

Autoregulation of the Human C/EBP α Gene by Stimulation of Upstream Stimulatory Factor Binding

N. TIMCHENKO,¹ D. R. WILSON,¹ L. R. TAYLOR,² S. ABDELSAYED,¹ M. WILDE,¹
M. SAWADOGO,³ AND G. J. DARLINGTON^{1,2*}

*Department of Pathology*¹ and *Department of Molecular and Human Genetics,*² *Baylor College of Medicine, and Department of Molecular Genetics, The University of Texas M. D. Anderson Cancer Center,*³ *Houston, Texas 77030*

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The human C/EBP α gene promoter shares significant sequence homology with that of the mouse but has a different mechanism of autoregulation. Activation of the murine promoter by direct binding of C/EBP α to a site within 200 bp of the transcriptional start was shown to elevate activity by approximately threefold (R. J. Christy, K. H. Kaestner, D. E. Geiman, and M. D. Lane, Proc. Natl. Acad. Sci. USA 88:2593-2597, 1991; K. Legraverend, P. Antonson, P. Flodby, and K. G. Xanthopoulos, Nucleic Acids Res. 21:1735-1742, 1993). Unlike its murine counterpart, the human C/EBP α gene promoter does not contain a *cis* element that binds the C/EBP α protein. Neither C/EBP α nor C/EBP β (NF-II-6) binds the human C/EBP α promoter within 437 bp. However, cotransfection studies show that C/EBP α stimulates transcription of a reporter gene driven by 437 bp of the C/EBP α promoter. Our studies show that the human C/EBP α protein stimulates USF to bind to a USF consensus element within C/EBP α promoter and activates it by two- to threefold. We propose that the human gene employs the ubiquitously expressed DNA-binding protein factor USF to carry out autoregulation. Autoregulation of the human C/EBP α promoter was abolished by deletion of the USF binding site, CACGTG. Expression of human C/EBP β following transfection did not stimulate USF binding. These studies suggest a mechanism whereby tissue-specific autoregulation can be achieved via a *trans*-acting factor that is expressed in all cell types. Thus, direct binding of the C/EBP α protein to the promoter of the C/EBP α gene is not required for autoregulation.

C/EBP α (CCAAT enhancer-binding protein α) belongs to a family of transcription factors (bZIP proteins) which contain a region rich in basic amino acids and a flanking leucine zipper domain that are necessary for DNA binding and dimer formation (22). A number of bZIP proteins have been cloned and sequenced (2, 8, 21, 29). At least three members of the C/EBP family of proteins show a high level of amino acid homology within the basic region and leucine zipper domains: C/EBP α , C/EBP β , and C/EBP δ (8). These three nuclear factors are able to form heterodimers that bind DNA (8). C/EBP α consists of four regions which are necessary for its transcriptional activity. Two transactivation domains located in the amino-terminal part of the molecule are important for transcriptional activation, while the basic and leucine zipper regions are necessary for binding to DNA (32). Expression of C/EBP α is regulated during rat liver development (13), adipocyte differentiation (6), and liver regeneration (14, 25). Several lines of evidence suggest a central role of C/EBP α in the maintenance of the quiescent, mature state of adult hepatocytes and adipocytes. A high level of C/EBP α expression is found to be limited to highly differentiated cells. For example, quiescent liver hepatocytes contain a high level of C/EBP α mRNA, but this level is decreased in regenerating hepatocytes (14, 25). C/EBP α regulates several genes expressed in differentiated cells, including the serum albumin (15), stearoyl coenzyme A desaturase (11), α 1-antitrypsin (12), insulin-responsive glucose transporter (19), and insulin-like growth factor II (33) genes. Umek et al. show that hormone-regulated increases of C/EBP α binding result in growth arrest of dividing adipocytes (32). Differenti-

ation of mouse preadipocytes into adipocytes is characterized by induction of C/EBP α expression (6, 32).

In the present paper we report the nucleotide sequence of the human C/EBP α 5'-flanking region and the investigation of important *cis* elements within this region. Using transient-cotransfection experiments, we show that the human C/EBP α protein can activate the human C/EBP α promoter. Our attempts to find a binding site for C/EBP proteins were unsuccessful. However, we found that a nuclear factor, upstream stimulatory factor (USF), binds to a specific sequence in the human C/EBP α promoter, and its binding activity increased in response to human C/EBP α but not human C/EBP β (NF-II-6) (2). We show that C/EBP α stimulates expression of a reporter gene promoted by the normal, but not a mutant, USF binding site from the C/EBP α promoter.

MATERIALS AND METHODS

Materials. The following oligonucleotides were used in this work: bZIP, 5'-CATGGATGGTATTGAGAAATCTG-3', containing the C/EBP binding site from the human C3 promoter (18, 35); m-c/ebp1, 5'-AGTCAGTGGCGGTTGC GCCACGATCTCT-3', corresponding to the sequence of the mouse C/EBP α promoter region from positions -200 to -173 (Fig. 1); h-c/ebp1, 5'-AGGCGG TGGGCGTTGCGCCGCGGCCT-3', containing the sequence of the human C/EBP α promoter from nucleotides -194 to -165 (Fig. 1); USF/Ad-ml, 5'-AC GGTGTAGGCCACGTGACCGGGTGT-3', corresponding to the nucleotide sequence of the adenovirus major late promoter which contains a high-affinity binding site for USF (16); USF/cebpb, 5'-TACCGACCACGTGGGCGCGGG GCGAC-3', having the nucleotide sequence of the human C/EBP α promoter from nucleotides -276 to -249; and Egr-1, 5'-TTGATCTCGGGGGCGAG GGGGATCAA-3', containing the binding site for the Egr-1 protein (9). The above oligonucleotides were synthesized in the Nucleic Acids Core Laboratory of the Department of Molecular and Human Genetics (Baylor College of Medicine). We also used oligonucleotides for Sp1 and AP2 obtained from Promega. Nucleotide sequences of these oligonucleotides are as follows: Sp1, 5'-ATTCC ATCGGGGCGGGGCGAG-3', and AP2, 5'-GATCGAACTGACCGCCCGCG GCGCGT-3'. For bandshift experiments, double-stranded oligonucleotides were labeled to a high specific activity with [³²P]dCTP by filling in with Klenow DNA

* Corresponding author. Phone: (713) 770-1868. Fax: (713) 770-1032. Electronic mail address (Internet): gretchen@msmail.his.tmc.tch.edu.

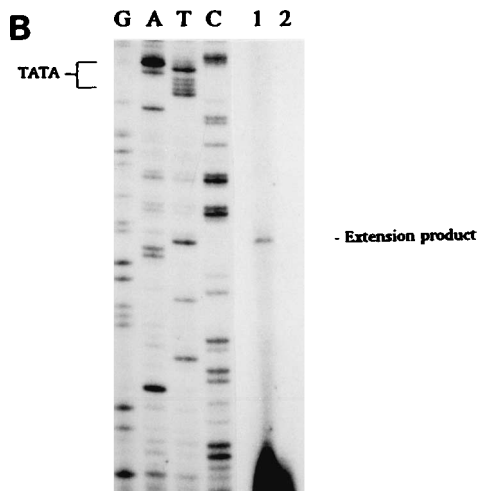
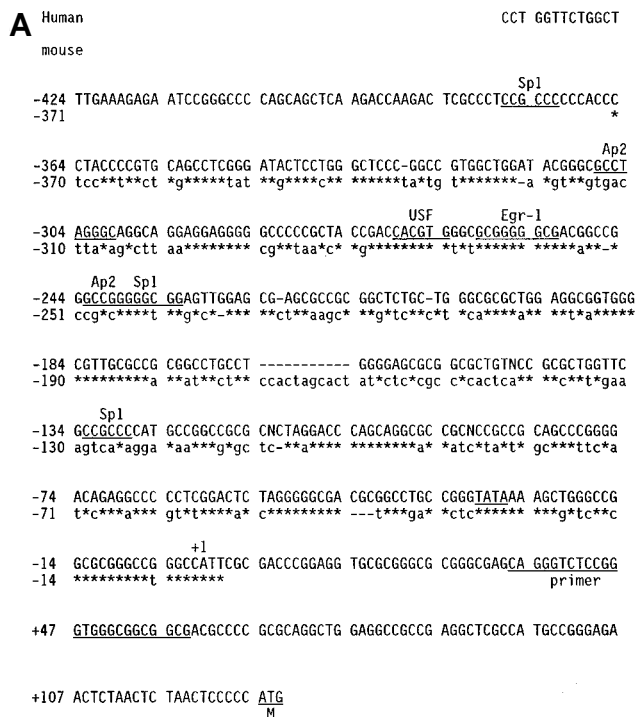


