Expression of Angiogenic Factor Cyr61 during Neuronal Cell Death via the Activation of c-Jun N-terminal Kinase and Serum Response Factor*

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The immediate early gene, *cyr61*, is transcriptionally activated within minutes by serum and serum growth factors. The encoded *cyr61* protein is secreted into the extracellular matrix and promotes cell adhesion and migration. In this study, we sought to examine the expression profile of *cyr61* gene during neuronal cell death induced by various toxic stimuli and the mechanisms involved. Our data show that toxic stimuli, such as etoposide, significantly increased *cyr61* mRNA levels in immortalized hippocampal progenitor (H19-7) cells. *Cyr61* transcriptional activation was corroborated at the protein level as well. To identify the upstream signaling cascades involved in *cyr61* gene induction, the blocking effect of either JNK or p38 kinase-signaling pathway on *cyr61* induction in response to etoposide was tested. Transfection of the cells with a kinase-deficient mutant of MEKK, an upstream activator of JNK, significantly decreased the *cyr61* expression induced by etoposide. In contrast, *cyr61* mRNA levels did not change after pretreatment with SB203580, the p38 kinase inhibitor. When the induction of *cyr61* was tested by using several of its deleted promoters driving the expression of reporter gene, the promoter activation occurred primarily within the region containing an SRE-like CARG box. In addition, the SRF, which binds to the CARG site, was directly phosphorylated by active JNK. Furthermore, the blockade of *cyr61* gene expression using an antisense encoding *cyr61* sequence significantly inhibited the cell death induced by etoposide. Overall, these results suggest that the induction of the immediate early gene, *cyr61*, is important for neuronal cell death in the central nervous system hippocampal progenitor cells, and JNK activation, but not of p38, as well as the subsequent SRF phosphorylation are involved in *cyr61* gene induction.

The immediate early gene (IEG), *cyr61*, encodes a secretory, growth regulatory, and heparin-binding protein that is associated with the cell surface and extracellular matrix (1, 2). It is a member of the CCN family that includes CTGF, Nov, Elm-1/WISP-Q, Cop-1/WISP-2, and WISP-3 (3–5). A remarkable feature of the CCN protein family is their organization into four conserved modular domains, which share sequence similarities with the insulin-like growth factor-binding protein, the von Willebrand factor type C repeat, and the thrombospondin type I repeat (6). *Cyr61* was originally identified in both mouse 3T3 fibroblasts and human umbilical vein endothelial cells, and its mRNA is rapidly and transiently expressed by the serum and the serum growth factors (1). At the molecular level, its recombinant protein is able to support cell adhesion and migration, enhances the proliferative effects of the basic fibroblast growth factor. *Cyr61* is expressed during embryogenesis of the circulatory system and the cartilaginous skeleton, and enhances chordogenesis in vitro (7). In addition, *cyr61* gene plays a role during neuronal differentiation (8) and promotes angiogenesis and the growth of certain tumors, probably through its angiogenic potential (9, 10).

An upstream 2-kb 5′-flanking DNA fragment of *cyr61* gene functions as a serum-inducible promoter (11). This DNA fragment contains a sequence that resembles the serum response element (SRE) originally identified in the c-fos promoter. A deletion of the *cyr61* SRE-like sequence abrogates its serum inducibility. Furthermore, this SRE-like sequence is sufficient to confer induction by the serum and growth factor and binds to a serum response factor (SRF). The SRE mediates c-fos induction in response to the growth factor, cytokines, and other extracellular stimuli that activate the MAPK pathways (12). The SRE in the c-fos promoter is comprised of an inner core known as the CARG box, which is recognized by a dimer of the SRF; and the ternary complex factor (TCF), a family of Ets-domain transcription factors (13). Elk-1 is a member of the TCF.

