (BD Biosciences) with emission detection at 488 nm (excitation) and 575 nm (peak emission). Data were analyzed using ModFit LT 2.0 (Verity Software House, Inc., ME) and WindMDI 2.8 (Joseph Trotter, The Scripps Research Institute).

MTT Assays—Confluent HEK293A cells grown on 10-cm culture dishes were transfected with pcDNA3.1-ZBTB2 expression vector or siZBTB2 RNA in the presence or absence of p53 expression vector. Cells (1.5×10^5 cells) were transferred to 6-well culture dishes and grown for 0–6 days. At 0, 2, 4, and 6 days, cells were incubated for 1 h at 37 °C with 500 μl/well MTT (2 mg/ml). Precipitates were dissolved with 1 ml of dimethyl sulfoxide. Cellular proliferation was determined from the conversion of MTT to formazan using a SpectraMAX 250 (Molecular Device Co.) at 570 nm. *p* value was calculated using the statistical analysis program SPSS (Statistical Package for the Social Sciences) (Chicago, IL).

Preparation of Anti-ZBTB2 Antibody—To obtain a rabbit polyclonal antibody against ZBTB2 protein, one white rabbit was immunized subcutaneously with a synthetic peptide (amino acids 500–514 of ZBTB2; VLASIKKEQETVLLD) three times at 3-week intervals. Blood was collected, incubated at 37 °C for 90 min, and centrifuged. The supernatant was incubated with the protein A/G-agarose beads (Santa Cruz Biotechnology). The beads were collected and washed, and the antibody was eluted. The titer of the antibody was tested by Western blot assay of the HEK293A cells transfected with the pcDNA3.1-ZBTB2 overexpression vector.

RESULTS

ZBTB2, a Novel POK Protein, Represses Transcription of ARF, p53, and p21 Genes of the p53 Pathway but Activates Transcription of HDM2—ZBTB2 cDNA encodes a protein composed of 514 amino acids (supplemental Fig. S1). ZBTB2 contains an N-terminal POZ domain at amino acids 24 to 117 and four zinc fingers at the C terminus. ZBTB2 mRNA was expressed in all male FVB mouse tissues examined, and was particularly high in the spleen (supplemental Fig. S2D). SAGE analysis by the Cancer Genomic Anatomy Project (CGAP) showed that ZBTB2 mRNA expression is higher in cancers derived from the retina, thyroid, liver, peritoneum, ovary, and muscle compared with normal tissues (nci.nih.gov). Immunocytochemistry in HEK293A cells detected ZBTB2 in both the cytoplasm and nuclear speckles (supplemental Fig. S2E). Although the calculated molecular mass of ZBTB2 is 57 kDa, Western blot analysis of the HEK293A cell lysate transfected with the pcDNA-FLAG-ZBTB2 expression vector yielded a 75-kDa

FIGURE 2. **ZBTB2 represses transcription activation by Sp1 on the minimal *p21* promoter and pG5-5x(GC)-Luc.** ZBTB2 competes with Sp1 to bind to the proximal GC-box 5/6. ZBTB2 interacts with Sp1 to weakly inhibit Sp1 binding. *A* and *B*, Sp1 activated transcription of pGL2-p21-Luc (−131 bp) and pG5-5x(GC)-Luc, and ZBTB2 repressed transcriptional activation by Sp1. *C*, EMSA. The ^{32}P-labeled Sp1 binding GC-box probes were incubated with GST-ZFZBTB2 (0.5 μg) and separated by 4% nondenaturing PAGE. *D*, ChIP assay in *Drosophila* SL2 cells transfected with pGL2-p21-Luc Mt, pPac PL-Sp1, and/or pPac PL-FLAG-ZBTB2. ZBTB2 could not bind to the mutated proximal promoter. *X*, mutated GC-box 5/6. *E*, ChIP assay of ZBTB2 binding on the *p21* Wt promoter in *Drosophila* SL2 cells. Cells were transfected with pGL2-p21-Luc Wt, pPac PL-Sp1, and increasing amounts of pPac PL-FLAG-ZBTB2. *F*, ChIP assay of the endogenous *p21* gene in human HEK293A cells transfected with pcDNA3-FLAG-ZBTB2. ZBTB2 competed with Sp1 to bind to the proximal promoter and inhibited Sp1 binding, but not in the 3′-untranslated region. *Bottom*, histogram of ChIP assays. *G*, co-immunoprecipitation of ZBTB2 and Sp1. Cell lysates prepared from HEK293A cells transfected with the pcDNA3-FLAG-ZBTB2 expression vector were co-immunoprecipitated using anti-FLAG antibody (*Ab*) and analyzed by Western blotting using anti-Sp1 antibody. *H*, *in vitro* GST fusion protein pull-down assays. Recombinant GST, GST-POZZBTB2, or GST-ZFZBTB2 was incubated with [^{35}S]methionine-labeled Sp1, pulled down, and resolved by a 10% SDS-PAGE. *Input*, 10% of the Sp1 added in the binding reactions. *I*, ChIP assay of endogenous ZBTB2 binding to the proximal GC-box 5/6 elements of endogenous *p21* in HEK293A cells. ChIP PCR primer sets are as in *F*. *J*, oligonucleotide pull-down assay of ZBTB2 binding to the proximal GC-box 5/6 elements of the *p21* gene promoter. HEK293A cell extracts were incubated with biotinylated double-stranded oligonucleotides. The mixtures were further incubated with streptavidin-agarose beads and precipitated by centrifugation. The precipitate was analyzed by Western blot (*WB*) assay using antibody against ZBTB2. *IP*, immunoprecipitation.

band, suggesting the possibility of post-translational modification of the protein.

Recently, several reports have implicated POZ domain proteins such as FBI-1, BCL-6, and Miz-1 in cell cycle regulation (10, 21). We investigated whether ZBTB2 regulates expression of the genes (*ARF, HDM2, p53,* and *p21*) of the p53 pathway, which is important in cell cycle regulation. In human HEK293A cells, ZBTB2 repressed transcription of three genes (*ARF, p53,* and *p21*) of the p53 pathway by more than 60–80%, and repression was particularly effective in the *p21* gene. In contrast, ZBTB2 increased transcription of *HDM2*, which could induce degradation of p53 (Fig. 1*A*) (33).