FIG. 1. Human C/EBP α promoter. (A) Nucleotide sequence of the 5'-flanking region of the human C/EBP α gene and its comparison with the mouse C/EBP α promoter. The transcription initiation site (+1), TATA box, and putative binding sites for nuclear proteins (Sp1, AP2, USF, and Egr-1) are indicated. The nucleotide sequence used in primer extension is underlined. Dashed lines indicate the presence of insertion/deletion in one sequence relative to the other. (B) Primer extension analysis documenting the transcription start site of human C/EBP α mRNA. The primer was annealed to 10 μ g of poly(A)⁺ RNA and extended by reverse transcriptase (lane 1). Lane 2, extension of primer by reverse transcription in the absence of RNA. Dideoxy sequencing of the C/EBP α promoter with the same primer. The position of the TATA box homology is shown on the left.

polymerase. Antibodies to C/EBP α , C/EBP β , and C/EBP δ were prepared in the laboratory of G. Darlington. Anti-C/EBP α serum was raised in rabbits to the C/EBP α peptide KGEPREEDEAKQLA. The anti-C/EBP β serum was similarly raised to the peptide SKAKKTVDKHSDEYKIRRC. This sequence resides in the leucine zipper domain, and antibodies to this portion of the protein disrupt dimerization and DNA binding. The antiserum to C/EBP δ was raised against the N-terminal amino acids 1 to 206 coupled to histidine. We also used antibodies to C/EBP α and to c-Myc from Santa Cruz Biotechnology. Antisera against human

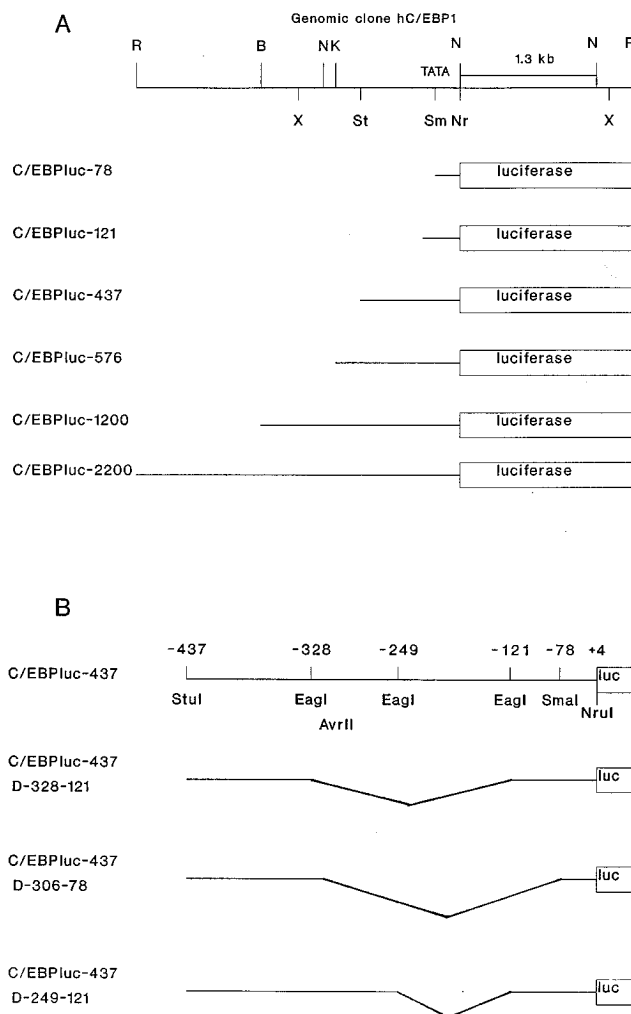


FIG. 2. Restriction map of the human C/EBP α promoter and construction of C/EBP-luciferase plasmids. (A) Restriction map of genomic clone hC/EBP1 and schematic representation of progressive deletion constructs of the C/EBP α promoter. R, *EcoRI*; B, *BamHI*; N, *NotI*; K, *KpnI*; X, *XhoI*; St, *StuI*; Sm, *SmaI*; Nr, *NruI*. The -2200 bp promoter region was cut by *EcoRI* and *NruI* and cloned into the *SmaI* site of the pXP1 vector (35). This plasmid was named C/EBPluc-2200. Using *BamHI*, *KpnI*, *StuI*, *EagI*, and *SmaI* enzymes, progressive deletion plasmids were constructed. (B) Construction of internal deletions within the -437 C/EBP α promoter.

43-kDa USF and 44-kDa USF were prepared in the laboratory of M. Sawadogo, as was an expression vector for the 43-kDa USF, PN3.

Cell culture and transient-transfection assay. Human hepatoma-derived Hep3B2 cells (1) were maintained as monolayers in M/M (three parts Eagle minimal essential medium, one part Waymouth MAB 87/3) plus 8% horse serum and 2% fetal bovine serum. General tissue culture methods were previously described (35). Coelectroporation of expression vectors was carried out with 5×10^6 cells per sample and 10 μ g of the reporter construct and 10 μ g of the expression vector. CaPO₄ transfection was carried out by a previously published protocol (35) and utilized 5 μ g of reporter and 5 μ g of the expression construct. The data summarize three to five separate experiments.

Stable clones. Clones of Hep3B2 cells were pooled following DNA-mediated gene transfer of a construct containing wild-type or mutant promoter elements coupled to luciferase as a reporter gene along with a plasmid containing the selectable neomycin resistance (Neo) marker. Analyses of transactivation by C/EBP α or by control DNA (CMV-stop) were carried out by electroporation of the expression vectors into the stable transformants. Luciferase activity was measured 24 h after delivery of the C/EBP α expression vector unless noted otherwise.

Preparation of constructs. The structures of the human C/EBP α gene and its 5'-flanking region are shown in Fig. 2. The coding region of the human C/EBP α gene (1.3 kb) was cut by *NruI* and *XhoI*. The fragment ends were blunted by

Klenow fragment and cloned into the *NotI* site of a cytomegalovirus (CMV) vector (24) that was restricted by *NotI* and blunted by Klenow fragment. The resulting plasmid was named CMV-C/EBP α . C/EBP α promoter fragments were inserted in front of the luciferase gene of the pXP1 plasmid (26) (Fig. 2). This vector showed low basal activity after transfection into mammalian cells (35). A plasmid, CMV-stop, containing only the CMV promoter was used as a negative control.

Preparation of WCE and NE. For the preparation of whole-cell extracts (WCE), 1×10^6 to 5×10^6 3B2 cells were harvested by scraping and washed twice with phosphate-buffered saline (PBS) without Ca or Mg ions. After pelleting, the cells were suspended in 300 μ l of solution E (50 mM Tris-HCl [pH 8.0], 0.1 mM EDTA, 1 mM dithiothreitol [DTT], 12.5 mM MgCl₂, 20% glycerol, 0.1 M KCl, 1% Triton X-100, protease inhibitors). After 5 min of incubation on ice, the lysed cells were centrifuged for 5 min at 10,000 rpm (Sorvall Microspin 12S). Supernatant (WCE) was collected, frozen in liquid nitrogen, and stored at -80°C . Nuclear extracts (NE) were prepared as described previously (18). In some cases the cells were scraped, washed with PBS, and suspended in 150 μ l of buffer A (10 mM Tris-HCl [pH 7.6], 1.5 mM MgCl₂, 10 mM KCl, 0.5 mM DTT). After 15 min of incubation on ice, cells were homogenized by pulling them through a 23-gauge needle (six to eight strokes), and the sample was centrifuged for 5 min at 10,000 rpm. Nuclei (pellet) were resuspended and salt extracted in 20 to 50 μ l of buffer B (20 mM Tris-HCl [pH 7.6], 25% sucrose, 0.420 M NaCl, 1.5 mM MgCl₂, 0.2 mM EDTA, 0.5 mM DTT) and incubated on ice 30 min. The nuclei were pelleted, and the supernatant (NE) was removed, dialyzed against buffer C (20 mM Tris-HCl [pH 7.6], 20% glycerol, 20 mM KCl, 1.5 mM MgCl₂, 0.2 mM EDTA), and used immediately.

Electrophoretic mobility shift assay (EMSA). Binding reactions were carried out at room temperature for 30 min. The reaction mixture (20 μ l) contained 0.2 to 0.4 ng of probe with or without a 100-fold molar excess of unlabeled oligonucleotides, 10 μ g of NE or 30 to 40 μ g of WCE, 2 μ g of poly(dI-dC) \cdot poly(dI-dC), 20 mM Tris-HCl (pH 7.6), 100 mM KCl, 5 mM MgCl₂, 1 mM DTT, and 10% glycerol. Antibodies were added to the reaction mixture before the addition of probe. Protein-DNA complexes were resolved on low-ionic-strength, native, 5% polyacrylamide (acrylamide/bisacrylamide ratio, 30:1.5) gels at room temperature. DNA fragments and oligonucleotides were end labeled by filling in with [³²P]dCTP and Klenow polymerase.