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† The abbreviations used are: IEG, immediate early gene; CAT, chloramphenicol N-acetyltransferase; DMEM, Dulbecco’s modified Eagle’s medium; GFP, green fluorescent protein; GST, glutathione S-transferase; JNK, c-Jun-N-terminal kinase; MAPK, mitogen-activated protein kinase; MK, MAPK-activated protein kinase; SRE, serum response element; SRF, serum response factor; TCF, ternary complex factor; ERK, extracellular signal-regulated kinase; CaM, calmodulin; CMV, cytomegalovirus; TUNEL, terminal deoxynucleotidyl transferase-mediated dUTP nick end labeling; NMDA, N-methyl-D-aspartic acid; RT, reverse transcriptase; MEKK, MAPK/ERK kinase kinase; SARP, secreted apoptosis-related protein; nt, nucleotide(s); MAPKAP, MAPK-activated protein.
family, which is phosphorylated by JNK and p38 as well as by ERK (14, 15). Several N-terminal phosphorylation sites have been identified within the SRF (16). Specifically, the Ser-133 residue in the SRF is phosphorylated by CaM kinase II and IV (17) and MAPKAP kinase 1 and 2 (also referred to as MK-1 and MK-2) (18). MK-2 is located downstream of the p38 kinase pathway. Although there have been several reports of situations where JNK and/or p38 activation can occur without influencing cell death (19–21), high levels of JNK and p38 activities have been correlated with the induction of apoptosis in many cases (22–24).

Based on these findings, the possibility of whether cyr61 is expressed during the neuronal cell death induced by various toxic stimuli was investigated. The cyr61 mRNA levels were found to increase, and its encoded proteins were expressed and subsequently secreted into the extracellular space during etoposide-induced neuronal cell death in the embryonic hippocampal progenitor cells. Furthermore, the induction of cyr61 was mediated by the JNK-dependent phosphorylation of SRF, and the blocking of cyr61 expression, through use of an antisense-expressing construct, suppressed the neuronal cell death induced by etoposide. These results suggest that the induction of the angiogenic factor cyr61 plays a key role during neuronal cell death.

**EXPERIMENTAL PROCEDURES**

**Materials**—Dulbecco’s modified Eagle’s medium (DMEM), the fetal bovine serum, and the LipofectAMINE reagents were purchased from Invitrogen. The U0126 was purchased from New England BioLabs. The SB203580 and 1.9-pyrazolonothrean were purchased from Calbiochem. Both the Protein A-Sepharose and glutathione-Sepharose 4B were purchased from Amersham Biosciences. The cyr61 promoter-chloramphenicol acetyltransferase (CAT) reporter fusion constructs (−2062cyr61/CAT, −1709cyr61/CAT, −529cyr61/CAT, −529cyr61/CAT, −529cyr61/CAT, −529cyr61/CAT) were prepared, as described previously (11). Plasmid encoding antisense Cyrl, pZeoSV-AS-cyr61, was constructed by inserting a 300-nucleotide antisense strand of cyr61 into the Xhol and EcoRI site of pZeoSV vector (Invitrogen, Carlsbad, CA), causing an over-lapping of transcriptional initiation of the start site and an exon 1 portion of the cyr61 gene. The fidelity of plasmid DNA was verified by nucleotide sequence in both strands. The plasmids encoding glutathione S-transferase (GST) fused to the whole SRF proteins (residues 1–508: pGST-SRF508), N-terminal peptide (residues 1–140: pGST-SRF140), or C-terminal peptide (residues 198–508: pGST-SRF198/508) were kindly provided by K. Sobue (Osaka University Graduate School of Medicine, Osaka, Japan). Mammalian expression vectors encoding kinase deficient JNK1 (pCMV5-JNK1) and JNK2 (p8-HA-JNK2) were provided by J. S. Chun (Kwangju Institute of Science & Technology, Kwangju, Korea). The heterologous plasmids for the SRF-c fos promoter/luciferase reporter gene (pWTGL3 and pnm18GL3) were provided by R. Prywes (Columbia University, New York, NY). The polyclonal anti-Cyr61 antibodies were prepared as described elsewhere (25).

**Cell Culture and DNA Transfection—**Immortalized hippocampal H19-7 cells were generated and cultured as described previously (26, 27). The H19-7 cells were grown in Dulbecco’s modified Eagle’s medium supplemented with 10% fetal bovine serum and then transiently transfected for 24 h using the LipofectAMINE reagents (Invitrogen) according to the manufacturer’s protocol. To prepare the H19-7 cells, clones, antisense cyr61 construct was transfected into H19-7 cells using calcium phosphate. Cells were cultured in medium containing 300 μg/ml Zeocin (Invitrogen), 10% fetal bovine serum in DMEM in 5% CO₂ at 33 °C for 14 days, and individual Zeocin-resistant clones were isolated.