Because all of the transcriptional regulatory effects of ZBTB2 on the p53 pathway converged onto expression of the *p21* gene, an important negative regulator of cell cycle progression, we investigated the molecular mechanisms of transcriptional regulation of the *p21* gene in detail. RT-PCR and Western blot analysis of HEK293A cells infected with either control adenovirus or recombinant virus overexpressing ZBTB2 showed that ZBTB2 repressed *p21* gene expression (Fig. 1*B*). Knock-down of ZBTB mRNA by RNA interference with four different siRNAs also resulted in derepression of *p21* gene transcription, particularly with ZBTB2 number 2 siRNA (Fig. 1, *C–E*). Taken together, these data suggest that ZBTB2 is a major negative transcription regulator of the p53 pathway and particularly of the *p21* gene. Furthermore, we mapped the cis-regulatory elements of the *p21* gene promoter responsible for transcriptional repression by ZBTB2. Transcription assays indicate that ZBTB2 can repress transcription by acting on the small proximal regulatory element concentrated with Sp1 binding GC-boxes (bp, −133 to approximately +30) (Ref. 26 and references therein). We observed more potent repression with the longer promoter constructs containing the distal p53 binding elements (Fig. 1, *F* and *G*).

ZBTB2 Competes with Sp1 to Bind to the Proximal Promoter GC-box 5/6 of the p21 Gene and ZBTB2

Interacts with Sp1—The above data suggested that Sp1 and the GC-boxes could be involved in repression by ZBTB2. Accordingly, we tested whether ZBTB2 could repress transcriptional activation by Sp1 on the short *p21* proximal promoter and artificial pG5-5x(GC)-Luc with the well characterized Sp1 binding GC-box (34) in HEK293A cells. Sp1 activated transcription of
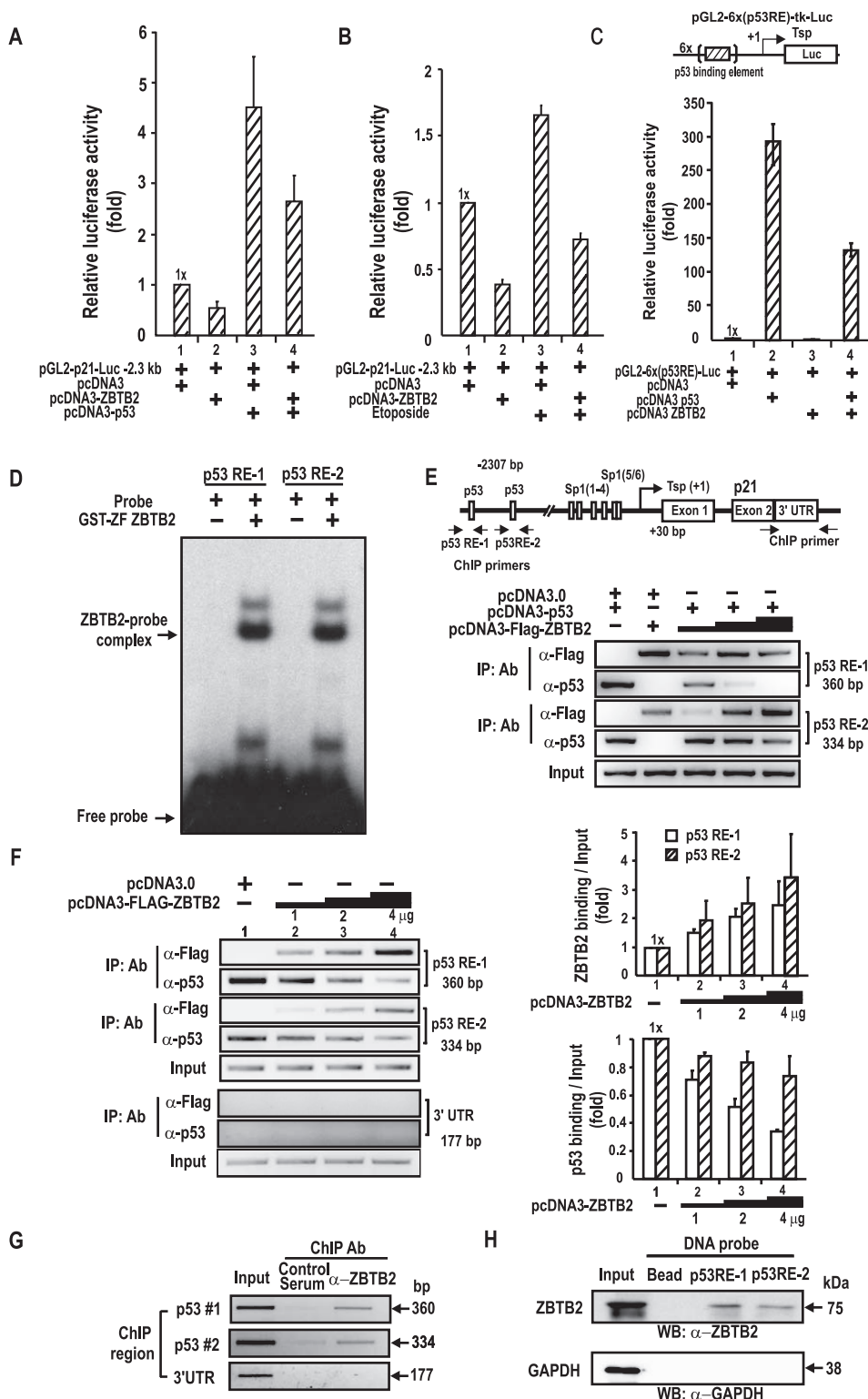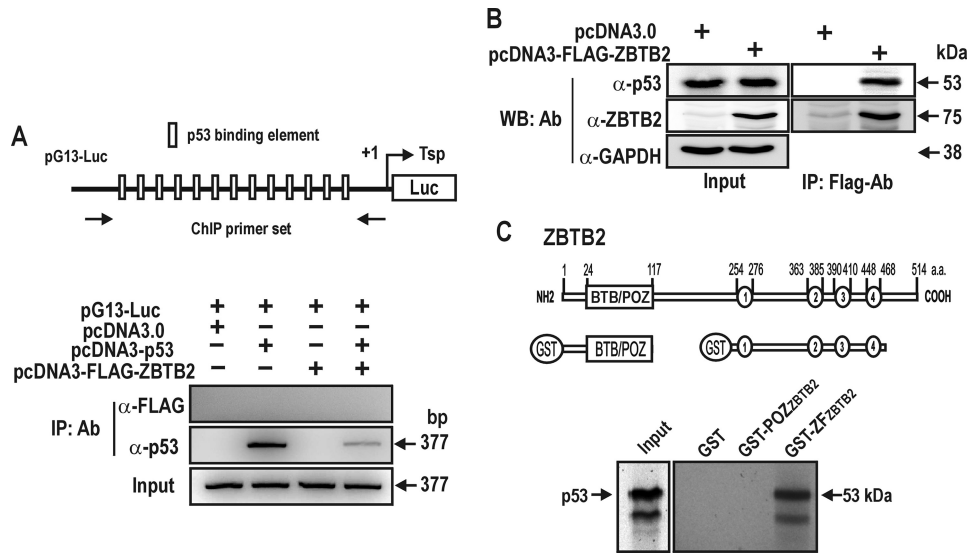
FIGURE 4. **ZBTB2 interacts directly with p53 and inhibits p53 binding by protein-protein interactions.** *A*, ChIP assay of ZBTB2 binding on the proximal promoter of pG13-Luc in Saos-2 cells. Although ZBTB2 itself could not bind to this p53 binding element (5'-CCAGGCAAGTCCAGGCAGG-3'), its presence still decreased p53 binding. *B*, co-immunoprecipitation of ZBTB2 and p53. HEK293A cell lysates prepared from cells transfected with FLAG-ZBTB2 expression vector were immunoprecipitated (*IP*) using anti-FLAG antibody and analyzed by Western blotting (*WB*) using anti-p53 antibody. *C*, *in vitro* GST fusion protein pull-down assay. Recombinant GST, GST-POZZBTB2, or GST-ZFZBTB2 was incubated with [35S]methionine-labeled p53, pulled down, and resolved by 10% SDS-PAGE. The gel was then exposed to x-ray film. *Input*, 10% of the p53 added in the binding reactions. *Ab*, antibody.