Southwestern (DNA-protein) analysis. Nuclear extracts of Hep3B2, HepG2, and HeLa cells were electrophoresed in sodium dodecyl sulfate (SDS)-10% polyacrylamide gels (20) and electroblotted onto nitrocellulose membranes. The membranes were blocked by 5% dry milk dissolved in 10 mM Tris-HCl (pH 7.6) with 1 mM DTT. The membranes were incubated at room temperature for 60 min in binding buffer which contained 10 mM Tris-HCl (pH 7.6), 10 mM MgCl₂, 100 mM KCl, 1 mM DTT, 0.25% dry milk, 0.1 mM EDTA, and 10⁶ cpm of ³²P-end-labeled oligonucleotides per ml. After incubation, the filter was washed with binding buffer without labeled oligonucleotides.

RNA isolation and primer extension. Poly(A)⁺ RNA was isolated from Hep3B2 cells by using the Fast Track mRNA Isolation Kit (Invitrogen). The synthetic oligonucleotide complementary to residues from +34 to +59 of the human C/EBP α mRNA (Fig. 1, underlined) was annealed to 10 μ g of poly(A)⁺ RNA at 80°C for 10 min and at 42°C overnight. Extension was carried out with 30 U of reverse transcriptase (Promega) under conditions previously described (30). The product was analyzed on an 8% sequencing gel.

Western blotting (immunoblotting). Proteins were electrophoresed in a 10% polyacrylamide gel containing 0.1% SDS and transferred to a nitrocellulose filter. Detection of immunoreactive proteins was performed with the enhanced chemiluminescence system (Amersham).

Site-directed mutagenesis. Deletion of the USF binding site, CACGTG, was carried out with a Transformer Site Directed Mutagenic Kit (Clontech) with the following modifications. The mutagenic primer 5'-CGTCCGCCCGCGC CGTCCGGTAGCGGGGC-3' from -249 to -284 (Fig. 1, CACGTG deleted) was annealed to the -437/luc and to the pT81-328-249 plasmids. A mutant DNA strand was synthesized with T4 DNA polymerase. After incubation for 1 h, fresh T4 DNA polymerase was added to the reaction mixture, and synthesis was continued for 2 h. Because the sequence CACGTG is a restriction site for *PmlI*, we used this enzyme for primary and secondary selection of mutant plasmids. Deletion of CACGTG was checked by resistance to *PmlI*, by sequencing, and by bandshift assay (see Fig. 10).

RESULTS

Nucleotide sequence of the human C/EBP α promoter. To study the activation of the human C/EBP α promoter, its nucleotide sequence was determined. Figure 1A shows the 5'-flanking region of the human C/EBP α gene from -437 to the first methionine codon. The promoter region of the human C/EBP α gene is GC rich (80%). A sequence with TATA box homology is located in the position identical to that of the mouse C/EBP α TATA box (10). The putative human C/EBP α mRNA cap site would be the adenine residue that is labeled

+1. Primer extension experiments demonstrated that the start position of C/EBP α mRNA is precisely as predicted (Fig. 1B). The length of 5' untranslated mRNA from +1 to the first ATG codon is 126 bp.

Comparison of human and mouse C/EBP α promoters indicated a relatively low level of similarity, although the transcribed regions of both genes are very similar (>80%) (unpublished data). Upstream of the TATA box, the mouse and human C/EBP α promoters possess only 53% sequence identity. The search for known nuclear factor binding sites within the human C/EBP α promoter identified several putative elements, including three GGGCGG boxes (the Sp1 binding site); a perfect binding site for zinc finger proteins, GCGGGGGCG (9); a binding site for helix-loop-helix (HLH)-bZIP (USF) family proteins, CACGTG; and two consensus sequences for AP2 (GCCNNNGGC). These sequences are underlined in Fig. 1A.

Four hundred thirty-seven nucleotides of the human C/EBP α promoter are sufficient for high-level expression of a C/EBP α -luciferase construct. In previous studies, we cloned the human C/EBP α gene and determined its chromosomal localization (17). To identify the region of the human C/EBP α promoter which was important for transcription of this gene, two series of constructs were prepared. In one series, different DNA fragments (with progressive or internal deletions of the C/EBP α promoter) were cloned in front of the luciferase gene of the pXP1 plasmid (Fig. 2). Luciferase activity from the longest promoter fragment (-2200) was consistently less than that of the -1200 and -576 constructs (Fig. 3A). Deletion of nucleotides to -78 resulted in a significant decrease of promoter activity (Fig. 3A). Subsequent analyses of promoter function concentrated on the region within 437 nucleotides of the human C/EBP α promoter. To test for the contributions of various regions to promoter activity, transient-transfection experiments with internal deletions were carried out. Deletion of nucleotides from -328 to -121, as well as from -306 to -78, decreased activity of the human C/EBP α promoter (Fig. 3B). However, a twofold increase of promoter activity was observed after deletion of nucleotides -249 to -121, suggesting the presence of a negative element(s) within this region (Fig. 3B).

Human C/EBP α can activate its own promoter. Autoregulation of mammalian transcription factors by direct binding of the gene product was first described for Jun (3). Mouse C/EBP α can bind to its own promoter (10) and activate expression of a luciferase construct (23). We tested whether or not autoregulation occurs for the human C/EBP α by cotransfection experiments of different C/EBP α -luciferase constructs (Fig. 2) with an expression vector for C/EBP α (CMV-C/EBP α) or control DNA (CMV-stop). Figure 3C shows that C/EBP α expression resulted in two- to threefold induction of activity of the cotransfected 437-bp C/EBP α promoter. Deletion of nucleotides -249 to -121 did not reduce activity substantially, while deletion of nucleotides -306 to -78 resulted in no induction. Autoregulation of the human C/EBP α promoter was observed also with stable clones containing -437 luc C/EBP α promoter integrated into chromosomal DNA (see below). These results suggested that the nucleotide sequence which is necessary for autoregulation is located between nucleotides -306 and -249 of the human C/EBP α promoter.

C/EBP α and C/EBP β do not bind to the promoter region of human C/EBP α . Because C/EBP α and C/EBP β bind to the same sequence (18), we have investigated the interaction of both with the promoter region of the human C/EBP α gene. The human C/EBP α promoter was divided into three pieces, -437 to -328, -328 to -249, and -249 to -121, which were subcloned into the pBluescript II KS(-) (Stratagene) vector