**Cell Death Assessment—**Cell death was quantified by the trypan blue staining method as described elsewhere (28). Statistical analyses were performed with the aid of the StatView II program for Macintosh computers (Abacus Concepts, Berkeley, CA). All data were analyzed by one-way analysis of variance, and preplanned comparisons with the control were performed by Dunnett’s t statistic.

**Detection of Apoptotic Cells—**Apoptotic cells were detected by terminal deoxynucleotidyl transferase-mediated dUTP fluorescein nick end-labelling (TUNEL) using the in situ death detection kit (Roche Molecular Biochemicals) following the protocol provided by the manufacturer. The cells were fixed for 30 min in fresh 4% paraformaldehyde in phosphate-buffered saline at room temperature. Endogenous peroxidase was inactivated by incubation with 0.3% hydrogen peroxide in methanol for 30 min at room temperature. The cells were then incubated in a permeabilizing solution (0.1% sodium citrate and 0.1% Triton X-100) for 2 min at 4 °C. The cells were labeled by incubation with the TUNEL reaction mixture for 60 min at 37 °C. After two washes with phosphate-buffered saline, cells were labeled with peroxidase-conjugated anti-goat antibody (Fab fragment) for 30 min at 37 °C and stained with a Vectastain ABC kit (Vector Laboratories). To detect intercellular DNA fragmentation, DNA fragmentation assay was performed as described elsewhere (45).

**RNA Preparations and Northern Blot Analysis—**The total cellular RNA from the H19-7 cells was isolated by the TRIzol reagent (Invitrogen) according to the manufacturer’s protocol. Total RNA (10 μg) was subjected to electrophoresis in a 1% agarose gel containing 37% formaldehyde for 2 h and transferred onto nylon membranes by capillary transfer. The cyr61 cDNA was labeled with [32P] using a Redi prime II kit (Amersham Biosciences) according to the procedure provided by the manufacturer and used as a hybridization probe. Prehybridization and hybridization were carried out in a solution containing 50% formamide, 5× Denhardt’s reagent, 6× SSPE, 0.5% SDS at 42 °C for 18 h. After hybridization, the nylon membrane was rinsed twice in 1× SSPE containing 0.1% SDS at 42 °C for 20 min, which was then subject to autoradiography at −70 °C for 3 days.

**RT-PCR—**For reverse transcription, a 2-μg aliquot of the total RNA was treated with a hexa-deoxyribonucleotide of the random primers (Invitrogen), and the first strand was synthesized using SuperScript™II Reverse Transcriptase (Invitrogen) according to the manufacturer’s protocol. The cDNA/mRNA hybrids were amplified with the sense and antisense primers by PCR. After an initial denaturation at 94 °C for 3 min, temperature cycling was initiated for each cycles follows: 94 °C for 30 s, 68 °C for 1 min, and 72 °C for 2 min for 25 cycles for cyr61, followed by a final elongation step at 72 °C for 10 min.

**Metabolic Labeling and Immunoprecipitation of Cyrl—**The H19-7 cells were incubated with 1 in 10% fetal bovine serum-containing DMEM without methionine prior to labeling. The cells were metabolically labeled with 50 μCi/ml [35S]methionine (ICN, Costa Mesa, CA) and chased for 85 μl of the etoposide for the indicated times. The cell lysates were prepared, and the recovered culture medium was concentrated using a Centricon YM-30 (with 30-kDa molecular size cut-off). The cell lysates and media were immunoprecipitated with the polyclonal anti-Cyr61 serum and analyzed as described elsewhere (27).

**Reporter CAT and Luciferase Assay—**The CAT assay was carried out with an enzyme-linked immunosorbent CAT assay kit (Roche Molecular Biochemicals) according to the manufacturer’s protocol. The luciferase activity was measured using a luciferase assay kit (Promega) and a luminometer.

**Western Blot Analysis with Anti-ERK, Anti-JNK, or Anti-p38 Antibodies—**Cell lysates were prepared from 85 μl of etoposide induced H19-7 cells. The lysates were separated by SDS-PAGE in a 10% polyacrylamide gel and transferred to a nitrocellulose membrane. The membrane was reacted with a 1/2,000 dilution of anti-phospho-JNK (New England BioLabs), 1/500 dilution of anti-phospho-p38 (Santa Cruz Biotechnology). Horseradish peroxidase-conjugated goat anti-rabbit and anti-mouse IgG were used as secondary antibodies.