the HEK293A cellular extract transfected with the FLAG-ZBTB2 expression vector showed that Sp1 and ZBTB2 interacted with each other *in vivo* (Fig. 2*G*). GST fusion protein pull-down assays also demonstrated that both the POZ and ZF domains of ZBTB2 interact directly with Sp1 (Fig. 2*H*). ZBTB2 not only competed with Sp1 to bind to the proximal GC-box 5/6 elements, but also interacted with Sp1 to inhibit Sp1 binding, repressing transcription of the *p21* gene.

We also examined whether endogenous ZBTB2 binds the proximal GC-box 5/6 of the endogenous *p21* gene by ChIP and oligonucleotide pull-down assays using antibody against ZBTB2. Apparently, endogenous ZBTB2 binds to the proximal promoter GC-box 5/6 of the endogenous *p21* gene (Fig. 2, *I* and *J*).

ZBTB2 Represses Transcription of p21 through Binding Competition between ZBTB2 and p53 on the Distal p53 Binding Elements and ZBTB2 Interacts with p53—Because more robust transcription repression was observed with pGL2-p21-Luc −2.3-kb and −1.5-kb constructs compared with pGL2-p21-Luc −131 bp (Fig. 1, *F* and *G*), we suspected that other repression mechanisms involving p53 and/or distal p53 binding elements might be possible. ZBTB2 repressed transcription of pGL2-p21-Luc by 50% in MB352 cells lacking endogenous p53. Ectopic p53 increased *p21* gene expression, which was repressed by ZBTB2 (Fig. 3*A*). In HEK293 A cells, treatment with the DNA damaging agent etoposide increased *p21* gene expression by inducing p53, which was again repressed by ZBTB2 (Fig. 3*B*). Additional transcriptional analysis of pGL2–6x(p53RE)-Luc with five copies of the p53 binding elements of the *p21* gene in the proximal promoter showed that ZBTB2 blocked transcription activation by p53 (Fig. 3*C*). These data suggest that ZBTB2 may inhibit transcription of the *p21* gene by directly acting on the distal p53 binding elements.

EMSA showed that the zinc finger DNA binding domain of ZBTB2 could bind to p53 RE-1 and 2, suggesting a potential binding competition between p53 and ZBTB2 (Fig. 3*D*). We investigated whether the two proteins competed with each

the reporter genes and ZBTB2 repressed transcriptional activation by Sp1 on the two promoter constructs (Fig. 2, *A* and *B*).

Often, transcription repression can be achieved by binding competition at the same DNA element or inhibition of transcription factor binding activity by protein-protein interactions. EMSA and ChIP in *Drosophila* SL2 cells transiently co-transfected with expression vectors of ZBTB2 and Sp1 and pGL2-p21-Luc Wt (−2.3 kb) or pGL2-p21-Luc Mt GC-box 5/6 (−2.3 kb) showed that ZBTB2 zinc fingers and Sp1 could bind to the proximal Sp1 binding GC-box 5/6 (Fig. 2, *C–E*). Mutation of the element prevented ZBTB2 from binding. Ectopic ZBTB2 weakly decreased Sp1 binding (Fig. 2*D*). Overall, the data imply that Sp1 and ZBTB2 may compete with each other to bind to the element. In human HEK293A cells, ectopic ZBTB2 binds to the proximal promoter of the endogenous *p21* gene but not to the control 3'-untranslated region. ZBTB2 competed with Sp1 to bind to the region and decreased Sp1 binding in a dose-dependent manner (Fig. 2*F*).