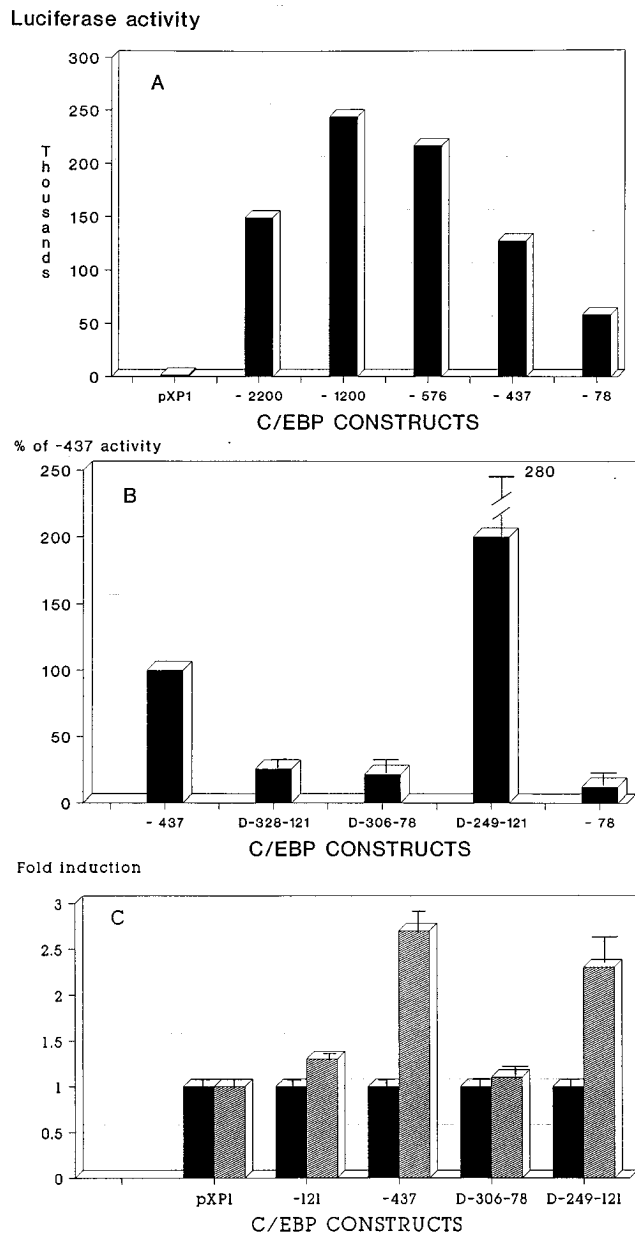


FIG. 3. (A) Four hundred thirty-seven nucleotides of the human C/EBP α promoter direct high-level expression of a C/EBP α -luciferase construct. C/EBP α -luciferase constructs containing different-length pieces of the human C/EBP α promoter were transfected into Hep3B2 cells. Luciferase activity (light units/microgram of cellular protein) was measured 16 h after transfection. (B) Promoter activity of deletion constructs. Luciferase activity is shown as a percentage of the -437 C/EBP α promoter activity. (C) C/EBP α stimulates its own promoter. Different C/EBP α -luciferase constructs were cotransfected into Hep3B2 cells with a C/EBP α expression vector (CMV-C/EBP α) and with the CMV-stop construct as a control. The fold induction was calculated as the increased luciferase activity in cells cotransfected with C/EBP α above that in cells cotransfected with control DNA (CMV-stop) for each construct.

and used in bandshift assays. For these experiments, WCEs with high levels of C/EBP α (WCE-C/EBP α) and C/EBP β (WCE-C/EBP β) binding activities were obtained by transfection of 3B2 cells with CMV-C/EBP α or CMV-C/EBP β constructs, respectively.

Several DNA-protein complexes were formed after incubation of C/EBP α promoter fragments and WCEs (Fig. 4A). To

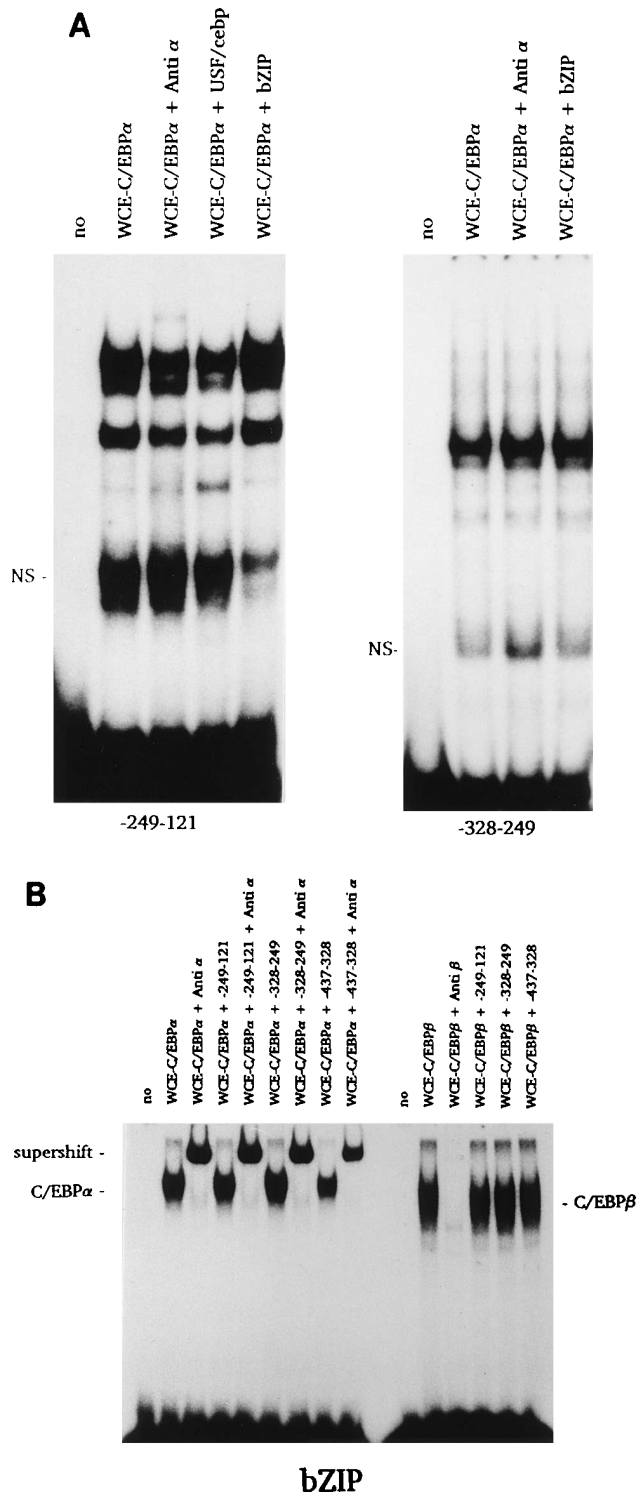


FIG. 4. C/EBP proteins do not bind to the human C/EBP α promoter. (A) EMSA of DNA-protein interactions of the human C/EBP α promoter with Hep3B2 WCE-C/EBP α which contains a high level of C/EBP α . Two promoter fragments (from -249 to -121 and from -328 to -249) were incubated with WCE-C/EBP α . Specific antibodies to C/EBP α and a competitor oligonucleotide, bZIP, were added to binding reaction mixtures before the addition of 32 P-labeled DNA probes. NS, nonspecific band (no self-competition was observed). (B) Competition EMSA of DNA-protein interactions. WCEs containing a high level of C/EBP α or - β were incubated first with unlabeled DNA fragments of the C/EBP α promoter and then a 32 P-labeled bZIP oligonucleotide (0.4 ng) was added at a molar ratio of 100:1 (unlabeled DNA fragment to 32 P-labeled bZIP). Specific antibodies to C/EBP α and to C/EBP β were added before 32 P-labeled bZIP. Lanes no, no proteins.