**In Vitro Immunocomplex Kinase Assay—**The cell extracts were prepared after the H19-7 cells were treated with the etoposide, washed twice with phosphate-buffered saline, and lysed with 300 μl of the lysis buffer (20 mM Tris, pH 7.9, 137 mM NaCl, 5 mM EDTA, 1% Triton X-100, 10% glycerol, 1 mM β-glycerophosphate (pH 7.4), 0.1 mM EDTA, 200 μM phenylmethylsulfonyl fluoride, 1 mM NaF, 1 mM Na3VO4, 1 μg/ml aprotinin, 1 μg/ml leupeptin). The cell lysates were pretreated with 1 μg of the transfectant H19-7 clone cDNA at 44 °C for 14 h 4 °C and added to the Protein A-Sepharose gels (Amersham Biosciences). After incubation for 2 h, the gels were washed four times with buffer A. The kinase reaction was carried out as described elsewhere. The gels were mixed with either the wild type or the deleted GST-SRF proteins in 20 μl of the kinase buffer (20 mM HEPES, pH 7.4, 10 mM MgCl2, 20 mM Tris, 1 mM EDTA, 200 μM phenylmethylsulfonyl fluoride, 2.5 μg/ml aprotinin, 2.5 μg/ml leupeptin, 1 mM NaF, 1 mM dithiothreitol, 20 μM ATP) and allowed to incubate at 30 °C for 1 h. After 2-h incubation, the Sepharose gels were treated with the 2% SDS sample buffer, and the proteins were separated by 8% SDS-PAGE. The resolved proteins were analyzed using an ImageQuant analyzer (Molecular Dynamics).
H19-7 cells with the etoposide and then applying them to the gel. All the gel renaturation and phosphorylation protocols were performed as previously described (27).

RESULTS

Various Toxic Stimuli Induce the Expression of Immediate Early Gene cyr61—To examine whether or not IEG cyr61 is induced by various toxic stimuli in H19-7 cells, cyr61 mRNA expression was measured in response to several neurotoxins, such as etoposide, NMDA, or glutamate. As shown in Fig. 1A, RT-PCR analysis clearly showed that the expression of a 361-bp fragment of cyr61 was abundantly amplified after being stimulated with 85 μM etoposide for 1 h. Furthermore, cyr61 gene expression increased significantly after stimulation with either 200 μM glutamate or 200 μM NMDA. As a positive control, cells were treated with basic fibroblast growth factor (10 ng/ml), which resulted in cyr61 induction, as previously reported (8). In a similar way, Northern blot analysis using the total RNAs isolated after being stimulated with the same concentration of etoposide, NMDA, and glutamate confirmed that IEG cyr61 is rapidly induced by these toxic stimuli (Fig. 1B).

Etoposide Induces Apoptosis in H19-7 Cells—To clarify the upstream signal transduction pathways leading to cyr61 induction, the effect of the DNA topoisomerase II inhibitor, etoposide (29), on cyr61 expression was examined. Etoposide stabilizes the DNA-topoisomerase II complexes by blocking DNA relagation. Initially, the alteration of cell viability was determined in response to various etoposide doses to test how etoposide affects cell viability in H19-7 cells (Fig. 2A). When 10–85 μM etoposide was added to the serum-containing medium, the cell viability decreased in a dose-dependent manner, as measured by the trypan blue staining method. Stimulation of the cells with 85 μM etoposide caused an approximate 51% decrease in cell viability, compared with the control cells. To determine whether the neuronal cell death was due to apoptosis or necrosis, the occurrence of DNA fragmentation was measured by means of in situ TUNEL method as well as the detection of internucleosomal DNA ladder formation. The treatment with 85 μM etoposide significantly increased the TUNEL-positive cells and DNA fragmentation (Fig. 2B). These results indicated that etoposide-treated H19-7 cells die by means of apoptosis.