ChIP assays in *Drosophila* SL2 cells showed that although ZBTB2 was not able to bind to the mutated GC-box 5/6, ZBTB2 still appeared to weakly inhibit Sp1 binding to the proximal promoter region, probably through an Sp1-ZBTB2 interaction (Fig. 2*D*). Co-immunoprecipitation and Western blot assays of

FIGURE 3. **ZBTB2 represses transcription of the *p21* gene by binding competition with p53 to the distal p53 binding elements *in vivo*.** *A*, transcription analysis. MB352 cells lacking *p53* were transiently co-transfected with expression vector of p53 and/or ZBTB2 and pGL2-p21-Luc Wt (−2.3 kb), and luciferase activity was measured. *B*, transcription analysis in human HEK293A cells. Etoposide treatment of cells increased *p21* gene transcription, which was repressed by ZBTB2. *C*, transcriptional activation of pGL2–6x(p53RE)-Luc by ectopic p53 was repressed by ZBTB2 in Saos-2 cells lacking *p53*. *p53RE*, distal p53-binding elements of the *p21* gene promoter. *D*, EMSA. Two 32P-labeled p53 binding element probes of the *p21* gene were incubated with GST-ZFZBTB2 (0.5 μg) and separated by 4% nondenaturing PAGE. *E*, ChIP assay of ZBTB2 binding on the distal p53 binding elements of the endogenous *p21* gene in Saos-2 cells lacking p53. The cells were transfected with p53 expression vector and increasing amounts of FLAG-ZBTB2 expression vector. *F*, *left*, ChIP assay of ZBTB2 binding on the distal p53 binding elements of the endogenous *p21* gene in HEK293A cells. Cells were transfected with increasing amounts of FLAG-ZBTB2 expression vector. *Right*, histograms of ZBTB2 and p53 binding on p53 binding elements 1 and 2. *G*, ChIP assay of endogenous ZBTB2 binding to the distal p53 binding elements of the endogenous *p21* gene in HEK293A cells. *H*, oligonucleotide pull-down assay of endogenous ZBTB2 binding to the distal p53 binding elements of the *p21* gene. *WB*, Western blot; *IP*, immunoprecipitation; *Ab*, antibody.
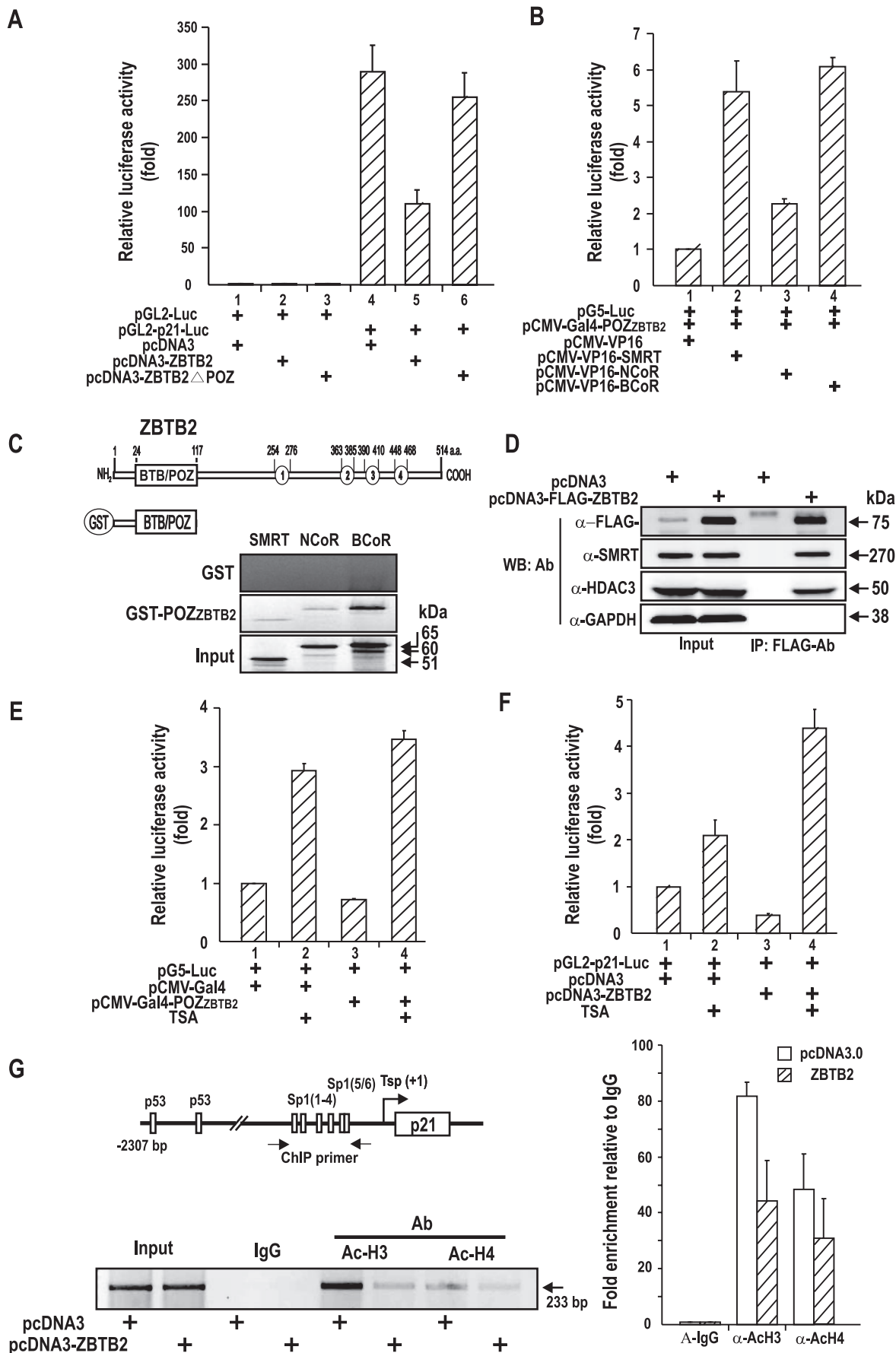
other for the sites of the endogenous *p21* gene using ChIP assays. Expression vectors of ZBTB2 and p53 were transiently co-transfected in Saos2 cells lacking p53. ZBTB2 bound to p53 RE-1 by competing with p53 in a dose-dependent manner, but binding competition between ZBTB2 and p53 at p53 RE-2 was less pronounced (Fig. 3*E*). We found a similar binding competition between ZBTB2 and p53 on the endogenous *p21* gene promoter in HEK293A cells, and again the binding competition on p53 RE-2 by ZBTB2 was also less effective (Fig. 3*F*).