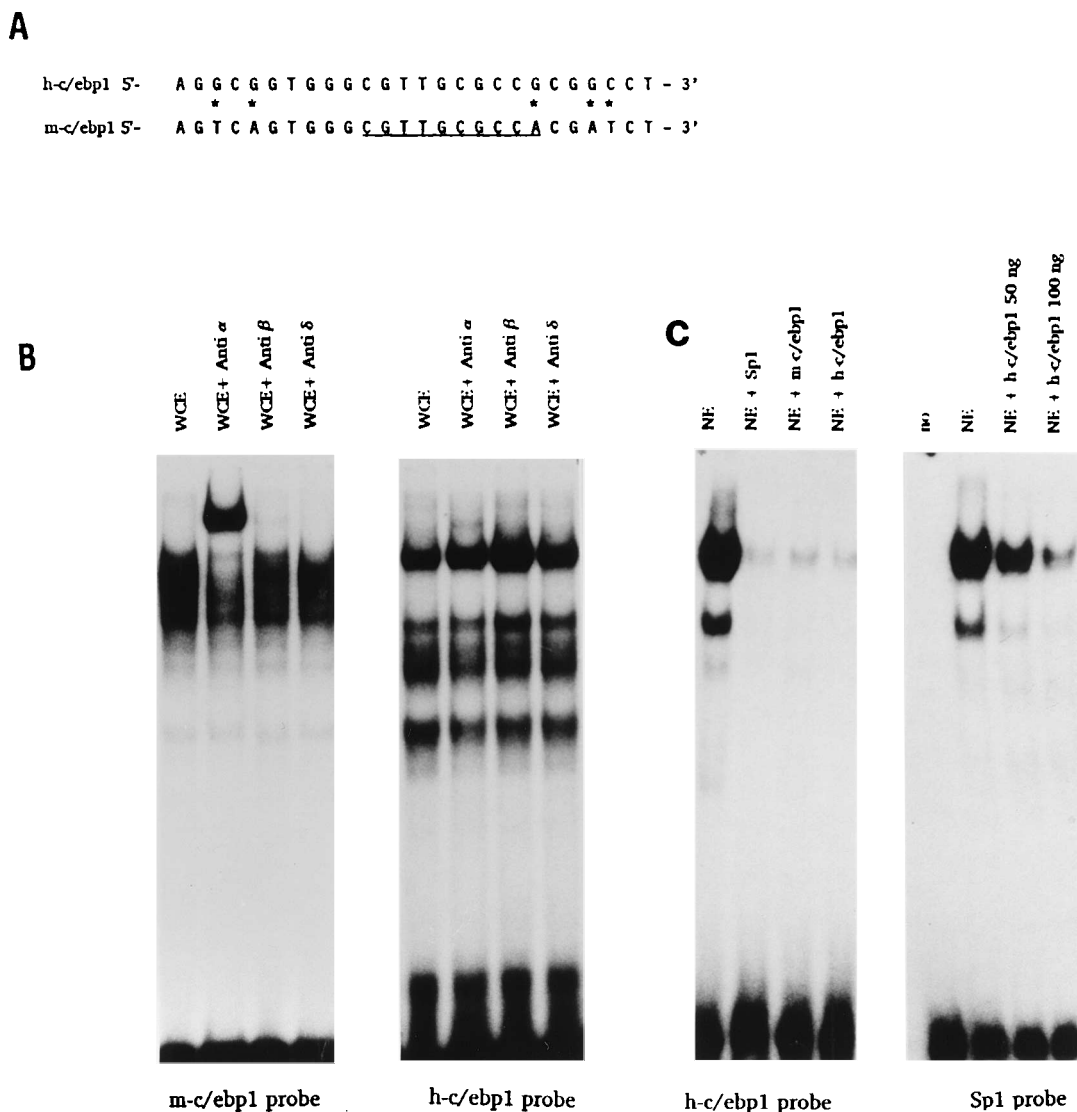


FIG. 5. Sp1-like proteins bind to the human and mouse C/EBP α promoters. (A) Nucleotide sequences of human (h-c/ebp1) and mouse (m-c/ebp1) oligonucleotides. Asterisks show nonhomologous nucleotides. The C/EBP α consensus is underlined. (B) EMSA of protein interactions with 32 P-labeled h-c/ebp1 and m-c/ebp1 oligonucleotides. These oligonucleotides were incubated with 20 μ g of the same WCE-C/EBP α in the presence and in the absence of antibodies specific to C/EBP proteins. Preimmune serum (1 μ l) was added to control mixtures that did not contain antiserum. The gel with m-c/ebp1 was exposed for 12 h, and the gel with the human probe was exposed for 48 h. (C) Competition EMSA of DNA-protein interactions. A total of 5 μ g of Hep3B2 NE was incubated with labeled h-c/ebp1 or Sp1 oligonucleotides in the presence of a 100-fold molar excess of different unlabeled oligonucleotides or increasing amounts of h-c/ebp1. Lane no, no proteins.

find possible C/EBP-DNA complexes, three different approaches were pursued: the use of antibodies specific to C/EBP α and β to supershift protein-DNA complexes, competition of complexes with the fragments by a 100-fold molar excess of unlabeled bZIP oligonucleotides, and EMSA analysis of bacterially expressed protein. Neither antibody changed the patterns of DNA-protein interactions (data for anti-C/EBP β not shown). Nor were any changes observed after the addition of a bZIP oligonucleotide to the reaction mixtures (Fig. 4A). As shown in Fig. 4B, WCEs prepared from transfected cells contained proteins with C/EBP-specific binding activities. Antibodies to C/EBP α supershifted DNA-protein complexes, while antibodies against C/EBP β neutralized the binding of the proteins to the bZIP oligonucleotide. Neither of the complexes was inhibited by fragments of the human C/EBP α promoter, suggesting that no C/EBP binding sites resided within the -437 to -121 region.

In addition, bacterially expressed human C/EBP α did not bind to different pieces of the human C/EBP α promoter, including DNA fragments from -328 to -249 and from -249 to -121, although the recombinant protein did bind to the m-c/ebp-1 and bZIP oligomers (data not shown). Thus, three lines of experiments failed to identify interaction of C/EBP α and C/EBP β with the human C/EBP α promoter.

Sp1-like nuclear factors recognized two sequences of the human C/EBP α promoter. The C/EBP binding region of the mouse C/EBP α promoter and the corresponding nucleotide sequence of the human C/EBP α promoter differ by a single nucleotide (Fig. 5A). The binding region of the mouse C/EBP α promoter contains a nucleotide sequence (underlined) almost identical to the C/EBP consensus, TT/GNNGNAAT/G (opposite orientation [Fig. 5A]). Although no C/EBP proteins were found to bind to human h-c/ebp1 sequence by EMSA, several protein-oligonucleotide complexes were formed with this oli-

gonucleotide (Fig. 5B). The addition of antibodies against C/EBP α to the binding reaction mixture resulted in a supershifted band only with the mouse sequence and not with the human sequence. No binding of C/EBP α to h-c/ebp1 was observed after a long exposure of the gel (in Fig. 5B exposure of the bandshift with the mouse probe was 12 h, and exposure with the human probe was 48 h). Supershift of the mouse oligonucleotide was due to a specific interaction with C/EBP α because no change was detected after the addition of antibodies to C/EBP β or δ with either oligonucleotide. These results confirmed the data of Christy et al. (10) regarding C/EBP binding to the mouse promoter and indicated that the corresponding region of the human C/EBP α promoter did not contain a binding site for C/EBP α . We have also found that human C/EBP β bound to the mouse oligonucleotide, m-c/ebp1, but did not bind to human h-c/ebp1 (data not shown).

With the exception of C/EBP α , the electrophoretic mobilities of the DNA-protein complexes are identical with both C/EBP oligonucleotides (human and mouse) (Fig. 5B). Different intensities of the complexes are the result of a longer exposure time. These oligonucleotides contained Sp1 consensus binding sites. Bandshift competition experiments (Fig. 5C) showed that a 100-fold excess of unlabeled Sp1 oligonucleotide inhibited the formation of these complexes with the h-c/ebp1 (Fig. 5C) and oligonucleotides, as did m-c/ebp1. This competition was specific because the addition of a 100-fold excess of other oligonucleotides (bZIP, AP2, USF/Ad-ml, and Egr-1) did not disrupt the complexes (data not shown). To verify the presence of an Sp1 binding site in the human promoter, the opposite competition was performed. A labeled Sp1 oligonucleotide was incubated with Hep3B2 nuclear extract in the presence of increasing amounts of unlabeled h-c/ebp1 oligonucleotide. Two DNA-Sp1 complexes were disrupted by h-c/ebp1 (Fig. 5C). Anti-Sp1 sera shifted only the more slowly migrating complex, suggesting that one complex is truly Sp1 and the faster complex contains an Sp1-like molecule (data not shown). Taken together, the above experiments indicated that the mouse C/EBP α promoter from -203 to -176 possessed binding sites for C/EBP α and β and for Sp1 or for an Sp1-like protein(s). In contrast, the human C/EBP α promoter did not contain a C/EBP α binding site in this region but contained a sequence recognized by Sp1 and an Sp1-like protein(s).

C/EBP α does not bind to other regions of the human C/EBP α promoter. Analysis of the human C/EBP α promoter region identified a short DNA fragment (-249 to -213) in which three consensus sites for nuclear factors were found: Sp1 (GGGCGG), AP2 (GCCGGGGGC), and a sequence closely resembling C/EBP α (TGGAGCGAG). In addition, the region between -249 and -213 was interesting because the corresponding region of the mouse promoter was bound by a nuclear protein(s) from undifferentiated adipocytes (10). Vas-seur-Cognet and Lane have shown that two proteins, C/EBP α undifferentiated protein (CUP) and an Sp1-like protein, interacted with the above region (34). To test for possible interaction of nuclear proteins in this region of the human C/EBP α promoter, a DNA fragment (-249 to -213) was used in EMSA with nuclear extract from HeLa cells transfected with CMV-C/EBP α . Two DNA-protein complexes were observed, and these were both inhibited specifically by the Sp1 oligonucleotide (Fig. 6). Thus, we conclude that the nuclear factor Sp1 and Sp1-like protein(s) can bind in vitro to at least two distinct regions of the human C/EBP α promoter: from -194 to -165 and from -249 to -213 .