The Synthesis of Cyr61 Protein Is Induced by Etoposide in H19-7 Cells—In addition, the effect of etoposide on cyr61 protein synthesis was also examined. Cyr61 protein is well known to be secreted into the extracellular space in a variety of cell types. The H19-7 cells were metabolically labeled with [35S]methionine and stimulated with 85 μM etoposide, and the cell lysates and cultured media were prepared. The cell lysates and media were immunoprecipitated with the Cyr61 polyclonal antibodies. As shown in Fig. 3, the presence of 42-kDa protein band can be seen, corresponding to the molecular size of Cyr61 in the cell lysates within 5–10 h after the cells were stimulated with etoposide, and up to 24 h after stimulation. In addition, its outer cellular presence was maintained until 48 h after post-etoposide stimulation (Fig. 3). These findings suggest the occurrence of rapid Cyr61 synthesis by etoposide. However, once produced inside the cells, Cyr61 appears to be translocated gradually into the extracellular media.

The Etoposide-induced Expression of cyr61 Occurs by JNK-dependent Pathway—Next we sought to elucidate the upstream signaling pathways leading to the induction of cyr61. Because the mitogen-activated protein kinases (MAPKs), consisting of JNK, p38 kinase, and ERK, are potential candidates for cyr61 gene activation, we first examined whether they are activated directly occurs by the JNK-signaling cascade, which selectively inhibits JNK activation. As shown in Fig. 4, both JNK1 and JNK2 were transiently activated within 5–15 min post-etoposide stimulation, whereas no significant levels of active p38 kinase or ERK were detected. To investigate whether the mRNA induction of cyr61 directly occurs by the JNK-dependent pathway, cells were transfected with kinase-inactive MEKK mutant, an upstream JNK kinase activator in the JNK-signaling cascade, which selectively inhibits JNK activation. As shown in Fig. 4B, the RT-PCR experiment revealed that blocking the JNK pathway results in a significant decrease in etoposide-induced cyr61 expression, compared with...
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Fig. 3. Induction of Cyr61 protein in H19-7 cells by etoposide.
While metabolically labeled with [35S]methionine, the H19-7 cells were stimulated with 85 μM etoposide for the indicated times. Where specified, Cyr61 in the cell lysates and culture media were immunoprecipitated using polyclonal anti-Cyr61 IgG, resolved by SDS-PAGE (8.0% gel), and visualized by autoradiography. Cyr61 synthesis in cell lysates (A) or media (B) is shown in the individual autoradiograph.

Fig. 4. Etoposide-induced expression of cyr61 is mediated by JNK-dependent signaling pathway. A, etoposide-induced activation of JNK, but not p38 or ERK. The H19-7 cells were treated with 85 μM etoposide for the indicated times. The cell extracts were then resolved by SDS-PAGE and transferred to a nitrocellulose membrane. After blocking, the membranes were incubated with antibodies specific to phosphorylated JNK, p38 kinase, or ERK. The membrane was incubated with peroxidase-conjugated secondary antibodies, and the bands representing phosphorylated JNK, p38 kinase, or ERK were visualized by enhanced chemiluminescence.

B, effect of JNK and p38 kinase pathway on the transcriptional activity of cyr61. 2.5 μg of cDNA probe for cyr61 was transiently transfected into the H19-7 cells. The cells were then stimulated with 85 μM etoposide. The activity of the expressed CAT enzyme in 50–70 μg of the cell lysate was measured as described under “Experimental Procedures.” Extracts prepared from the mock-transfected cells were used as a negative control. The results are plotted as a mean plus the range of samples from two independent experiments.

Fig. 5. Inhibition of transcriptional activation of cyr61 by blocking JNK. A, time course of transcriptional activation of cyr61 by etoposide in H19-7 cells. The −2062cyr61/CAT fusion plasmid (5 μg) was transiently transfected into the H19-7 cells. The cells were then stimulated with 85 μM etoposide. The activity of the expressed CAT enzyme was measured using an enzyme-linked immunosorbent CAT assay kit according to the manufacturer’s protocol.

Transcriptional Activation of the cyr61 Gene Functions as a Serum-Inducible Promoter (11). This DNA fragment contains a sequence resembling the serum response element. The transcriptional activation of the cyr61 gene was examined using a CAT reporter plasmid linked to a 2062-bp cDNA fragment of cyr61. The resulting DNA fusion plasmid (−2062cyr61/CAT) transiently expressed in H19-7 cells. Treatment of the H19-7 cells with 85 μM etoposide rapidly stimulated cyr61 transcription, which reached a plateau after 4 h.