Using newly prepared antibody against ZBTB2, we also investigated whether endogenous ZBTB2 could bind to the distal p53 binding elements of the endogenous *p21* gene using ChIP and oligonucleotide pull-down assays. ZBTB2 binds specifically to p53 RE-1 and p53 RE-2 (Fig. 3, *G* and *H*).

We then used ChIP to determine whether ZBTB2 and p53 competed with each other on the well characterized pG13-Luc, which has 13 copies of the p53 binding element (5′-CCAG-GCAAGTCCAGGCAGG-3′) in the proximal promoter (24). Expression vectors of ZBTB2, p53, and pG13-Luc reporter plasmids were transiently co-transfected in p53-null Saos2 cells, and chromatin was immunoprecipitated using the indicated antibodies. Contrary to our expectations, ZBTB2 did not bind to the pG13-Luc reporter gene, possibly reflecting the binding specificity of ZBTB2 to only some p53 binding sequences (such as those of the *p21* gene). ZBTB2 did, however, decrease p53 binding to the pG13-Luc reporter gene quite effectively (Fig. 4*A*). The data suggest that ZBTB2 may repress transcription of the *p21* gene by directly interacting with p53, and thus interfering with p53 binding on the proximal promoter of pG13-Luc. Co-immunoprecipitation and Western blot assays of HEK293A cells transfected with the FLAG-ZBTB2 expression vector revealed that ZBTB2 and p53 interact with each other *in vivo* (Fig. 4*B*). GST fusion protein pull-down assay also showed that the GST-ZFZBTB2 domain, not GST-POZZBTB2, interacted with p53 *in vitro*, suggesting that p53 and ZBTB2 interact directly with p53 via its zinc fingers of ZBTB2 (Fig. 4*C*).

The POZ Domain of ZBTB2 Interacts with the Corepressor-HDAC Complex to Deacetylate Histones Ac-H3 and -H4 at the Proximal Promoter—ZBTB2 repressed transcription by direct binding competition with transcription activators such as Sp1 and p53, but it was not clear how it repressed transcription once bound to the proximal and/or distal regulatory elements. To map the domain of ZBTB2 important in transcription repression, we prepared a mutated ZBTB2 construct with the POZ domain deleted (ZBTB2ΔPOZ). ZBTB2 repressed transcription of the *p21* gene but the mutant ZBTB2ΔPOZ did not, indi-

cating that the POZ domain of ZBTB2 is required in transcriptional repression (Fig. 5*A*).

Transcriptional repressors, including some POZ domain proteins such as PLZF and BCL-6, often repress transcription through interaction with corepressors such as SMRT, NCoR, BCoR, and mSin3A. Mammalian two-hybrid assays in CV-1 cells using pG5-Luc, pGal4-POZZBTB2, and pVP16-corepressor fusion protein expression vectors demonstrated that the POZ domain of ZBTB2 interacts with SMRT, NCoR, and BCoR (Fig. 5*B*). In addition, GST fusion protein pull-down assays showed that POZZBTB2 can interact directly with SMRT, NCoR, and BCoR (Fig. 5*C*). Corepressor complexes recruited by transcriptional repressors often contain HDAC proteins. These HDACs deacetylate the histones of nearby nucleosomes to repress transcription. Co-immunoprecipitation and Western blot analysis of HEK293A cell extracts transfected with the FLAG-ZBTB2 expression vector using anti-SMRT and anti-HDAC3 antibodies revealed that ZBTB2 and SMRT-HDAC interacted with each other *in vivo* (Fig. 5*D*), indicating that ZBTB2 may repress transcription of the *p21* gene by interacting directly with the corepressor-HDAC complex via its POZ domain.

HDAC inhibitor trichostatin A treatment of CV-1 or HEK293A cells co-transfected with pG5-Luc and pGal4-POZZBTB2 or pGL2-p21-Luc and ZBTB2 expression vectors significantly affected transcriptional repression by ZBTB2 or the POZ domain of ZBTB2 on both pG5-Luc and pGL2-p21-Luc, resulting in a significant increase in transcription (Fig. 5, *F* and *G*). These data implicate the involvement of HDACs in transcriptional repression by ZBTB2.

Corepressor-HDACs recruited by the repressors may deacetylate the histones of nearby nucleosomes around the proximal promoter. Accordingly, we used ChIP to examine whether the acetylation status of histones H3 and H4 at the proximal promoter of the endogenous *p21* gene was altered by ZBTB2-corepressor-HDACs complexes in HEK293A cells transfected with the FLAG-ZBTB2 expression vector. The complex significantly decreased acetylated histones H3 and H4 at proximal promoter 4 (Fig. 5*H*).