C/EBP α , but not C/EBP β , induces binding activity of a nuclear factor which interacts with the CACGTG sequence of the human C/EBP α promoter. Our attempts to identify the

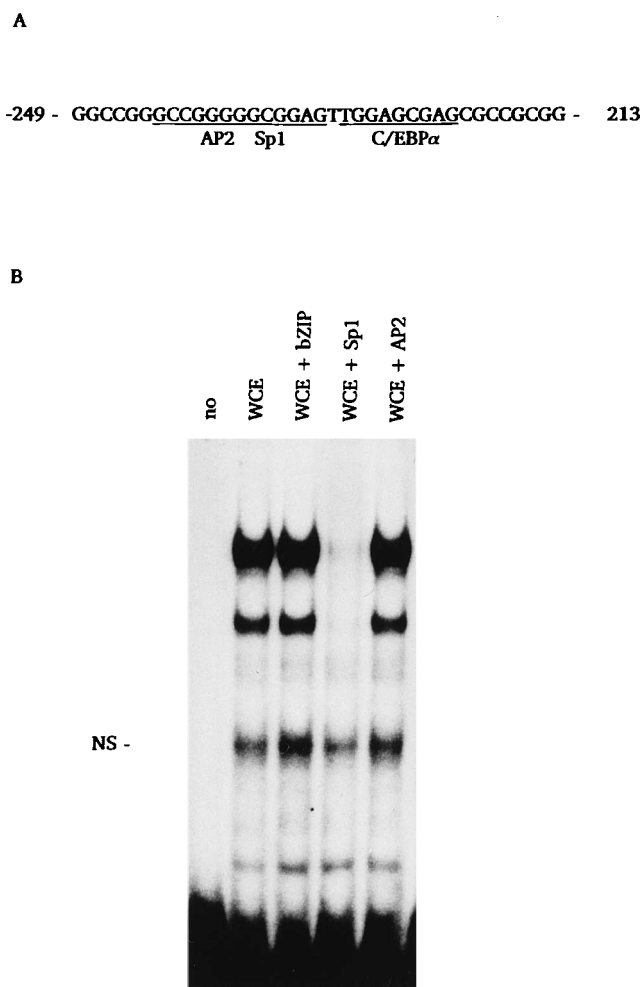


FIG. 6. The promoter fragment from -249 to -213 of the human C/EBP α promoter binds Sp1-like proteins but not C/EBP or AP2. (A) Nucleotide sequence of the -249 to -213 DNA fragment. Putative binding sites for AP2, Sp1, and C/EBP α proteins are underlined. (B) EMSA of DNA-protein interactions on the -249 to -213 DNA fragment. The end-labeled DNA fragment was incubated with WCE isolated from HeLa cells after transfection with the CMV-C/EBP α expression vector. A molar excess (100-fold) of unlabeled oligonucleotides bZIP, Sp1, and AP2 was added. Lane no, no proteins. NS, nonspecific complex (no self-competition was observed).

binding of C/EBP α and β to the human C/EBP α promoter suggested that neither protein binds within -437 to -121 bp of the proximal sequence. Nevertheless, C/EBP α can stimulate transcription of luciferase constructs (Fig. 3C) containing this same promoter region. We hypothesized that C/EBP α acted indirectly by stimulating activity of another nuclear protein(s) which transactivated the human C/EBP α promoter. To test this possibility, the interactions of WCE-C/EBP α and WCE-C/EBP β with the promoter region were studied. As a control, we used extracts (WCE-stop) from Hep 3B2 cells after transfection with the CMV-stop construct (Fig. 7). No significant difference in the binding activities of the three WCEs to DNA fragments -437 to -328 or to -249 to -121 was observed (for DNA fragment -437 to -328 , data not shown). In contrast, DNA fragment -328 to -249 showed increased binding activity of one nuclear protein in WCE-C/EBP α (Fig. 7A, complex IC). WCE-C/EBP β contained only a low level (identical to WCE-stop) of this binding activity. This observation was con-

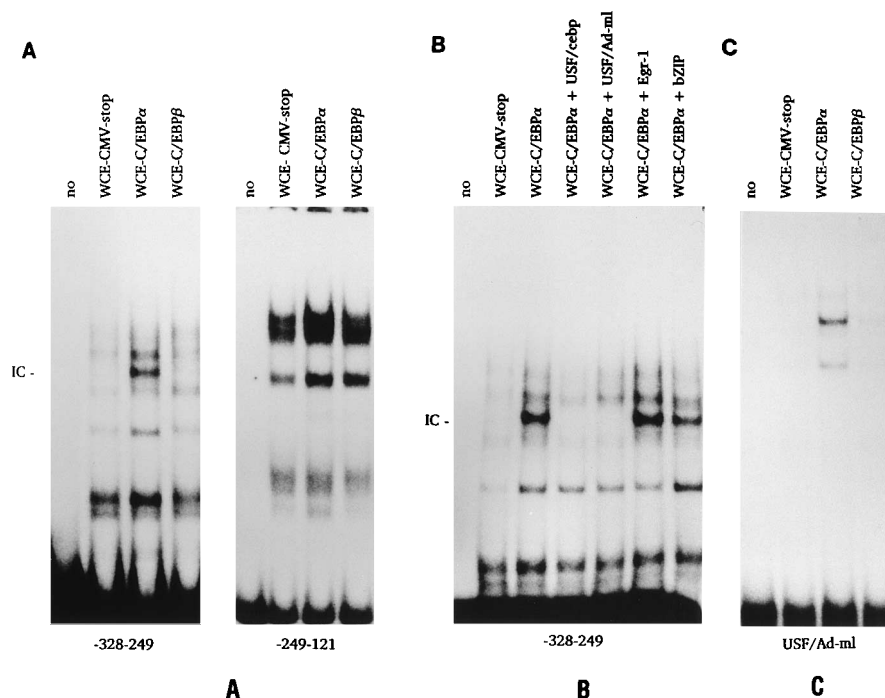


FIG. 7. C/EBP α increased binding activity of a nuclear factor which interacts with the C/EBP α promoter. (A) Interaction of WCE-C/EBP α and WCE-C/EBP β with the human C/EBP α promoter. End-labeled DNA fragments -328 to -249 and -249 to -121 were incubated with these WCEs and analyzed by EMSA. The position of the inducible complex (IC) is indicated. (B) Competition EMSA of binding of inducible protein to an end-labeled -328 to -249 promoter fragment. (C) USF binding activity is increased in WCE-C/EBP α but not in WCE-C/EBP β . 32 P-labeled USF/Ad-ml oligonucleotide which contained a high-affinity binding site for USF (16) was incubated with $20 \mu\text{g}$ of WCEs and analyzed by EMSA. Lanes no, no proteins.

sistent with the cotransfection experiments (Fig. 3C) and suggested that C/EBP α increased binding activity of this inducible protein with the C/EBP α promoter, different unlabeled oligonucleotides were added to the binding mixtures. Because the -328 to -249 DNA fragment contained putative binding sites for the HLH-bZIP family proteins (CACGTG) and for zinc finger proteins (GCGGGGCG) (Fig. 1), we tested oligonucleotides containing well-known high-affinity binding sites for these proteins: USF/Ad-ml and Egr-1 (see Materials and Methods). Oligonucleotides USF/cebp and bZIP were also examined. The results of competition studies are shown in Fig. 7B. Oligonucleotides USF/Ad-ml and USF/cebp, in a 100-fold excess, inhibited the inducible complex (IC), while Egr-1 and bZIP did not. Because oligonucleotides USF/Ad-ml and USF/cebp share only one common element, CACGTG, we concluded that the core binding element for the inducible protein is likely to be CACGTG. Thus, C/EBP α induced binding activity of a nuclear factor which can recognize the CACGTG nucleotides of the human C/EBP α promoter. USF/Ad-ml was used in bandshift experiments (Fig. 7C). After a short exposure, binding activity of this nuclear factor is observed only in WCE-C/EBP α . Upon longer exposure, this binding activity is observed in all lanes. Thus, human C/EBP α can stimulate binding activity of a nuclear factor which recognizes a CACGTG site in the human C/EBP α promoter.

The nuclear factor binding to the CACGTG sequence of the human C/EBP α promoter is identical to USF. The CACGTG sequence is a target for several transcription factors, including USF (16), TFE 3 (5), Myc/Max (7, 28), and Max/Mad and Max/Mxi (4, 36). To determine the nature of the inducible nuclear factor which binds to CACGTG in the human C/EBP α promoter, we initially estimated its molecular weight by using

the Southwestern method. Nuclear extracts of 3B2, HepG2, and HeLa cells were electrophoresed under denaturing conditions, blotted onto membrane, and probed with 32 P-labeled USF/cebp oligonucleotide. One major protein of different nuclear extracts interacted with the nucleotide sequence of USF/cebp oligonucleotide (Fig. 8A). Its molecular mass was about 43 kDa, corresponding to one of the USF proteins (16, 27). Figure 8B indicates that this nuclear factor was heat stable, as has been reported for USF (16). Two polyclonal antisera, one against 43-kDa USF and the other against 44-kDa USF were used in EMSA to confirm the identity of USF. The specificities of these antibodies have been described (31). The complex was supershifted upon the addition of either of the antibodies to USF proteins, while no effect was detected upon the addition of antibodies to c-Myc or to C/EBP α (Fig. 8C). Thus, molecular weight, heat stability, target sequence specificity to CACGTG, and interaction with specific antibodies to USF revealed that the inducible nuclear factor was identical to USF.