The blocking effect of MAPK pathways on the transcriptional activity of cyr61 was tested using either the chemical inhibitors of the MAPK pathways or the plasmid encoding kinase inactive mutant MEKK (mMEKK) (Fig. 5B). Following pretreatment of the H19-7 cells with either 30 μM SB203580, 10 μM U0126, or 30 μM U0126, the activation of the cyr61 promoter was unaffected. However, when a plasmid encoding kinase-deficient MEKK mutant and −2062cyr61/CAT-construct were co-transfected by the JNK-dependent pathway but not by either the ERK or p38 kinase pathway.
into the cells, stimulation with 85 μM etoposide caused significant inhibition of cyr61 induction, compared with control cells transfected with -2062cyr61/CAT alone. This indicates that the etoposide-induced transcriptional activation of the cyr61 gene is mediated at least in part by JNK but not by p38 kinase or ERK activation.

Cis-regulatory Serum Response Element in cyr61 Promoter Is Required for Its Induction by Etoposide—The results described above indicate that the 2062-bp cyr61 promoter contains a domain responsive to a JNK-dependent signaling pathway, which is activated by etoposide. To identify these domains, the cyr61 promoter was subjected to deletion analysis (Fig. 6A). The cyr61 promoter has one SRF-binding domain (SRE or CArG box) between -1950 and -1900. Deleting this SRE (-1763cyr61/CAT) resulted in a complete loss of the etoposide-activated transcription of cyr61, compared with the -2062cyr61/CAT-transfected cells (Fig. 6B). A further deletion of the promoter up to -529 (−529cyr61/CAT) had no effect, whereas an intact SRE-containing construct with an internal deletion (ΔBglIIcyr61/CAT) showed a significant increase in cyr61 promoter activity, compared with the -2062cyr61/CAT construct (Fig. 6B). The SRE enhancer region of the cyr61 promoter was further analyzed by linking it to the 529-bp fragment (CArG/−529cyr61/CAT). The results suggest that a domain containing a CArG box is sufficient for the full cyr61 transcriptional activation by etoposide.

The SRE was then tested to determine whether it is sufficient for cyr61 induction or other serum-inducible cis-regulatory elements, such as the TCF-binding motif where its presence appears to be crucial for inducing IEGs during neuronal cell death (27, 30). In addition, the TCF-binding motif was examined to determine if it acts together with the SRE to mediate a cyr61 induction in a synergistic way. To test this possibility, two heterologous SRE-c-fos promoter/luciferase constructs involving either the SRE alone (ppm18GL3) or a combined TCF-SRE-c-fos promoter (pWTGL3) were further analyzed (Fig. 7A). The plasmids, pWTGL3 and ppm18GL3, containing the 285 region of the murine c-fos promoter were cotransfected into the cells, stimulation with 85 μM etoposide caused significant inhibition of cyr61 induction, compared with control cells transfected with -2062cyr61/CAT alone. This indicates that the etoposide-induced transcriptional activation of the cyr61 gene is mediated at least in part by JNK but not by p38 kinase or ERK activation.

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Cis-regulatory Serum Response Element in cyr61 Promoter Is Required for Its Induction by Etoposide—The results described above indicate that the 2062-bp cyr61 promoter contains a domain responsive to a JNK-dependent signaling pathway, which is activated by etoposide. To identify these domains, the cyr61 promoter was subjected to deletion analysis (Fig. 6A). The cyr61 promoter has one SRF-binding domain (SRE or CArG box) between -1950 and -1900. Deleting this SRE (-1763cyr61/CAT) resulted in a complete loss of the etoposide-activated transcription of cyr61, compared with the -2062cyr61/CAT-transfected cells (Fig. 6B). A further deletion of the promoter up to -529 (−529cyr61/CAT) had no effect, whereas an intact SRE-containing construct with an internal deletion (ΔBglIIcyr61/CAT) showed a significant increase in cyr61 promoter activity, compared with the -2062cyr61/CAT construct (Fig. 6B). The SRE enhancer region of the cyr61 promoter was further analyzed by linking it to the 529-bp fragment (CArG/−529cyr61/CAT). The results suggest that a domain containing a CArG box is sufficient for the full cyr61 transcriptional activation by etoposide.