ZBTB2 Stimulates HeLa Cell Proliferation and Increases the Percentage of Cells in S-phase—A major regulator of cell cycle arrest, p21, was potently repressed by ZBTB2 at the transcriptional level. HeLa cells stably expressing ZBTB2 showed a significant increase in cell proliferation (Fig. 6*A*). MTT assays revealed that whereas ZBTB2 overexpression significantly increased cell proliferation, ZBTB2 knock-down by siRNA decreased cell proliferation in the presence or absence of p53 (Fig. 6, *B–F*). FACS analysis also showed that ZBTB2 stimulated cell cycle progression and

FIGURE 5. The POZ domain of ZBTB2 is important in transcription repression and interacts directly with corepressors. ZBTB2-corepressor-HDAC complexes deacetylate histones Ac-H3 and -H4. *A*, transcription assays. The reporter pGL2-p21-Luc and expression plasmids of ZBTB2 or its POZ domain deletion mutant ZBTB2ΔPOZ, were transiently co-transfected into HEK293A cells and luciferase activity was measured. *B*, mammalian two-hybrid assays of protein-protein interactions between the POZ domain and corepressor proteins. CV-1 cells were transfected with pG5-Luc, pGal4-POZZBTB2, and pVP16-corepressor expression plasmids and luciferase activity was measured. *C*, *in vitro* GST fusion protein pull-down assays. Recombinant GST or GST-POZZBTB2 was incubated with [³⁵S]methionine-labeled corepressors, pulled down, and resolved by 10% SDS-PAGE. The gel was then exposed to x-ray film. *Input*, 10% of the corepressors added in the binding reactions. *D*, co-immunoprecipitation of ZBTB2 and SMRT-HDAC3. Cell lysates prepared from HEK293A cells transfected with FLAG-ZBTB2 expression vector were immunoprecipitated (*IP*) using anti-FLAG antibody and analyzed by Western blotting (*WB*) using anti-SMRT and HDAC3 antibodies. *E* and *F*, trichostatin A (*TSA*) treatment derepressed transcription repression of pG5-Luc and pGL2-p21-Luc by the POZ domain or full-length ZBTB2. Plasmid mixtures of pG5-Luc and the pGal4-POZZBTB2 expression plasmid or pGL2-p21-Luc and the ZBTB2 expression plasmid were transiently co-transfected into CV-1 or HEK293A cells. *G*, *left*, ChIP assays of histone modification at the proximal promoter of the endogenous *p21* gene using antibodies against Ac-H3 and -H4. Cells were transfected with FLAG-ZBTB2 and immunoprecipitated with the indicated antibodies. *Right*, histogram of ChIP assays. *Ab*, antibody.
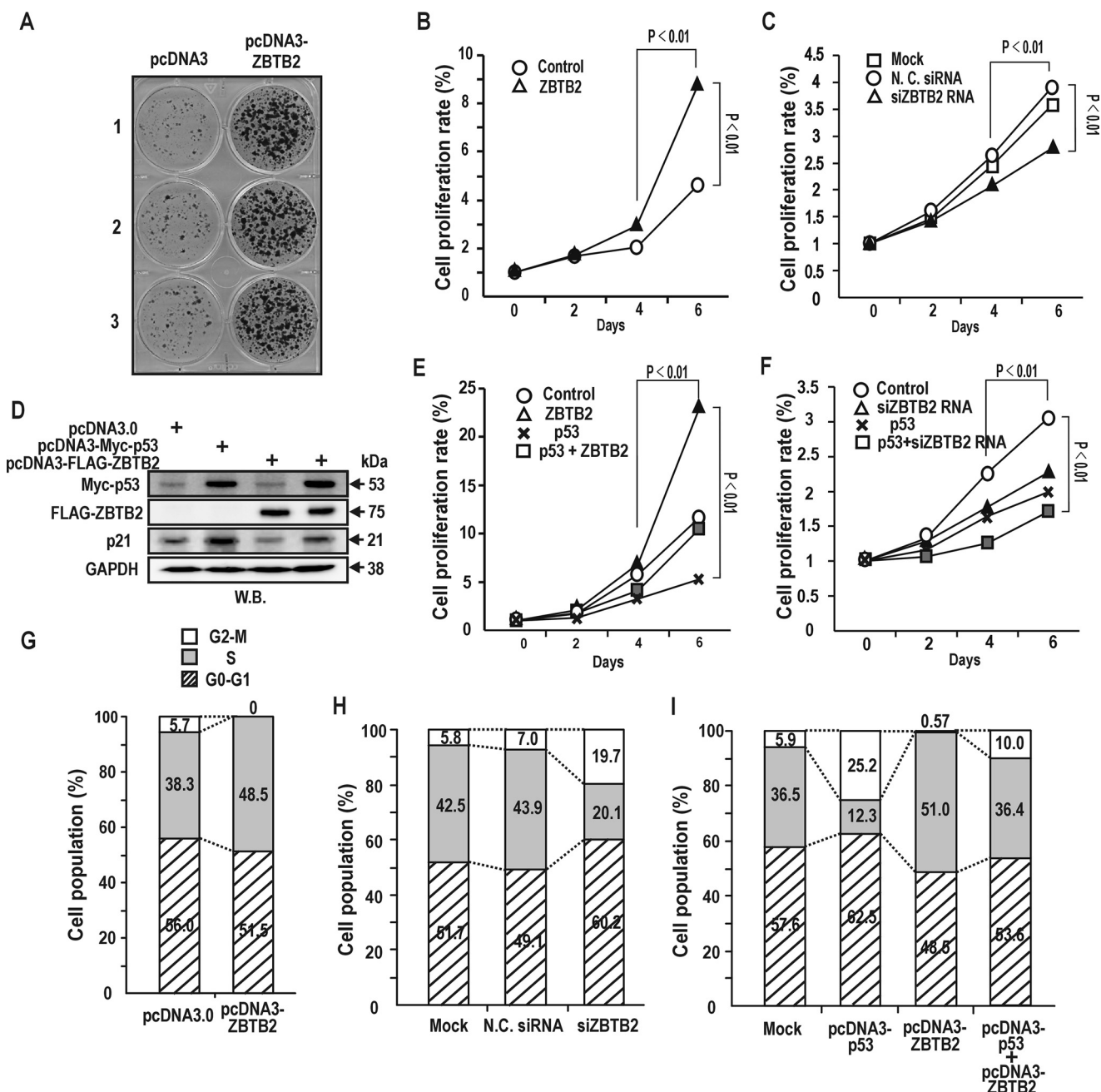
FIGURE 6. ZBTB2 stimulates cell proliferation and cell cycle progression. *A*, foci-formation assays. HeLa cells transfected with the ZBTB2 expression vector were cultured in G418 medium and stained with 0.1% crystal violet. HeLa cells stably expressing ZBTB2 showed an increase in cell proliferation. *B* and *C*, MTT assay of HEK293A cells grown for 2, 4, or 6 days. Cells were transfected with either the control vector or ZBTB2 expression vector and analyzed for cell growth. Alternatively, cells were treated with either negative control siRNA or ZBTB2 siRNA. All assays were performed in triplicate. Error bars are included but too tight to see. *p* values are <0.001. *D*, Western blot (*W.B.*) analysis. HEK293A cells were transfected with the expression vector of FLAG-ZBTB2 and/or Myc-p53. And the cell extracts were analyzed for p21, p53, and ZBTB2 expression. GAPDH, control. *E* and *F*, MTT assay. Cells were transfected with either control vector or ZBTB2 expression vector in the absence or presence of p53 expression vector and analyzed for cell growth. Assays were performed as in *B* and *C. G–I*, FACS analysis of cell cycle progression. HEK293A cells were transfected with ZBTB2 expression vector or control vector, cultured, and stained with propidium iodide. Cell proliferation was measured by FACS. Alternatively, cells were transfected with siRNA against ZBTB2 mRNA and cell cycle progression was analyzed. The same FACS analysis was performed after cells were transfected with or without p53 expression vector. *Mock*, transfection without siRNA. *N.C.*, scrambled negative control siRNA.