It is known that the nucleotide sequence CACGTG is a target for Myc family transcription factors (7, 28). By using monoclonal antibodies to human c-Myc protein, we tested the possible interaction of Myc/Max heterodimers of different cells with the CACGTG sequence of the human C/EBP α promoter. Nuclear extracts of Hep 3B2, HepG2, and HeLa cells did not contain Myc/Max DNA-binding complexes which were able to be detected by EMSA with the CACGTG oligonucleotide (Fig. 8C and data not shown). Nevertheless, we cannot exclude this interaction *in vivo*.

C/EBP α induces binding activity of USF. Given that overexpression of human C/EBP α in Hep3B2 cells increased USF binding, we compared the protein levels of USF in cells transfected with the C/EBP α expression vector, CMV-C/EBP α , and in the cells transfected with CMV-stop constructs. NE were

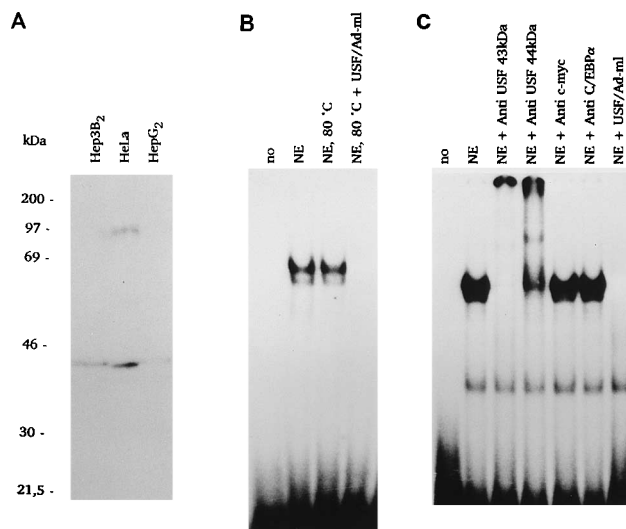


FIG. 8. The inducible nuclear factor is identical to USF. (A) Southwestern gel blotting analysis of interaction of USF/cebpa oligonucleotide with NE from Hep3B2, HeLa, and HepG2 cells. A total of 100 μ g of each NE was analyzed as described in Materials and Methods. The positions of marker proteins are shown on the left. (B) The inducible nuclear factor is heat stable, as is USF. Hep3B2 NE was heated at 80°C for 10 min, incubated with labeled USF/cebpa, and analyzed by EMSA. The addition of specific competitor USF/Ad-ml abolishes binding. (C) Antibodies to USF recognize the inducible nuclear protein. The 32 P-labeled USF/cebpa probe was incubated with Hep3B2 NE in the presence of antibodies to different nuclear factors and analyzed by EMSA. Lanes no, no proteins.

isolated 20 h after transfection and used in both bandshift and Western experiments (Fig. 9). Binding activity of USF in NE from cells overexpressing human C/EBP α was three- to four-fold higher than that in NE from control cells. Antibodies to 43-kDa USF supershifted the inducible complex, confirming these results.

Western analysis of NE isolated from Hep3B2 after transfection with CMV-C/EBP α , CMV-stop, and PN3 (a construct which codes for human 43-kDa USF) was performed. The 43-kDa immunoreactive protein corresponds to full-length human USF; the smaller protein presumably was a product of degradation. As shown, the level of immunoreactive 43-kDa polypeptide is almost the same in the extracts from CMV-C/EBP α and CMV-stop transfected cells. These results indicated that overexpression of human C/EBP α in Hep3B2 cells resulted in an increase of USF binding but did not substantially change its protein level.

The USF binding site is crucial for activation of the human C/EBP α promoter by C/EBP α . To investigate the role of the USF binding site in regulation and autoregulation of the C/EBP α gene, two expression constructs of the human C/EBP α promoter which deleted the CACGTG USF binding site were made. One mutant construct, -437 luc mut, contained the entire C/EBP α promoter from +1 to -437 but lacked the CACGTG sequence. We also deleted the USF binding site within pT81-328-249, a plasmid that contained a basal, 81-bp thymidine kinase promoter region coupled to a piece of the C/EBP α promoter from -328 to -249. A bandshift assay with normal and mutant -328 to -249 DNA fragments is shown in Fig. 10A. The mutant DNA fragment did not contain a USF binding site. The same result was observed with the -437 luc mut plasmid (data not shown).

Normal and mutant pT81-328-249 plasmids were tested for activation by USF in transient-cotransfection experiments with the USF expression vector, PN3. As shown in Fig. 9, transfection

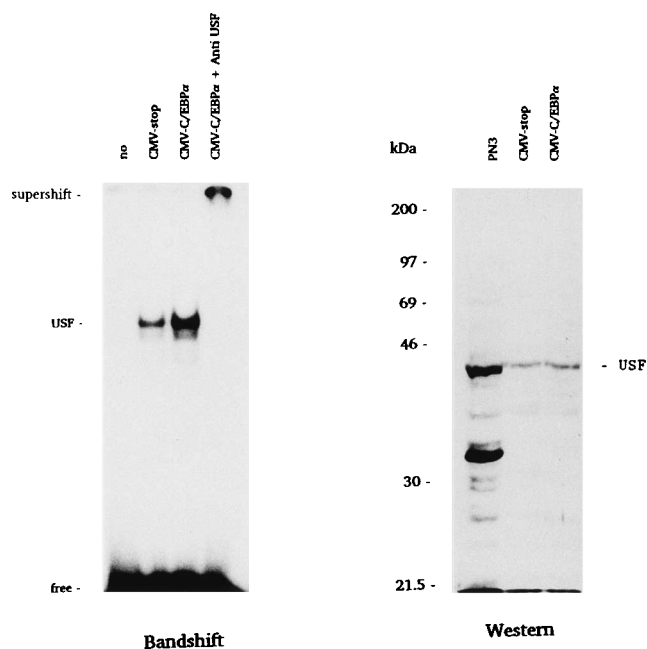


FIG. 9. C/EBP α increases binding activity of USF. NEs isolated from Hep3B2 after transfection with CMV-stop or with CMV-C/EBP α were used in a bandshift experiment (left) and in Western blot analysis (right). (Bandshift) A total of 5 μ g of NEs was incubated with 0.1 ng of USF/Ad-ml probe under the conditions described in Materials and Methods and loaded on a 5% polyacrylamide gel. Antibodies to the 43-kDa USF protein were added before the addition of probe. (Western) Proteins were separated in a 10% polyacrylamide gel with 0.1% SDS, blotted onto nitrocellulose filter, and probed with antibodies to 43-kDa USF. The positions of marker proteins are shown on the left. PN3 is a NE of Hep3B2 transfected with the PN3 construct, which codes for human 43-kDa USF. Lane no, no proteins. free, free probe.

of PN3 into Hep3B2 resulted in a high level of expression of 43-kDa human USF. Under these conditions, the cotransfected normal pT81-328-249 construct showed a 3.5-fold induction of luciferase activity, whereas the mutant construct did not register changes in activity (Fig. 10B). Therefore, USF activated the reporter construct through binding to the CACGTG nucleotides (USF binding site).

To test the contribution of USF to C/EBP α promoter activity within Hep3B2 cells, normal and mutant (CACGTG-deleted) -437 luc constructs and pT81-328-249 constructs were integrated into chromosomal DNA as described in Materials and Methods. Populations of G418-resistant stable clones were pooled and assayed for luciferase activity. Baseline luciferase activity of normal and mutant, stably transformed populations showed that deletion of the USF binding site resulted in loss of activity (Fig. 11A). Transient-transfection experiments and the identification of nuclear proteins interacting with the human C/EBP α promoter allowed us to suggest that C/EBP α increases the binding activity of USF, which then transactivates the C/EBP α promoter. To test this hypothesis, we used the populations of stable clones containing normal and mutant C/EBP α promoter/luciferase constructs to study their activation by C/EBP α . C/EBP α activated its own wild-type promoter threefold in cells stably transfected with a wild-type promoter, -437 luc normal, but did not change the activity of the mutant construct lacking the CACGTG USF binding site (Fig. 11B). These results indicated that autoactivation of the C/EBP α promoter was abolished by deletion of the USF binding site and led us to propose that C/EBP α activates its own promoter through a USF binding site.