The SRE was then tested to determine whether it is sufficient for cyr61 induction or other serum-inducible cis-regulatory elements, such as the TCF-binding motif where its presence appears to be crucial for inducing IEGs during neuronal cell death (27, 30). In addition, the TCF-binding motif was examined to determine if it acts together with the SRE to mediate a cyr61 induction in a synergistic way. To test this possibility, two heterologous SRE-c-fos promoter/luciferase constructs involving either the SRE alone (ppm18GL3) or a combined TCF-SRE-c-fos promoter (pWTGL3) were further analyzed (Fig. 7A). The plasmids, pWTGL3 and ppm18GL3, containing the 285 region of the murine c-fos promoter were cotransfected into the cells, stimulation with 85 μM etoposide caused significant inhibition of cyr61 induction, compared with control cells transfected with -2062cyr61/CAT alone. This indicates that the etoposide-induced transcriptional activation of the cyr61 gene is mediated at least in part by JNK but not by p38 kinase or ERK activation.
the H19-7 cells stimulated with 85 μM etoposide and, consequently, immunoprecipitated with the anti-JNK antibodies. Subsequently, the immunocomplex kinase assay was performed using bacterially recombinant glutathione S-transferase (GST) proteins fused to the whole SRF proteins (residues 1–508: GST-SRF508), the N-terminal SRF peptide (residues 1–140: GST-SRF140), or the C-terminal SRF peptide (residues 198–508: GST-SRF198/508) as a substrate (32). As shown in Fig. 8A, the in vitro kinase assay showed that the SRF is phosphorylated by JNK immunocomplexes. Interestingly, SRF phosphorylation significantly increased when GST-SRF508 and GST-SRF198/508 were used as substrates but not with the N-terminal SRF peptide (GST-SRF140) (Fig. 8A). To test the possibility that one or more other kinases beside JNK in the JNK immunocomplexes phosphorylates the SRF in response to etoposide, an in vitro gel kinase assay was performed using a polyacrylamide gel prepared in the presence of either the GST-SRF508 or GST-SRF140 proteins as a phosphorylation substrate. Equal protein-containing anti-JNK-IgG immunoprecipitates from the H19-7 cells, which had been stimulated with 85 μM etoposide for 60 min, were resolved by SDS-PAGE, renatured, and assayed for the SRF phosphorylation in the gel. The results showed the 46- and 54-kDa bands corresponding to the molecular size of JNK-1 and -2 phosphorylate GST-SRF508 in the gel (Fig. 8B). No significant kinase activity was detected when the N-terminal SRF peptide with its C-terminal 141–508 residues deleted was used as a substrate (Fig. 8B). Furthermore, to determine whether JNK could phosphorylate SRF in a selective way upon the stimulation with etoposide, the cells were either transiently co-transfected with expression vectors encoding kinase-deficient JNK1 and JNK2. The cells were then treated with 85 μM etoposide for 60 min, as indicated. The cell extracts containing 100- to 150-μg proteins were immunoprecipitated with the anti-JNK antibodies, and the immunocomplex proteins were resolved by SDS-PAGE on a 10% gel containing either 50 μg of the bacterially expressed wild type GST-SRF (wSRF) or the C-terminal-deleted GST-SRF104 peptide (SRF-N) per milliliter. The in-gel kinase renaturation assay was performed as described under “Experimental Procedures.” The final eluates from the beads were resolved by SDS-PAGE in 8.0% gel and visualized by autoradiography. B, the in vitro in-gel kinase assay. The H19-7 cells were untreated (C) or treated with 85 μM etoposide (E) for 60 min, as indicated. The cell extracts containing 100- to 150-μg proteins were immunoprecipitated with the anti-JNK antibodies, and the immunocomplex proteins were resolved by SDS-PAGE on a 10% gel containing either 50 μg of the bacterially expressed wild type GST-SRF (wSRF) or the C-terminal-deleted GST-SRF104 peptide (SRF-N) per milliliter. The in-gel kinase renaturation assay was performed as described under “Experimental Procedures.” JNK1 and JNK2 that were activated by etoposide are indicated by arrows. C, the blocking effect of JNK on SRF phosphorylation. The H19-7 cells were mock-transfected (No T, Cont, and JI) or transiently transfected with 3 μg of each pcCMV5-mJNK1 and pSR-HA-mJNK2 plasmid-encoding kinase-deficient JNK1 and JNK2, respectively (mJ12). Where indicated, the cells were pretreated with 300 μM 1,9-pyrazoloanthrone, a cell-permeable and selective JNK inhibitor (J1) for 30 min prior to stimulation. The cells were then stimulated with 85 μM etoposide for 60 min, immunoprecipitations were performed by using JNK antibodies, and immunocomplex kinase assays were done with 50 μg of recombinant wild type GST-SRF (wSRF) as a substrate.