increased the number of HEK293A cells in S-phase (38.3% in control *versus* 48.5% in HEK293A-ZBTB2). Furthermore, the number of cells in the G_2-M phase decreased from 5.7 to 0% (Fig. 6*G*). Knock-down of endogenous ZBTB2 mRNA resulted in a decrease in the number of cells in S-phase and a concomitant increase in the number of cells in G_0-G_1 and G_2-M phases (Fig. 6*H*). We also observed similar changes in cell cycle progression in the presence

of p53, and ZBTB2 reversed the cell cycle arrest effect of p53 as in the MTT assays (Fig. 6*I*).

DISCUSSION

Our investigation revealed that ZBTB2 represses transcription of *ARF*, *p53*, and *p21* and activates transcription of *HDM2*. Potent repression of *ARF* and activation of the *HDM2* gene can
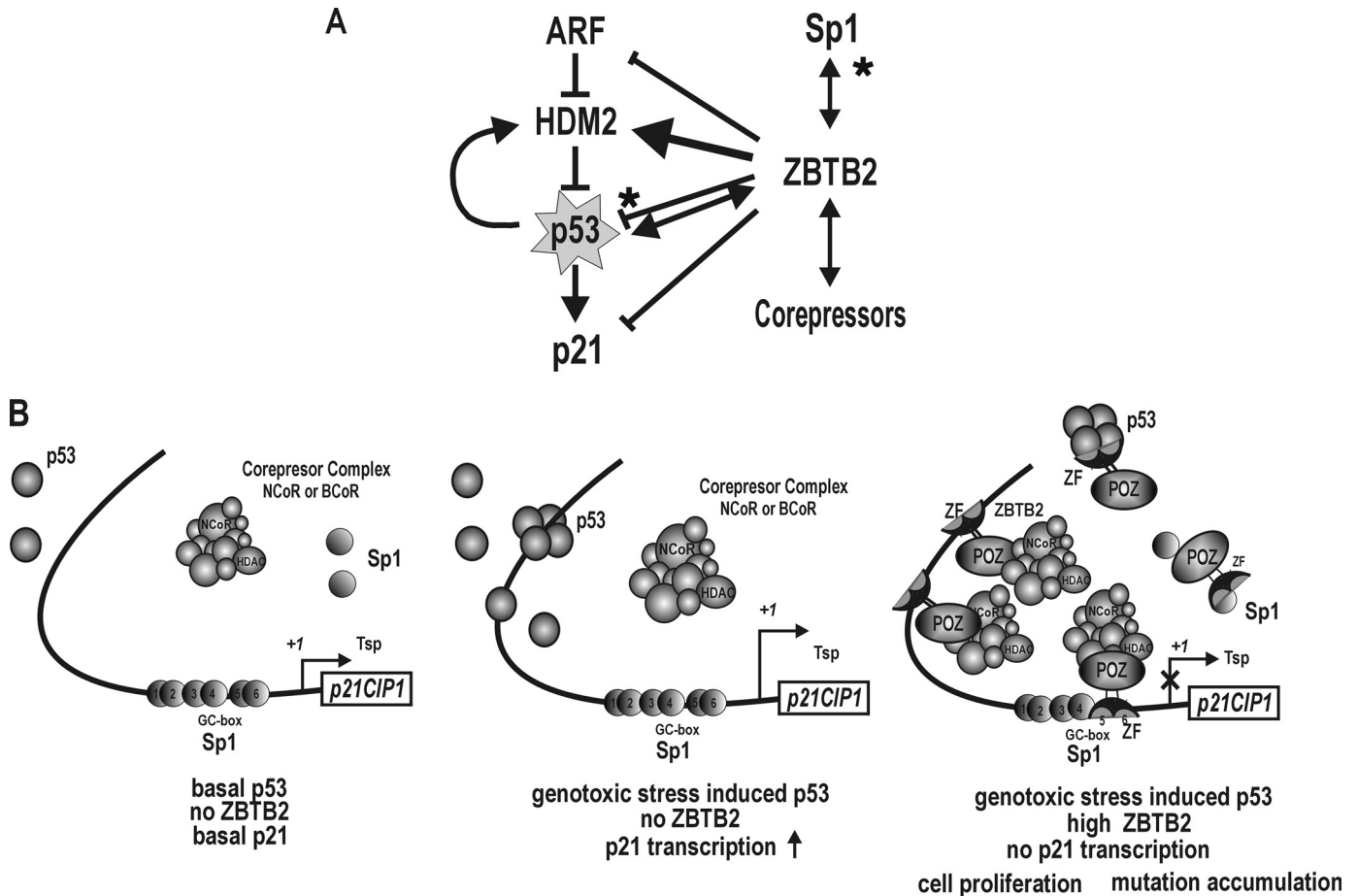
FIGURE 7. **Hypothetical model of transcriptional regulation of the *p21* gene and p53 pathway.** *A*, p53 pathway and ZBTB2 targets. ZBTB2 repressed transcription of the *ARF, p53,* and *p21* genes and activated *HDM2* gene transcription. *Solid line with arrowhead* (→), transcriptional activation; *solid line* with ⊥, transcriptional repression. *Solid line with double arrowhead* (↔), molecular interaction; *, inhibition of transcription factor binding. *B*, hypothetical model of transcriptional regulation of *p21* by ZBTB2 under three different cellular conditions. ZBTB2 represses transcription of the cell cycle arrest gene *p21* by binding to the proximal GC-box 5/6 elements and the two distal p53 binding elements by competition with either Sp1 and/or p53. ZBTB2 interacts with p53 via its zinc fingers and also interacts with Sp1 via its POZ domain and zinc fingers. These protein-protein interactions inhibit Sp1 or p53 binding to their respective binding elements. ZBTB2 attacks the three critical elements that are important in basal constitutive and inducible expression. ZBTB2 recruits co-repressor-HDAC complexes, which deacetylate histones Ac-H3 and -H4 at the proximal promoter to repress transcription. *Tsp* (+1), transcription start site.