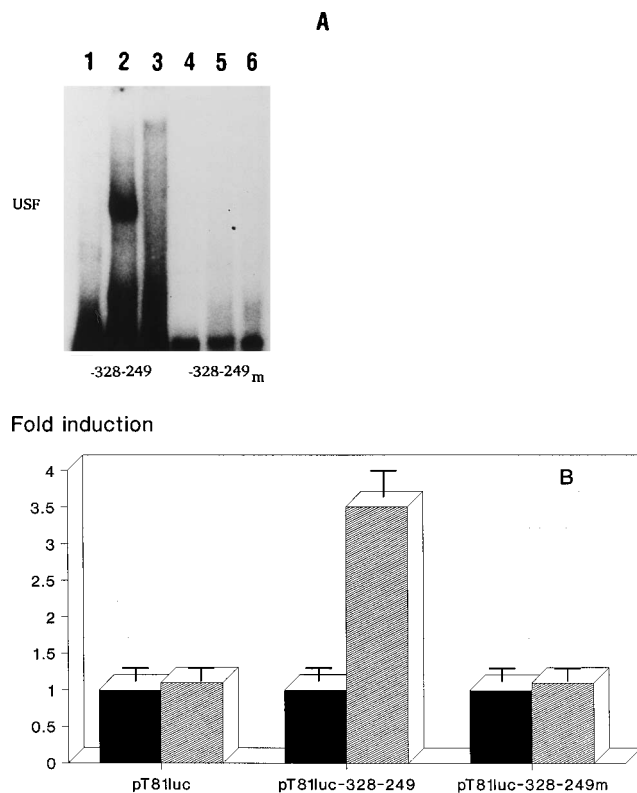


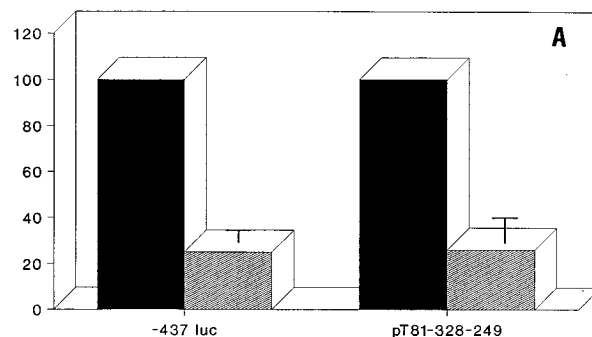
FIG. 10. USF activates the C/EBP α promoter by binding to the CACGTG sequence. (A) Binding of USF to normal and mutant C/EBP α promoter fragment -328 to -249 . DNA fragments were end labeled and incubated with PN3 NE. Lanes 1 and 4, mixtures without proteins; lanes 2 and 5, incubation with PN3 NE; lanes 3 and 6, incubation with PN3 NE in the presence of specific competitor USF/Ad-ml. The position of the USF-DNA complex is shown on the left. (B) USF activates the wild-type C/EBP α promoter and does not activate the promoter lacking the CACGTG consensus site. Normal and mutant pT81-328-249 constructs were cotransfected with PN3 (the USF expression vector) into Hep3B2, and luciferase activity was measured 16 h after transfection. The pT81 vector was used as a control. \blacksquare , CMV-stop; \square , PN3.

DISCUSSION

In this paper we describe the nucleotide sequence of the human C/EBP α promoter and an investigation of nuclear factors that regulate human C/EBP α gene expression. Sequence comparison of mouse and human C/EBP α promoters indicated a relatively low level of identity ($\sim 55\%$). Transient-transfection experiments indicated that the first 437 nucleotides of the human C/EBP α promoter contained elements necessary for high-level expression of this gene. A search for known target sequences showed the presence of several putative binding sites for nuclear factors. Here we show that a USF site is likely to be an important component in the regulation of human C/EBP α expression.

In the case of Jun, the mechanism of autoregulation included a direct interaction of DNA-binding proteins with their promoter regions. Autoregulation of the mouse C/EBP α protein has been described (10, 23). The human C/EBP α promoter has a potential C/EBP binding site in the same position as does the mouse promoter, and C/EBP α can activate the human 437-bp C/EBP α promoter (Fig. 3). However, no direct binding of C/EBP proteins to the part of the human promoter corresponding to the binding site in the mouse promoter was found. Although several specific complexes were formed as result of protein-DNA interaction, specific antibodies to

Relative luciferase activity (%)



Fold induction

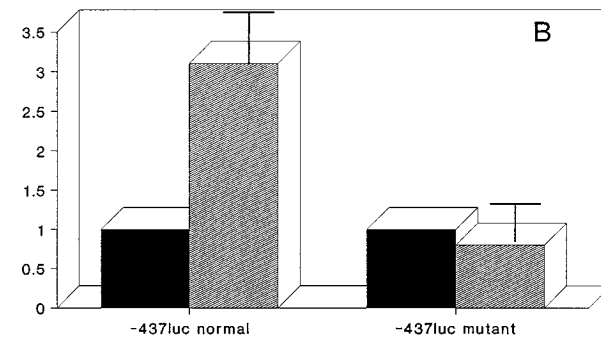


FIG. 11. (A) The USF binding site CACGTG within human C/EBP α promoter is crucial for its activity in Hep3B2 cells. Normal (\blacksquare) and mutant (\square) plasmids -437 luc and pT81-328-249 were transfected into Hep3B2 cells and placed under G418 selection for 2 weeks. G418-resistant colonies were pooled and assayed for baseline luciferase activity (A) and activity induced by electroporation of either CMV-stop (\blacksquare) or CMV-C/EBP α (\square) (B). Luciferase activity was determined 16 h after delivery of plasmids.

C/EBP proteins did not recognize any of these proteins (Fig. 4 and 5). An additional loose consensus C/EBP α binding site (-229 to -221) (Fig. 6) was also incapable of interacting with C/EBP proteins. Instead, an Sp1 or Sp1-like protein(s) bound both sequences of interest. An Sp1-like protein(s) also bound to the corresponding region of a mouse C/EBP α promoter (Fig. 5). Christy et al. have shown that interaction of an oligonucleotide identical to m-c/ebp1 with nuclear extracts from adipocytes resulted in the formation of four DNA-proteins complexes, two of which were complexes with C/EBP α (10). It is possible that the other two were complexes with an Sp1-like protein(s). The identification of two distinct recognition sequences for Sp1-like proteins was not surprising, because the human C/EBP α promoter was GC rich and contained several putative Sp1 binding sites (Fig. 1).

Vasseur-Cognet and Lane have identified within the mouse C/EBP α promoter a bipartite *cis* element-containing binding sites for CUP and an Sp1-like GT box binding protein (34). We have studied binding of nuclear proteins from HeLa cells (containing a high level of CUP) to the corresponding region of the human C/EBP α promoter (from -249 to -213). We found specific interaction of Sp1-like proteins but failed to determine any interaction with other nuclear proteins. The differences between the mouse and the human C/EBP α promoters almost certainly result in different mechanisms of regulation and autoregulation.

Our data clearly demonstrate that C/EBP α and C/EBP β could not bind to the -437 to -121 promoter region of the

human C/EBP α gene. We suggest that the mechanism of activation of the human C/EBP α promoter by C/EBP α includes induction of the DNA-binding activity of the USF nuclear factor. Two different forms of USF, 43-kDa USF1 and 44-kDa USF2, are encoded by two distinct genes and are expressed in virtually all cells (27, 31). We have shown that the DNA-binding activity of USF was stimulated by overexpression of human C/EBP α . Human C/EBP β did not stimulate USF binding. Transient-transfection experiments indicated a 3.5-fold induction of the C/EBP α promoter by USF (Fig. 10B). Construction of deletion mutants allowed the investigation of the role of the CACGTG USF binding site in regulation and autoregulation of C/EBP α promoter. Expression of a reporter in transient assays and in stable clones showed that the USF binding site is an important element of the C/EBP α promoter. Its deletion decreased C/EBP α promoter activity 70 to 75%. This observation is in good agreement with the data of Legraverend et al., indicating significant contribution of USF to mouse C/EBP α promoter activity (23). Deletion of the CACGTG nucleotides within the human C/EBP α promoter abolished activation of the promoter by C/EBP α and suggested that the human C/EBP α gene activates its own promoter through the USF binding site. It is possible that other sites also activate the C/EBP α promoter. It should also be noted that we have not investigated the role of TFE 3, whose activity is also mediated through a similar binding sequence. As gel shift analysis would not detect TFE 3, it is formally possible that C/EBP α also activates TFE 3 binding.

Our findings provide a paradigm of tissue-specific autoregulation that utilizes a general, ubiquitous factor (USF) which is stimulated by a tissue-restricted nuclear factor (C/EBP α). The mechanism by which C/EBP α enhances USF binding and transactivation is currently under study. It is clear that enhancement by C/EBP α is specific, as we were not able to detect any alteration of USF binding activity in cells after transfection by C/EBP β , another bZIP protein. This mode of autoregulation is novel. The generality of this mechanism needs to be examined in other genes that show autoregulatory properties. It is possible that autoregulation by direct binding of the gene product may work in concert with activation of more generally expressed factors such as USF.

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