**DISCUSSION**

It has been known that, as members of the CCN and IEG families, both cyr61 and CTGF are induced by the serum, basic fibroblast growth factor, and the platelet-derived growth factor in fibroblasts and neuronal H19-7 cells (1, 6, 8, 33). Both cyr61 and CTGF are associated with the extracellular matrix, share a 45% amino acid sequence identity, and bind to heparin (6). Although CTGF is known to induce apoptosis in the breast cancer cell line by transforming growth factor-β (34), the physiological role of cyr61 during cell death is unknown. Cyr61 regulates cell adhesion, migration, proliferation, differentiation, and chondro-
Fig. 9. Effect of antisense cyr61 expression on etoposide-induced neuronal cell death. A, while metabolically labeled with [35S]methionine, either stable H19-7 cell lines to express 300-nucleotide antisense Cyr61 to block the endogenous cyr61 expression (asCyr61) or control cells transfected with parental empty expression vectors (parental) were stimulated with 85 μM etoposide for 24 h. Newly synthesized Cyr61 proteins in the cell culture media were immunoprecipitated using anti-Cyr61 antibodies, resolved by SDS-PAGE, and visualized by autoradiography. B, where indicated, H19-7 cells stably transfected with parental empty control vector (parental) or antisense cyr61-expressing cells (asCyr61) were either untreated (Cont) or stimulated with 85 μM etoposide (Etop), and the extent of cell death was quantified. Data are expressed as mean ± S.E. from three independent experiments conducted in triplicates. Asterisks indicate significant differences compared with parental vector-transfected control values (*p < 0.001).

Induction of IEG Cyr61 during Neuronal Cell Death

Cyr61 can provide a negative regulation of cell growth. The induction of cyr61 appears to play an important role during etoposide-induced neuronal cell death in the hippocampal H19-7 cells. The cyr61 gene encodes a secretory protein. In accord with this property, the maximum level of Cyr61 synthesis was also observed in the cell lysates after 5 h of etoposide-stimulation in H19-7 cells and was maintained for approximately until 10 h. Once synthesized inside the cells, the Cyr61 proteins were presumably translated into the extracellular space, and were solely detected in the culture media 24 and 48 h after etoposide stimulation but not in cell lysates. In contrast to this study, the heparin-binding Cyr61 protein in mouse fibroblasts is associated with the cell surface and the extracellular matrix but not the culture media. These findings indicated that the localization of the synthesized Cyr61 during cell death is distinct from that in the serum-induced cell growth. The induction of another secretory protein, the secreted apoptosis-related proteins (SARPs), has been reported during cell death. The SARF family resembles growth factors and cytokines, and their tissue-specific expres-
Induction of IEG Cyr61 during Neuronal Cell Death

Seshan depends on the physiological state of cells. Human breast adenocarcinoma MCF7 cells stably transfected with sarp1 became more resistant, whereas cells transfected with sarp2 displayed an increased sensitivity to different proapoptotic stimuli such as tumor necrosis factor and ceramide. A family of transmembrane receptors, Frizzled proteins, is homologous to a family of secreted proteins (41). Furthermore, expression of the SARP family modulates the intracellular levels of β-catenin, suggesting that the SARP family interfere with the Wnt-frizzled protein signaling pathway (41). All members of the SARP family have a cysteine-rich domain that is homologous to the cysteine-rich domain in the transmembrane frizzled proteins.

We are currently investigating the molecular mechanisms of how the secretory Cyr61 protein may cause or potentiate cell death. This will provide new insights into another biological function of cyr61 during neuronal cell death. In summary, cyr61 is expressed during the etoposide-induced neuronal cell death in neuronal H19-7 cells, and the SRE-like CARG domain in the upstream cyr61 promoter is necessary for its induction by etoposide.

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Expression of Angiogenic Factor Cyr61 during Neuronal Cell Death via the Activation of c-Jun N-terminal Kinase and Serum Response Factor
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