result in an overall increase in *HDM2* gene expression, which can decrease p53 activity or stability. The mechanism of repression of the p53 pathway by ZBTB2 is directed toward the inhibition of p53 activity or stability. In addition to potently modulating expression of *ARF* and *HDM2* and thereby eventually affecting *p21* expression by down-regulating p53 expression, ZBTB2 directly repressed transcription of the *p21* gene (Fig. 7*A*). Although details of the transcription regulation of *ARF*, *p53*, and *HDM2* by ZBTB2 remains largely unexplored and requires further investigation, ZBTB2 may be a master control gene of the p53 pathway and thus of cell proliferation, cell cycle progression, and oncogenesis.

Our investigation of regulation of the cell cycle arrest gene *p21* revealed that *p21* is the direct target of ZBTB2, with a complex molecular mechanism of transcription repression that involves Sp1, p53, proximal GC-box 5/6, and two distal p53 binding elements of *p21*. ZBTB2 competes with Sp1 to bind to the proximal Sp1 binding GC-box 5/6, which is a direct target of regulation by Sp1 and Sp family members. Intriguingly, ZBTB2 binds to this particular site to repress transcription activation by Sp1.

Our data also showed that ZBTB2 binds to distal p53 binding elements by competing with p53, and that ZBTB2 also interacts with p53 directly to inhibit p53 binding and to repress the contribution of p53 to transcription. The site was shown to mediate the induction of p21 by genotoxic stresses. Accordingly, DNA damaging signals that result in p53-medicated induction of p21 can be blocked by ZBTB2. Overall, these molecular features of ZBTB2 may explain how ZBTB2 acts as a master control gene of cell proliferation by potently blocking the p53 pathway.

Based on our finding, we propose a hypothetical model of transcriptional regulation of the *p21* gene by ZBTB2 (Fig. 7). Under normal cellular conditions where p53 is expressed at low basal levels and ZBTB2 is not present or low compared with Sp1, the *p21* gene is expressed at low basal levels driven by Sp1, and cells proliferate normally. Challenge with a genotoxic stress induces production of tumor suppressor p53, which binds to the distal p53 response elements and activates transcription of *p21* by interacting with the Sp1 bound at the proximal GC-box. The induced p21 arrests cell cycle progression, allowing cells to repair DNA damage. In cells without DNA damage where ZBTB2 expression is high, ZBTB2 represses transcription

directly by binding to both the proximal GC-box 5/6 and distal p53 binding elements. ZBTB2 bound to the regulatory elements recruits the corepressor-HDAC complex, causing deacetylation of histones Ac-H3 and -H4 around the proximal promoter and repressing transcription. When cells are under genotoxic stress and ZBTB2 expression is high or in cancerous tissues that have high levels of p53 and ZBTB2, ZBTB2 represses transcription directly by binding to both the proximal GC-box 5/6 and distal p53 binding elements. Although p53 expression is also highly induced under these conditions, p53 has to compete with ZBTB2 to bind to the distal p53 binding elements and is also affected by molecular interactions between p53 and ZBTB2 that further impede binding. Although p53 is present, transcription of the *p21* gene is potently repressed by ZBTB2. Cells proliferate without cell cycle arrest, mutations accumulate, and cells are likely to undergo oncogenic transformation.

ZBTB2 has characteristics of Sp1-family Krüppel-like zinc finger proteins and binds to some of the GC-boxes that are similar to the GC-boxes recognized by Sp1. This finding suggests that GC-boxes recognized by Sp1 may be transcriptional repression targets of ZBTB2, and that Sp1-ZBTB2 binding competition may be a general mechanism of transcriptional repression of some ZBTB2 target genes. Molecular interactions occurring both in the proximal and distal promoter of the *p21* gene are unique and may be also relevant to the transcription regulation of other genes of the Arf-HDM2-p53-p21 pathway. How ZBTB2 potently activates (as much as 80-fold under our assay conditions) transcription of the *HDM2* gene (which has a p53 binding element in the P2 promoter and is activated by p53) remains unclear and needs further investigation. The strong induction of the *HDM2* gene may induce rapid degradation of p53, significantly blocking the protective effect of p53 in the cellular response to DNA damage. Taken together, our findings suggest that ZBTB2 may play a critical role in regulating important biological processes such as DNA repair, cell growth, differentiation, and apoptosis by regulating the transcription of *p21* and other genes of the p53 pathway.

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